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Longitudinal analysis of cumulative residual feed intake in Nellore cattle

Abstract – The objective of this work was to evaluate random regression models with linear spline functions for the estimation of genetic parameters of residual feed intake (RFI) in Nellore bovines. The RFI was estimated across five test periods (at 0–14, 0–28, 0–42, 0–56, and 070–days) in 929 Nellore bulls. The variance components were estimated, and the models were compared using the deviance information criterion. Rankings and the percentage of the top 10% animals across all periods were assessed using Spearman's correlations. The best-fit model included linear splines and heterogeneous residual variance (four classes). Heritability estimates for RFI ranged from 0.39 to 0.55, with high genetic (0.83–0.98) and phenotypic (0.82–0.98) correlations between adjacent periods. Rankings were consistent between 56 and 70 days (Spearman's correlations = 0.99; 93.55% overlap). The test period can be shortened to 56 days without compromising genetic parameters, optimizing feed intake evaluations. The random regression models effectively model the RFI, showing sufficient genetic variance for selection.

Index terms: beef cattle, feed efficiency, random regression, spline.

Análise longitudinal do consumo alimentar residual acumulado em bovinos Nelore

Resumo – O objetivo deste trabalho foi avaliar modelos de regressão aleatória com funções *spline* lineares, para estimar parâmetros genéticos de consumo alimentar residual (RFI) em bovinos Nelore. O RFI foi estimado em cinco períodos de teste (aos 0–14, 0–28, 0–42, 0–56 e 0–70 dias), em 929 touros Nelore. Os componentes de variância foram estimados, e os modelos foram comparados por meio do critério de informação de desvio. As classificações e a percentagem dos 10% dos melhores animais em todos os períodos foram avaliadas por meio das correlações de Spearman. O modelo de melhor ajuste incluiu *splines* lineares e variância residual heterogênea (quatro classes). As estimativas de herdabilidade para RFI variaram de 0,39 a 0,55, com altas correlações genéticas (0,83–0,98) e fenotípicas (0,82–0,98) entre períodos adjacentes. As classificações foram consistentes entre 56 e 70 dias (correlações de Spearman = 0,99; sobreposição de 93,55%). O período de teste pode ser encurtado para 56 dias sem comprometer os parâmetros genéticos, otimizando as avaliações de consumo de ração. Os modelos de regressão aleatória modelam efetivamente o RFI, mostrando variância genética suficiente para seleção.

Termos para indexação: bovino de corte, eficiência alimentar, regressão aleatória, *spline*.

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Introduction

In the beef cattle industry, feed costs represent the largest operational expense. Improving feed efficiency is therefore a critical strategy for enhancing the profitability of beef production (Brunes et al., 2021), which includes optimizing feed management and identifying animals that utilize nutrients more effectively. Raising animals that require less feed, without compromising growth rate or slaughter weight, can significantly reduce inputs related to feeding costs, without affecting the final product quality and quantity (Sainz et al., 2024).

Feed efficiency can be quantified using various methodologies, among which residual feed intake (RFI) has emerged as a prominent and widely adopted metric (Brunes et al., 2021; Soares et al., 2025). Selection to improve RFI allows of the identification of animals with lower maintenance energy requirements, contributing to reducing feed costs without negatively affecting the productivity (Seymour et al., 2020; Sainz et al., 2024). Accurate RFI measurement requires specific test periods, to collect precise individual data on body weight, dry matter intake, and average daily gain. However, extended test durations increase costs, due to the need of specialized feedlot systems equipped with electronic feed intake monitoring, which demands a significant financial investment and limits large-scale data collection. Culbertson et al. (2015) showed that 42 days is the minimum necessary to evaluate feed intake and, at least 56 days to calculate RFI in *Bos taurus* cattle. Nevertheless, recent findings suggest that shorter test periods may still maintain sufficient accuracy for selecting efficient animals (Ramos et al., 2024).

