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Genetic parameters and selection responses for feed efficiency, growth, and carcass traits in performance-tested Nellore cattle

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Abstract

Improving feed efficiency is a key strategy for increasing the biological and economic sustainability of beef cattle production systems. This study aimed to estimate genetic parameters and characterize additive genetic associations and expected correlated responses among feed intake, growth, and carcass traits in performance-tested Nellore cattle. Phenotypic records from 1,394 Nellore males evaluated in 14 performance tests conducted by the Embrapa Geneplus breeding program between 2016 and 2024 were analyzed, together with pedigree information comprising 7,168 animals. The evaluated traits were dry matter intake (DMI), body weight (BW), average daily gain (ADG), residual feed intake (RFI), ribeye area (REA), and subcutaneous fat thickness (SFT). Genetic parameters were estimated using a Bayesian six-trait animal model, including performance test as a fixed effect, age at the beginning of the test as a linear covariate, and additive genetic animal effect as a random effect. Posterior mean heritability estimates were 0.373 ± 0.076 for DMI, 0.744 ± 0.070 for BW, 0.213 ± 0.066 for ADG, 0.277 ± 0.078 for RFI, 0.630 ± 0.087 for REA, and 0.402 ± 0.090 for SFT, indicating exploitable additive genetic variation for all evaluated traits. Residual feed intake showed a moderate positive additive genetic correlation with DMI (0.58) and ADG (0.42), whereas its associations with BW (− 0.17), REA (− 0.27), and SFT (− 0.11) were low to moderate and negative. Ranking based on estimated breeding values showed similar patterns, with Spearman correlations of 0.33, 0.65, − 0.28, − 0.29, and − 0.21 between RFI and DMI, ADG, BW, REA, and SFT, respectively. The comparison between extreme RFI breeding-value groups demonstrated that genetically more efficient animals (lowest RFI decile) exhibited lower genetic propensity for DMI (− 0.41) and ADG (− 0.65), but greater genetic merit for BW (+ 0.80) and REA (+ 0.71) compared with genetically less efficient animals. These results demonstrate that RFI represents an exploitable source of additive genetic variation for improving feed efficiency in Nellore cattle. However, the antagonistic association with growth rate highlights the importance of multi-trait selection strategies integrating feed efficiency, growth, and carcass attributes to achieve balanced genetic progress.

1. Introduction

Feed represents the major variable cost in beef cattle production systems, and improving biological efficiency has become a central objective of genetic improvement programs worldwide. The identification and selection of animals capable of converting feed resources into body tissue more efficiently can contribute to reducing production costs, increasing resource-use efficiency, and improving the sustainability of beef production systems. This challenge is particularly relevant in tropical production systems based on Nellore cattle, which represent the predominant genetic resource for beef production in Brazil and other regions with similar environmental conditions.

Feed efficiency is a complex biological trait influenced by multiple physiological processes, including feed intake regulation, digestion, nutrient absorption, energy metabolism, maintenance requirements, and body composition. Among the available indicators of feed efficiency, residual feed intake (RFI) has received considerable attention because it represents the difference between observed feed intake and

the expected intake required to maintain a given level of production and body size (Koch et al., 1963). Unlike ratio-based measures of efficiency, RFI is calculated independently of production traits included in its adjustment model, allowing the identification of animals that consume less feed than expected while maintaining comparable productive performance (Arthur and Herd, 2008; Herd and Arthur, 2009).

The incorporation of RFI into breeding programs requires a comprehensive understanding of its genetic architecture and its relationships with economically relevant traits. Although RFI is conceptually designed to be independent of growth and body size, genetic associations with performance and carcass characteristics may still occur due to differences in population structure, selection history, methodology used for RFI calculation, and biological mechanisms underlying feed utilization efficiency. Previous studies in beef cattle have demonstrated that RFI generally presents low to moderate heritability, indicating the existence of exploitable additive genetic variation, but its association with growth and carcass traits remains variable among populations (Arthur and Herd, 2008; Herd and Arthur, 2009; Santana et al., 2014; Moraes et al., 2019; Brunes et al., 2023).

In Nellore cattle, improving feed efficiency represents a particular challenge because selection objectives must simultaneously consider production efficiency, growth potential, and carcass value. Although genetic evaluations for feed efficiency have advanced considerably, most studies have focused primarily on estimating heritability and genetic correlations among traits. These parameters are essential for understanding the genetic relationships among traits; however, they do not directly describe the magnitude and direction of expected correlated responses when animals with contrasting genetic merit for feed efficiency are selected. Therefore, complementary approaches that translate genetic parameters into practical selection scenarios are necessary to improve the interpretation and application of feed efficiency traits in breeding programs.