Residual feed intake, as a measure of feed efficiency, can be evaluated throughout the productive life of an animal, characterizing it as a longitudinal trait. Longitudinal data are commonly analyzed using random regression models (RRMs), as they allow for the estimation of genetic parameters at any point along the trajectory (Toral et al., 2019; Wang et al., 2022). The RRM takes advantage of all available records, capturing dynamic changes in trait expressions and genetic variances over time. Theoretically, they provide more accurate definition of covariances between repeated measurements, in comparison with the multitrait model (Toral et al., 2019; Paneru et al., 2024). Among the various covariance functions used

in RRM, spline functions have gained prominence due to their flexibility and computational efficiency. Splines provide direct estimates of genetic and environmental parameters directly at specific trajectory points, enabling accurate modeling of temporal trends in (co)variances. This is particularly beneficial for the genetic evaluation of longitudinal traits in herds under sequential selection (Toral et al., 2019). These characteristics are essential for identifying the most informative time points during the feed efficiency test period, helping to refine test duration and improve selection accuracy (Begli et al., 2016; Ramos et al., 2024). Moreover, they support a more precise genetic evaluation at critical developmental stages (Wang et al., 2022; Ramos et al., 2024).

The objective of this work was to evaluate random regression models (RRMs), with linear spline functions, to estimate genetic parameters for residual feed intake in Nellore bulls.

Materials and Methods

Feed efficiency data were collected from Nellore bulls born between 2010 and 2013, raised at Rancho da Matinha farm, located in the municipality of Uberaba, in the state of Minas Gerais, Brazil (19°39'S and 48°09'W, at 823 m altitude). The climate is monsoon-influenced humid subtropical (Cwa, by the Köppen-Geiger's classification), typical of the Cerrado biome, with 21.9°C average annual temperature, 1,476.3 mm annual rainfall, and 73% relative air humidity, according to the Instituto Nacional de Meteorologia (2025).

The dataset included records from seven feed efficiency tests conducted between 2011 and 2014. Each test lasted an average of 73 ± 3.46 days, including a 14-day adaptation period for diet and facilities. On average, 133 animals participated in each test. At the start of the tests, the bulls were 304 ± 43 days old and weighed 313 ± 46 kg. The animals were selected from a herd bred for carcass quality (since 2002), reproductive precocity and weight gain (since 1995), and feed efficiency (since 2011). The database comprised records for 929 bulls, progeny of 39 sires, and 413 dams. Pedigree information for 3,559 animals, provided by the Brazilian association of Zebu breeders (Associação Brasileira de Criadores de Zebu - ABCZ, Uberaba, MG, Brazil), was used to construct a relationship matrix.

The animals were housed in two paddocks with similar structures, solar exposure, and soil type, each one equipped with eight Growsafe system (AZTX Cattle Co, Hereford, Texas, USA) troughs to measure dry matter intake (DMI). The animal-to-feeder ratio was maintained at eight. Feed and water were provided *ad libitum*. Over the years, the diet included corn silage, ground corn, soybean meal, and a mineral supplement formulated as a total mixed ration with about 70% total digestible nutrients, 13% crude protein, and 43% dry matter. Feed was offered twice daily. Animals were weighed (without fasting) at the start of the test and every 14 days using a calibrated digital scale.

To ensure data consistency, only animals with known parentage and complete test participation were included. Based on batch and test data, contemporary groups were formed with only groups containing at least five animals, from at least three sires considered. This resulted in 14 contemporary groups.

Five cumulative evaluation periods (0-14, 0-28, 0-42, 0-56, and 0-70 days) were analyzed to assess variances throughout the test. Each period started on the first day of the test and increased in duration by 14-day intervals. For each period, dry matter intake (DMI), average daily gain (ADG), metabolic body weight ($BW^{0.75}$), and estimated dry matter intake (DMI_e) were calculated using average observations.

The RRM was used to analyze residual feed intake across the evaluation periods. Linear spline functions (LS) with knots placed at 14, 28, 42, 56, and 70 days were applied to the model, as well as to the average trajectory, additive genetic effects, and permanent environment. For n knots at points T_i ($i = 1, \dots, n$), where $T_i \leq t < T_{i+1}$, the (co) variables at knots i and $i + 1$ were calculated using the following equations:

$$\phi_i(t) = \frac{T_{i+1}-t}{T_{i+1}-T_i} \text{ and } \phi_{i+1}(t) = 1 - \frac{T_{i+1}-t}{T_{i+1}-T_i},$$