Recent studies have reinforced the importance of integrating feed efficiency traits with genomic, longitudinal, and multi-trait selection approaches to optimize genetic progress in beef cattle populations (Santana et al., 2014; Brunes et al., 2023; Ramos et al., 2024). In addition, studies evaluating Nellore cattle have indicated that selection for feed efficiency can be compatible with improvements in productive and carcass traits when appropriate selection objectives are established (Moraes et al., 2019). However, further studies are required to quantify the expected changes in economically relevant traits when animals at the extremes of the RFI distribution are compared.

We hypothesized that animals with contrasting genetic merit for RFI would exhibit distinct genetic profiles for feed intake, growth, and carcass traits, allowing the quantification of potential correlated responses under selection.

Therefore, the aim of this study was to estimate genetic parameters and characterize additive genetic associations among dry matter intake, residual feed intake, growth, and carcass traits in performance-tested Nellore cattle using a Bayesian multivariate animal model. Additionally, animals were classified according to their RFI breeding values, and the contrast between extreme efficiency groups was

evaluated to quantify the expected correlated genetic responses associated with selection for feed efficiency.

2. Materials and Methods

Phenotypic and pedigree records used in this study were provided by the Embrapa Geneplus breeding program under a formal confidentiality and data-use agreement for scientific research purposes. The dataset comprised Nellore males evaluated in 14 performance tests conducted between 2016 and 2024 at Campo Grande, Mato Grosso do Sul, Brazil. The performance tests were conducted under standardized management conditions to evaluate feed intake, growth performance, feed efficiency, and ultrasound carcass traits.

Animals entered the evaluation after a 21-day adaptation period followed by an 84-day feed efficiency test. During the test period, animals were maintained under ad libitum access to feed and water. Individual feed intake was recorded continuously using automated feeding systems, and body weights were collected periodically according to the procedures established by the Embrapa Geneplus performance testing protocol.

Individual dry matter intake (DMI) was obtained using Intergado® electronic feed bunks equipped with radio-frequency identification systems. The system automatically identified individual animals through electronic ear tags and recorded feed consumption during each visit to the feeding unit, allowing the estimation of daily feed intake.

Before genetic analyses, phenotypic records were subjected to data editing procedures. Observations outside ± 3 standard deviations within each performance test and trait were removed to minimize the influence of extreme records. Additionally, animals from sires represented by fewer than three progeny in the dataset were excluded to ensure adequate estimation of additive genetic effects. After editing, the final phenotypic dataset consisted of 1,394 animals, and the pedigree file used to construct the numerator relationship matrix included 7,168 animals.

The evaluated traits were dry matter intake (DMI, kg/day), mean body weight during the test period (BW, kg), average daily gain (ADG, kg/day), residual feed intake (RFI, kg DM/day), ribeye area (REA, cm^2), and subcutaneous fat thickness (SFT, mm).

Dry matter intake was defined as the average daily dry matter consumption recorded during the feed efficiency test. Mean body weight was calculated as the arithmetic mean of body weights obtained throughout the evaluation period. Average daily gain was calculated as the difference between final and initial body weight divided by the number of days on test.

Residual feed intake was calculated after phenotypic data editing as the difference between observed and expected dry matter intake (DMI): RFI = DMI−DMIp, where DMIp is the expected dry matter intake. Expected DMI was estimated according to Koch et al. (1963) using a multiple linear regression of DMI on

average daily gain and metabolic body weight ($BW^{0.75}$): $DMIp = \mu + b_1ADG + b_2BW^{0.75}$, where μ represents the intercept and b_1 and b_2 are the regression coefficients associated with ADG and metabolic body weight, respectively. The regression model was fitted separately within each performance test to account for differences among test editions in environmental conditions, management practices, and contemporary groups. Therefore, RFI represented the deviation of observed DMI from the intake expected for each animal according to its growth performance and metabolic body size within its respective evaluation group. Animals with negative RFI values were considered genetically more efficient because they consumed less feed than expected for their production level and body size.

Ribeye area (REA) and subcutaneous fat thickness (SFT) were obtained by ultrasound measurements during the performance tests following the standardized procedures adopted by the Embrapa Geneplus breeding program. Ultrasound images were collected between the 12th and 13th ribs by certified technicians using high-resolution equipment and specific image-analysis software for carcass evaluation.