For values outside the range T_i to T_{i+1} , $\phi_i(t) = 0$, when the evaluation period matched the adjusted node exactly, the following equation was used:

$$\phi_i(T_k) = \begin{cases} 1 & \text{if } i=k \\ 0 & \text{if } i \neq k \end{cases}$$

Fixed effects included contemporary groups, regression coefficients at each node for average trajectory, and animal age at the start of the test

(linear covariate). Random effects, modeled with LS coefficients, included additive genetic effects, permanent environment, and residual variances (homogenous and heterogeneous). The random regression model is represented as:

$$y_{ijklm} = gc_i + b_1 id_j + \sum_{k_1=0}^H f_{k_1} \phi_{k_1}(id_j^*) + \sum_{k_2=0}^H a_{lk_2} \phi_{k_2}(id_j^*) + \sum_{k_3=0}^H p_{lk_3} \phi_{k_3}(id_j^*) + e_{ijklm},$$

where: gc_i represents the contemporary group; id_j is the linear effect of the animal's age at the test start; f_{k_1} , a_{lk_2} , and p_{lk_3} are regression coefficients for the average RFI trajectory, additive genetic effects, and permanent environment, respectively; $\phi_k(id_j^*)$ are linear spline polynomials for the studied periods; H is the number of knots; and e_{ijklm} is the residual for each observation.

In matrix form, the model for the five test periods (0 to 14, 0 to 28, 0 to 42, 0 to 56, and 0 to 70 days) is:

$$y = X\beta + Z_1\alpha + Z_2\epsilon + \varepsilon,$$

where: y is the vector of RFI observations; α and ϵ are vectors of random regression coefficients for additive genetic and permanent environment effects; and ε is the vector of residuals. The incidence matrices for β , α , and ϵ are X , Z_1 , and Z_2 respectively. The following assumptions were considered:

$$\alpha|A, G \sim N(0, G \otimes A); \epsilon|I_p, P \sim N(0, P \otimes I_p) \text{ and } \varepsilon|R \sim N(0, R)$$

The inverted Wishart distributions below were assumed for genetic covariance matrices, permanent environment, and residual

$$G \sim IW(\sum_a^2, n_a), P \sim IW(\sum_p^2, n_p) \text{ and } R \sim IW(\sum_e^2, n_e),$$

where: $\sum_a^2$, $\sum_p^2$, $\sum_e^2$, n_a , n_p , and n_e are the hyperparameters of the inverted Wishart distributions.

The random regression models were represented using the notation $LS_{k_b k_a k_{ep} \in}$, where: LS denotes the linear spline polynomial; k_b , k_a , k_{ep} , and $\in$ represent the number of knots used to model the average trajectory of the RFI, the covariance functions for additive genetic and permanent environment effects, and the number of residual variance classes, respectively.

Variance components were estimated using the GIBBS3F90 software (Misztal et al., 2014). A total of 710,000 iterations were performed, with a burn-in period of 210,000 iterations and a thinning interval of

10 iterations. Posterior means and the highest-posterior density intervals (HPD) were calculated using the samples generated and stored in the Gibbs sampling procedure. The number of iterations was determined based on preliminary analyses using the BOA package (Smith, 2016) in R software (R Core Team, 2025). Convergence was assessed using the Geweke test available in the BOA package (Smith, 2016), as well as by visual inspection.

Model selection was based on the deviance information criterion (DIC). The initial comparison used the most parameterized model, with a 5-knot spline for all random effects and a heterogeneous residual variance. The average trajectory model was optimized first by varying the number of knots (5, 4, 3, and 2), while holding constant the number of knots of other effects ($k = 5$) and the residual variance structure. After optimizing the average trajectory, the same procedure was applied sequentially to the additive genetic effects, permanent environment effects, and residual variance. The residual variance was assessed across different classes: five (0–14, 0–28, 0–42, 0–56, and 0–70 days); four (0–28, 0–42, 0–56, and 0–70 days); three (0–28, 0–42, and 0–70 days); two (0–42, and 0–70 days), and homogeneous variances (0–70 days). The model with the lowest DIC was selected.