Genetic parameters were estimated using a Bayesian multivariate animal model. A six-trait animal model was fitted jointly for dry matter intake (DMI), mean body weight during the test period (BW), average daily gain (ADG), residual feed intake (RFI), ribeye area (REA), and subcutaneous fat thickness (SFT). This approach allowed the simultaneous estimation of additive genetic and residual (co)variance components and additive genetic correlations among feed intake, growth, feed efficiency, and carcass traits.

The statistical model was defined as: $y = X\beta + Za + e$, where y is the vector of phenotypic observations; β is the vector of fixed effects and covariates; a is the vector of random additive genetic effects; e is the vector of residual effects; and X and Z are the incidence matrices relating observations to fixed and additive genetic effects, respectively. The model included performance test as a fixed effect and age at the beginning of the test as a linear covariate (20.14 ± 1.83 months). The additive genetic effect of the animal was included as a random effect.

The vector of additive genetic effects was assumed to follow a multivariate normal distribution: $a \sim N(0,G)$, Where $G = A \otimes G_0$, with A representing the numerator relationship matrix constructed from the pedigree of 7,168 animals, G_0 representing the additive genetic variance–covariance matrix among the six traits, and ⊗ denoting the Kronecker product.

Residual effects were assumed to follow: $e \sim N(0,R)$, where $R = I \otimes R_0$, with I representing an identity matrix and R_0 representing the residual variance–covariance matrix among the six traits.

Both G_0 and R_0 were assigned inverse-Wishart prior distributions. Fixed effects were assumed to follow $\beta \sim N(\mu\beta, \Sigma\beta)$, with diffuse hyperparameters, i.e., a priori mean equal to zero and a variance–covariance matrix of large magnitude, representing weakly informative priors. The joint posterior distribution was defined as: $p(\beta, a, G_0, R_0 \mid y) \propto p(y \mid \beta, a, R_0) \cdot p(a \mid G_0) \cdot p(\beta) \cdot p(G_0) \cdot p(R_0)$.

Posterior distributions of variance and covariance components were obtained using Markov chain Monte Carlo (MCMC) through Gibbs sampling implemented in GIBBS1F90 (Misztal et al., 2014). A single Gibbs chain of 5,000,000 iterations was generated, with the first 1,000,000 iterations discarded as burn-in. Samples were retained at intervals of 200 iterations, resulting in 20,000 posterior samples for inference.

Convergence and mixing of the Markov chain were assessed using effective sample size (ESS), autocorrelation, and the Geweke diagnostic. Effective sample sizes for additive genetic covariance components ranged from approximately 12,000 to 19,000, whereas ESS values for residual covariance components were greater than 14,000. Autocorrelation at lag 50 was close to zero for the evaluated components, and Geweke diagnostic values were close to zero, providing no evidence of relevant non-stationarity. Monte Carlo errors were below 0.001 for the main posterior estimates. Collectively, these diagnostics indicated adequate chain mixing and convergence, supporting the reliability of the posterior inferences.

Posterior means, posterior standard deviations, and 95% highest posterior density (HPD) intervals were obtained for additive genetic variances, residual variances, heritability, and additive genetic correlations among the six evaluated traits. Heritability was estimated from the ratio of additive genetic variance to total phenotypic variance.

Spearman rank correlations among estimated breeding values (EBVs) were calculated to evaluate the consistency of animal ranking among traits. Additionally, a contrast analysis between extreme RFI breeding-value groups was performed to quantify the expected correlated genetic responses associated with selection for feed efficiency. Animals were ranked according to their EBVs for residual feed intake (RFI) and classified into ten deciles based on the distribution of RFI EBVs. The first decile (D1) comprised animals with the lowest RFI EBVs, representing genetically more efficient animals, whereas the tenth decile (D10) included animals with the highest RFI EBVs, representing genetically less efficient animals.

For each evaluated trait, including dry matter intake (DMI), body weight (BW), average daily gain (ADG), ribeye area (REA), and subcutaneous fat thickness (SFT), mean EBVs were calculated within the extreme groups. Genetic divergence between efficient and less efficient groups was quantified as the difference between the average EBVs of D1 and D10 animals: $\Delta EBV = EBVD1 - EBVD10$. The magnitude and direction of ΔEBV were interpreted according to the biological meaning of each trait. Positive values indicated greater EBV estimates in genetically more efficient animals, whereas negative values indicated lower EBV estimates in the efficient group.

The standard error of each contrast was estimated based on the variability of EBVs within the two extreme groups, providing an assessment of the precision of the estimated genetic differences. This approach was used to characterize the magnitude and direction of expected correlated genetic responses associated with selection for RFI, integrating feed intake, growth performance, and carcass traits into the interpretation of feed efficiency improvement.

3. Results and Discussion

The descriptive statistics of the evaluated traits are presented in Table 1. The dataset comprised 1,394 Nellore males evaluated under standardized performance testing conditions. Mean DMI was 11.9 kg/day, with animals presenting an average BW of 550.72 kg and ADG of 1.62 kg/day. Residual feed intake presented a mean close to zero (0.00 kg DM/day), as expected due to its calculation as the deviation between observed and expected feed intake. Carcass traits showed mean values of 86.15 cm² for REA and 5.37 mm for SFT.

Table 1
Number of observations (N), means and standard deviations (SD), minimum (Min) and maximum (Max) values for the following traits: dry matter intake (DMI), body weight (BW), average daily gain (ADG), residual feed intake (RFI), ribeye area (REA), and subcutaneous fat thickness (SFT).

Trait	N	Unit	Mean	SD	Min	Max
DMI	1394	kg/day	11.9	1.21	8.23	15.51
BW	1394	Kg	550.72	65.42	347.49	739.07
ADG	1394	kg/day	1.62	0.37	0.36	2.56
RFI	1394	kg DM/day	0	0.85	-2.35	2.16
REA	1393	cm²	86.15	11.2	51.9	116.8
SFT	1390	mm	5.37	1.93	1.1	10.3

Posterior means of additive genetic variance, residual variance, and heritability estimates are presented in Table 2. All evaluated traits showed significant additive genetic variation, indicating the presence of genetic differences among animals that can be exploited through selection. Additive genetic variance was detected for all traits, although its magnitude differed substantially among traits. The highest heritability estimates were observed for BW (0.744 ± 0.070) and REA (0.630 ± 0.087), followed by SFT (0.402 ± 0.090). Moderate heritability estimates were obtained for DMI (0.373 ± 0.076) and RFI (0.277 ± 0.078), whereas ADG presented the lowest estimate (0.213 ± 0.066).

Table 2
Posterior means of additive genetic variance (Va), residual variance (Ve), heritability (h^2), and 95% highest posterior density intervals (HPD) for feed efficiency, growth, and carcass traits in Nellore cattle.

Trait		mean	SD	95% HPD interval	h^2	SD	95% HPD interval
DMI (kg/day)	Va	0.535	0.118	0.307–0.765	0.373	0.0758	0.229–0.517
	Ve	0.885	0.103	0.679–1.075	–	–	–
BW (kg)	Va	2711.8	316.2	2068–3313	0.744	0.0702	0.593–0.895
	Ve	899.6	235.4	430–1362	–	–	–
ADG (kg/day)	Va	0.0279	0.0090	0.0112–0.0471	0.213	0.0663	0.081–0.345
	Ve	0.0944	0.0081	0.0795–0.1108	–	–	–
RFI (kg DM/day)	Va	0.221	0.065	0.095–0.345	0.277	0.0782	0.106–0.448
	Ve	0.522	0.054	0.417–0.628	–	–	–
REA (cm^2)	Va	64.24	10.38	44.0–84.0	0.630	0.0873	0.460–0.800
	Ve	49.09	10.93	32.4–69.7	–	–	–
SFT (mm)	Va	1.565	0.381	0.874–2.318	0.402	0.0899	0.225–0.579
	Ve	1.958	0.333	1.392–2.474	–	–	–

DMI (dry matter intake), BW (body weight), ADG (average daily gain), RFI (residual feed intake), REA (ribeye area), and SFT (subcutaneous fat thickness).

Body weight showed the highest heritability estimate (0.744 ± 0.070; 95% HPD: 0.593–0.895), followed by ribeye area (REA; 0.630 ± 0.087; 95% HPD: 0.460–0.800) and subcutaneous fat thickness (SFT; 0.402 ± 0.090; 95% HPD: 0.225–0.579). The magnitude of the posterior distributions indicates that a considerable proportion of the phenotypic variation in these traits was attributable to additive genetic effects. The high heritability for BW is consistent with the substantial genetic determination of body size in beef cattle and indicates considerable opportunity for direct response to selection. Likewise, the estimate for REA indicates strong additive genetic control of variation in muscularity, whereas the moderate heritability for SFT confirms the presence of exploitable genetic variation in fat deposition.