Pearson correlations between evaluation periods were calculated using the R software (R Core Team, 2025). Direct and correlated responses to selection were estimated using variance component samples, targeting the top 10% of the most efficient animals based on RFI (selection intensity of 1.76). The direct responses were calculated as follows:

$$\Delta G_h = i_h h_h^2 \sigma_{ph},$$

where: ΔG_h is the expected genetic gain per generation; i_h is the selection intensity; h_h^2 is the heritability of the selected trait; and σ_{ph} is the phenotypic standard deviation of the trait.

The correlated responses were calculated by the following equation:

$$\Delta G_{YX} = r_{ayax} h_y h_x i_x \sigma_{py},$$

where: ΔG_{YX} is the expected correlated response in trait Y, when selecting for trait X; r_{ayax} is the genetic correlation between Y and X; h_x and h_y are the square

root of heritability for X and Y; i_x is the selection intensity for X, and σ_{py} is the phenotypic standard deviation of Y.

The relative selection efficiency of indirect selection was assessed by comparing correlated and direct responses, as follows:

$$\frac{\Delta G_{YX}}{\Delta G_h} = \frac{h_x}{h_y} r_{ayax}.$$

Results and Discussion

In the performance tests of Nellore cattle, the descriptive statistics for feed efficiency and growth traits showed substantial phenotypic variability across contemporary groups, particularly for RFI (Table 1). As expected by its definition, the mean RFI was approximately zero in all groups, with 0.00 global average and 0.72 standard deviation. The observed RFI values ranged from -3.48 to 3.13 kg of DM per day, highlighting marked differences for feed efficiency among animals. These results are generally consistent with previous studies on Zebu cattle. Batalha et al. (2020) reported RFI values ranging from -1.47 to 2.36 kg of DM per day in Nellore bulls, while Sainz et al. (2024) observed a wider range, from -7.10 to 3.14 kg of DM per day. Differences for RFI ranges across studies may reflect the variation of test environments and animal genetic backgrounds, due to differences for selection intensity applied within each breeding program. Since the datasets originate from distinct genetic evaluation systems, the intensity and direction of selection for direct and correlated feed efficiency traits likely influenced the observed variability of RFI.

The proposed adjustment criterion for the model comparison highlighted the importance of using five knots to describe the average trajectory of RFI, over the evaluation period, and to model the additive genetic random effect (Table 2). Although the DIC penalizes models with a greater number of parameters, the observed reduction of DIC indicates that the improvement of the model fit outweighed the increase in complexity. In this context, the DIC reduction suggests that higher-order linear spline models provided the best representation of the data. The random effect of the permanent environment was optimally modeled using only two knots. Additionally, models that accounted for heterogeneous residual

Table 1. Descriptive statistics for feed efficiency and growth traits in performance tests of Nellore cattle.

Test	Trait ⁽¹⁾	NA	NO	Min	Max	$\bar{X}$	SD
001	DMI (kg)	128	8960	0.25	20.25	9.15	1.65
	ADG (kg per day)		640	-0.43	2.43	1.11	0.31
	IBW (kg)		128	274	483	369.57	37.61
	FBW (kg)		128	341.22	543.07	446.24	37.35
	RFI (kg DM per day)		640	-2.88	3.13	0.00	0.79
003	DMI (kg)	140	9800	0.72	13.91	6.98	1.37
	ADG (kg per day)		700	0.09	1.67	0.90	0.25
	IBW (kg)		140	216	351	280.22	29.11
	FBW (kg)		140	238.33	452.01	350.42	38.08
	RFI (kg DM per day)		700	-1.81	1.65	0.00	0.55
004	DMI (kg)	125	8750	0.92	15.30	5.90	1.05
	ADG (kg per day)		625	-0.86	1.89	0.71	0.35
	IBW (kg)		125	261	442	318.40	36.29
	FBW (kg)		125	279.78	503.07	371.87	41.85
	RFI (kg DM per day)		625	-1.38	1.28	0.00	0.45
006	DMI (kg)	143	10010	0.34	15.36	8.19	1.59
	ADG (kg per day)		715	-0.43	2.43	1.20	0.31
	IBW (kg)		143	235	385	299.26	30.09
	FBW (kg)		143	283.51	483.69	384.20	38.00
	RFI (kg DM per day)		715	-3.48	1.82	0.00	0.82
007	DMI (kg)	132	11088	0.18	15.76	7.98	1.72
	ADG (kg per day)		660	-0.64	2.29	1.24	0.33
	IBW (kg)		132	217	451	318.13	48.76
	FBW (kg)		132	285.83	548.84	395.60	49.30
	RFI (kg DM per day)		660	-2.67	2.40	0.00	0.80
009	DMI (kg)	127	8890	1.52	12.83	6.78	1.37
	ADG (kg per day)		635	-1.07	2.64	0.88	0.39
	IBW (kg)		127	207	338	278.08	29.49
	FBW (kg)		127	237.50	415.41	333.84	37.53
	RFI (kg DM per day)		635	-3.10	2.01	0.00	0.84
010	DMI (kg)	134	9380	1.64	13.19	6.77	1.48
	ADG (kg per day)		670	-2.07	2.50	1.02	0.40
	IBW (kg)		134	231	490	315.25	48.37
	FBW (kg)		134	262.29	558.91	371.28	57.51
	RFI (kg DM per day)		670	-2.86	2.32	0.00	0.67
Overall mean	DMI (kg)	132	9554	0.80	15.23	7.39	1.46
	ADG (kg per day)		663	-0.77	2.26	1.01	0.33
	IBW (kg)		132	234.43	420.00	311.27	37.10
	FBW (kg)		132	275.49	500.71	379.06	42.80
	RFI (kg DM per day)		663	-3.48	3.13	0.00	0.72

⁽¹⁾DMI, dry matter intake; ADG, average daily gain; IBW, initial body weight; FBW, final body weight; and RFI, residual feed intake. NA, number of animals; NO, number of trait observations; Min, minimum; Max, maximum; $\bar{X}$, mean; SD, standard deviation.

variance across four classes (14, 28, 42, and 56–70 days) resulted in a lower DIC. Thus, the model with the best goodness of fit employed a linear spline function with heterogeneous residual variance (referred to as LS₅₅₂₄). Based on these findings, a RRM LS₅₅₂₄ was selected for the estimation of genetic parameters and prediction of genetic values.

The model aligned closely with the expected biological trajectory of residual feed intake over time. Similar findings were reported by Begli et al. (2016) and Ramos et al. (2024), showing that random regression models using linear spline yield produced

more accurate estimates of genetic parameters for feed efficiency traits. Models assuming heterogeneous residual variances showed superior fit, suggesting significant changes in the residual variance during the feedlot period.

The posterior mean values and the highest posterior density intervals (HPD) for permanent environmental and residual variances decreased over the test period (Table 3). While additive genetic variance remained stable across most test periods, it increased at 42 days. Permanent environmental variance followed a downward trend, though not statistically significant, due to overlapping HPD intervals.

Genetic parameters remained relatively stable throughout the test period. Posterior mean estimates of additive genetic variances exceeded those reported by Moraes et al. (2017), who used a single-trait model for total period evaluations. The higher additive genetic variances in the present study, combined with low residual variances, led to high heritability estimates. High additive genetic variance benefits breeding programs by enhancing selection precision and maximizing genetic gain.

Random regression models effectively capture the variance heterogeneity, improving the model accuracy (Esfandiyari & Jensen, 2021). Boligon et al. (2012) emphasized that data structure and distribution over the evaluation interval influenced residual variance heterogeneity. Posterior means estimates of residual variances declined from the start of the test until 28 days, peaked at 42 days, and then stabilized until the end (Table 3). The increase of residual variance at 42 days suggests environmental fluctuations during the evaluation phases.

Heritability estimates fluctuated throughout the performance test, with an increase from 14 to 28 days,

Table 2. Number of knots, residual variance classes, and deviance information criterion (DIC), in random regression models for residual feed intake analysis of Nellore cattle, over the evaluation period.

Model	N _b ⁽¹⁾	n _a	n _{ep}	e	DIC
LS ₅₅₅₅	5	5	5	5	-3635.4210
LS ₄₅₅₅	4	5	5	5	-4849.6183
LS ₃₅₅₅	3	5	5	5	-5055.6002
LS ₂₅₅₅	2	5	5	5	-4948.6147
LS ₅₄₅₅	5	4	5	5	-3812.5791
LS ₅₃₅₅	5	3	5	5	-815.3895
LS ₅₂₅₅	5	2	5	5	-965.7051
LS ₅₅₄₅	5	5	4	5	-3585.2682
LS ₅₅₃₅	5	5	3	5	-2517.2147
LS ₅₅₂₅	5	5	2	5	-905.2482
LS ₅₅₂₄	5	5	2	4	907.8764
LS ₅₅₂₃	5	5	2	3	1309.3562
LS ₅₅₂₂	5	5	2	2	1423.1871
LS ₅₅₂₁	5	5	2	1	2523.7447

⁽¹⁾n_a, n_b, and n_{ep}: linear spline knots for the average residual feed intake trajectory, additive genetic effects, and permanent environment effects, respectively; e, residual variance classes; and LS, random regression model with linear spline functions.

Table 3. Posterior means (the highest posterior density intervals) of direct additive, residual, and heritability for residual feed intake, across different test periods (14, 28, 42, 56, and 70 days) in Nellore cattle.

Test period	σ^2_a	σ^2_{ep}	σ^2_e	h ²
14	0.21 (0.093; 0.352)	0.28 (0.1864; 0.365)	0.037 (0.033; 0.041)	0.39 (0.203; 0.611)
28	0.22 (0.106; 0.345)	0.22 (0.1362; 0.294)	0.024 (0.018; 0.031)	0.46 (0.272; 0.692)
42	0.26 (0.148; 0.389)	0.17 (0.098; 0.244)	0.19 (0.180; 0.220)	0.41 (0.265; 0.575)
56	0.23 (0.120; 0.343)	0.14 (0.069; 0.211)	0.043 (0.028; 0.059)	0.54 (0.342; 0.755)
70	0.21 (0.102; 0.319)	0.12 (0.049; 0.195)	0.043 (0.028; 0.059)	0.55 (0.322; 0.774)

Components of variance: σ^2_a , additive variance; σ^2_{ep} , permanent environmental variance; σ^2_e , residual variance; h², heritability.

a decrease at 42 days, and stabilization thereafter. The posterior means ranged from 0.39 to 0.55, indicating a substantial genetic variability for selection. These values are comparable with those found in other studies, varying from 0.33 (Moraes et al., 2019) to 0.68 (Santana et al., 2014).

The heritability estimates for RFI observed in the present study also align with those reported by Moraes et al. (2017), who found heritability above 0.40, using data from the same herd adjusted for fat. Similarly, Esfandyari & Jensen (2021), applying a one-step Bayesian approach to longitudinal feed intake, reported stable heritability estimates about 0.50 for both daily and accumulated RFI, reinforcing the substantial genetic variability underlying this trait. In contrast, Ramos et al. (2024) reported lower heritability (0.03 to 0.26), using a B-spline function to model feed efficiency in Nellore cattle, highlighting how differences in modeling approaches, population structure, environmental factors (Toral et al., 2019; Paneru et al., 2024), and the method used for measuring RFI can influence genetic parameter estimation.

Although point estimates of heritability decline at 42 days, coinciding with a peak in residual variance, the highest posterior density intervals (HPD) across all periods largely overlapped, indicating that such fluctuations may not be statistically significant. Nevertheless, the temporary drop of heritability may reflect physiological transitions in the animals during mid-test, such as changes of metabolic efficiency. Esfandyari & Jensen (2021) observed a gradual increase in the heritability of daily RFI over the test period, from approximately 0.40 at the beginning (225 days of age) to about 0.58 at the end (391 days of age), suggesting that the expression of feed efficiency becomes more stable as animals adapt to test conditions.

In contrast, Ramos et al. (2024) reported an increase of heritability estimates at 42 days (from 0.09 at 28 days to 0.30), suggesting that this period may be biologically relevant for the evaluation of feed efficiency in specific contexts. Although no statistically significant changes of heritability were observed in the present study, the fluctuation observed – along with reported feeding behavioral differences between low- and high-RFI animals (Garcia et al., 2024) – underscores the importance of considering the temporal dynamics of RFI. These results support the application of longitudinal modeling approaches, to better characterize the complexity and time-dependent nature of RFI expression throughout the performance test.

Genetic and phenotypic correlations across evaluation days were positive and high, ranging from 0.83 to 0.98 and 0.82 to 0.98, respectively (Table 4). The correlations decreased as the evaluation interval increased, while correlations between adjacent periods remained high. This pattern aligns with findings for broiler feed efficiency (Begli et al., 2016), beef cattle weight (Toral et al., 2019), and meat sheep weight (Paneru et al., 2024).

The decline of genetic correlations with increasing intervals was expected, since RFI measurements in one period (for instance 14 days) contribute to subsequent periods (for instance, 70 days), due to the cumulative nature of its calculation. Nonetheless, the highest genetic correlations (0.98) occurred between 56 and 70 days, suggesting that the same gene groups regulate residual feed intake throughout the test stages. Conversely, Esfandyari & Jensen (2021) observed that genetic correlations between RFI, measured at different ages, decreased to negative values mid-test, and subsequently approached zero, reflecting temporal changes in genetic expression possibly due

Table 4. Posterior means (highest posterior density intervals) of the genetic (above the diagonal) and phenotypic (below the diagonal) correlations between the different test periods (14, 28, 42, 56, and 70 days).

Test periods	14	28	42	56	70
14		0.95 (0.918; 0.982)	0.83 (0.722; 0.948)	0.84 (0.722; 0.945)	0.83 (0.682; 0.955)
28	0.97 (0.968; 0.982)		0.96 (0.937; 0.983)	0.96 (0.923; 0.990)	0.93 (0.870; 0.988)
42	0.91 (0.893; 0.943)	0.97 (0.966; 0.986)		0.98 (0.977; 0.997)	0.95 (0.907; 0.989)
56	0.87 (0.847; 0.902)	0.95 (0.941; 0.968)	0.97 (0.965; 0.987)		0.98 (0.975; 0.997)
70	0.82 (0.780; 0.865)	0.91 (0.871; 0.942)	0.93 (0.902; 0.963)	0.98 (0.977; 0.993)	

to physiological acclimation. Ramos et al. (2024) reported negative genetic correlations between test days in Nellore cattle, highlighting the potential impact of differing RFI calculation methods. Specifically, Ramos et al. (2024) included metabolic body weight as a fixed effect, while Esfandyari & Jensen (2021) derived RFI using a one-step Bayesian approach, differing from the methodology applied in the present study. These results indicate that shorter performance tests assess the same genetic trait as longer trials, with minimal animal re-ranking.

Data collected from the same animal over a shorter period tend to show high correlations (Esfandyari & Jensen, 2021). Likewise, RFI data derived from the same animal, throughout the test, exhibit a comparable pattern. Consequently, RFI shows a high genetic correlation across evaluation periods. This stability indicates minimal re-ranking in later test stages, suggesting that selecting animals based on shorter-duration tests can reliably identify genetically superior individuals for feed efficiency. Reducing test durations, while increasing the number of feed efficiency tests conducted annually, could optimize selection strategies.

The Spearman correlation coefficients between genetic values, across the evaluation periods, showed a clear pattern of increasing concordance as test duration

progressed (Table 5). Correlations between early and later periods, such as 14 vs. 70 days, were lower, whereas comparisons between adjacent or longer intervals (for instance, 56 vs. 70 days) exhibited high agreement (0.99, $p < 0.001$). This indicates that genetic rankings of superior animals become more stable with longer test durations. Culbertson et al. (2015) and Kriese-Anderson et al. (2016) report similar findings, with a Spearman correlation of around 0.95 for 56-day tests for cattle of different ages, suggesting minimal re-ranking beyond this point. Likewise, Manafiazar et al. (2017) observed a correlation of 0.95, when comparing a 49-day to a 70-day test, reinforcing the notion that performance rankings stabilize after approximately seven weeks of evaluation. Additionally, the authors showed that reducing the test length to 42 days led to the estimate of 7% change in animal rankings compared to 84-day reference, echoing our observation that early evaluations (at 14 days) are prone to greater ranking instability. In the present study, the top 10% rankings showed that only 65.59% of animals ranked at the top 10%, at 14 days remaining in the same group at 70 days, while this overlap increased to 93.55% between 56 and 70 days (Table 6). This finding suggests that a test duration of at least 56 days (6.45% changes in rankings) provides a greater stability in genetic ranking,

Table 5. Spearman's correlation of genetic values (below the diagonal) for residual feed intake, across different test periods (14, 28, 42, 56, and 70 days), in Nellore cattle.

Test periods	14	28	42	56	70
14					
28	0.9611**				
42	0.8613**	0.9663**			
56	0.8713**	0.9681**	0.9936**		
70	0.8710**	0.9572**	0.9735**	0.9928**	

**p-value < 0.001.

Table 6. Ranking of the 10% superior animals for number of animals in common (above the diagonal) and percentage in common (below the diagonal) for the residual feed intake, across different test periods (14, 28, 42, 56, and 70 days) in Nellore cattle.

Test periods	14	28	42	56	70
14		73.00	62.00	61.00	61.00
28	78.49		80.00	79.00	77.00
42	66.66	86.02		86.00	80.00
56	65.59	84.95	92.47		87.00
70	65.59	82.79	86.02	93.55	

optimizing the performance testing by balancing accuracy and evaluation costs. This result aligns with evidence from Manafiazar et al. (2017), who found that shortening test periods to 42 days could preserve an acceptable accuracy; however, longer durations (56–70 days) could result in higher repeatability and ranking consistency; these authors highlighted the importance of optimizing the test length to increase genetic gain, by enabling the evaluation of a larger number of animals, without compromising selection precision. Similarly, Culbertson et al. (2015) and Ramos et al. (2024) supported the feasibility of shorter tests durations (56 days), but acknowledged that longer evaluations enhance the stability of estimated breeding values (EBVs). This is consistent with the findings of Esfandyari & Jensen (2021), who reported that RFI measured early in the test is not predictive of genetic merit for feed intake.

Short-test durations may capture transient effects related to feed adaptation or social stress, potentially distorting true genetic merit. The greater agreement in rankings, observed after 56 days, likely reflects physiological stabilization and a more reliable expression of genetic potential. From the perspective of a breeding program, a 56-day test appears to strike an optimal balance between cost-effectiveness and selection accuracy, contributing to faster the genetic progress. The relative efficiency of the correlated response increased throughout the evaluation period, despite a reduction at 42 days (Table 7). The performance test efficiency improved from 0.708 at 14 days to 0.983 at 56 days, supporting the assertion that a longer test enhances the selection accuracy. As reported by Manafiazar et al. (2017) and Ramos et al. (2024), reducing the evaluation period from 84 to 42 days led to approximately 7% loss in ranking

consistency. Their findings suggest that a 42-day test would not significantly affect the residual feed intake selection, while allowing for more tested animals. Expanding the number of animals tested within a 56-day window could increase the selection intensity.

The variation observed in residual feed intake ensures a meaningful response to selection. Selecting animals based on 56-day RFI data appears to be a viable alternative to the full 70-day test, with heritability estimates remaining high, and Spearman correlations with 70-day evaluation reaching 0.99. Additionally, the overlap of 93.55% in the top 10% rankings between these periods underscores the reliability of this shortened duration. Nonetheless, further studies are warranted, to assess whether shortening the test impacts other economically relevant traits genetically correlated with RFI. These findings highlight the need to assess residual variance heterogeneity and heritability fluctuations, when designing selection strategies in beef cattle breeding programs.

Conclusions

1. Random regression models with linear spline polynomials and heterogenous residual variance prove effective in describing the variance component patterns of residual feed intake in Nellore cattle.

2. The estimates of variance components and genetic parameters show minimal variation throughout the evaluation periods from 14 to 70 days.

3. The test period can be shortened from 70 to 56 days without compromising the genetic gain, thereby enhancing the efficiency and feasibility of large-scale feed efficiency evaluations.

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Table 7. Posterior means (highest posterior density intervals) of comparisons between correlated responses and direct responses for residual feed intake, across different test periods (14, 28, 42, 56, and 70 days) in Nellore cattle.

Correlated response/direct response	Relative efficiency
$\Delta G_{70,14}/\Delta G_{70}$	0.708 (0.507; 0.9080)
$\Delta G_{70,28}/\Delta G_{70}$	0.856 (0.712; 1.0009)
$\Delta G_{70,42}/\Delta G_{70}$	0.816 (0.729; 0.905)
$\Delta G_{70,56}/\Delta G_{70}$	0.983 (0.935; 1.033)

ΔG , genetic response.

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No generative artificial intelligence (AI) was used in this study.

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