Dry matter intake (DMI) showed moderate heritability (0.373 ± 0.076; 95% HPD: 0.229–0.517), indicating that individual differences in feed consumption were partly attributable to additive genetic effects. This level of genetic control provides a basis for selection aimed at modifying feed intake, although the biological consequences of such selection depend on the genetic relationships between DMI and productive traits. Average daily gain exhibited the lowest heritability among the traits evaluated (0.213 ± 0.066; 95% HPD: 0.081–0.345). The estimate nevertheless indicates the presence of additive genetic

variation for growth rate, although a comparatively larger proportion of its phenotypic variation was associated with residual and environmental sources.

Residual feed intake (RFI) presented a heritability of 0.277 ± 0.078 (95% HPD: 0.106–0.448), indicating moderate additive genetic control. This estimate is within the range generally reported for RFI in beef cattle and supports its potential use as a selection criterion for feed efficiency (Arthur and Herd, 2008; Herd and Arthur, 2009; Moraes et al., 2019; Brunes et al., 2023; Almeida et al., 2024; Sainz et al., 2024). The presence of additive genetic variation in RFI is particularly relevant because the trait is constructed from feed intake after accounting for production requirements, allowing genetic differences in feed consumption relative to expected intake to be characterized.

Differences in heritability estimates among studies may arise from differences in population structure, genetic background, age at evaluation, feeding and management conditions, selection history, trait definition, and statistical procedures used to estimate variance components (Lee and Kim, 2004; Weik et al., 2022; Pauling et al., 2023). For RFI specifically, the methodology used to estimate expected feed intake can also affect the resulting genetic parameters. Brunes et al. (2023) demonstrated that differences in the variables included in the RFI adjustment model may influence estimates of genetic variance and relationships with economically relevant traits in Nellore cattle.

The heritability estimate for SFT (0.402 ± 0.090) was consistent with values previously reported for Nellore populations (Moraes et al., 2019; Marestone et al., 2022). Variation among estimates reported in different populations may reflect differences in genetic background, age at measurement, nutritional management, degree of fat deposition, and environmental conditions (Elzo et al., 1998; Pereira et al., 2023). The moderate additive genetic control observed in the present study indicates that SFT can respond to selection and may be incorporated into breeding objectives when carcass composition is considered alongside growth and feed-efficiency traits.

The contrasting heritability estimates among DMI, RFI, and ADG also emphasize the biological complexity of feed efficiency. Although DMI is influenced by appetite, maintenance requirements, growth, and energy metabolism, RFI represents the residual component of feed intake after accounting for production-related requirements. Consequently, genetic variation in RFI may reflect differences in several physiological processes involved in nutrient utilization, digestion, energy metabolism, physical activity, and thermoregulation (Herd and Arthur, 2009). This complexity may contribute to the moderate rather than high heritability observed for RFI.

The present estimate of RFI heritability is also consistent with evidence from Nellore cattle indicating that the trait can be incorporated into genetic evaluation programs (Moraes et al., 2019; Brunes et al., 2023; Almeida et al., 2024; Ramos et al., 2024; Sainz et al., 2024). However, the existence of additive genetic variation alone does not establish the consequences of selection for RFI on other economically relevant traits. The genetic relationships among RFI, feed intake, growth, and carcass traits therefore provide an essential complement to the univariate heritability estimates and are considered below.

Additive genetic correlations (above diagonal) and Spearman rank correlations among EBVs (below diagonal) are presented in Fig. 1. Genetic correlations ranged from − 0.29 to 0.71, demonstrating heterogeneous genetic relationships among feed intake, growth, and carcass traits. Spearman rank correlations generally followed the same direction as additive genetic correlations; however, differences in magnitude were observed for some trait combinations, indicating that the consistency of animal ranking based on EBVs does not necessarily reflect the exact magnitude of the underlying additive genetic associations.

Residual feed intake (RFI) showed a moderate positive additive genetic correlation with dry matter intake (DMI) (0.58), indicating that animals genetically predisposed to higher RFI also tended to present greater genetic merit for feed consumption. This relationship is consistent with the biological definition of RFI, which represents the deviation between observed and expected intake after accounting for production requirements and metabolic body size (Koch et al., 1963). Similar positive genetic associations between RFI and DMI have been reported in Nellore cattle, indicating that although RFI is adjusted for production level, part of its genetic variation remains associated with voluntary feed intake (Santana et al., 2014; Moraes et al., 2019). Nevertheless, differences among estimates may occur due to population structure, the variables included in the prediction model, and methodological procedures used for RFI calculation (Brunes et al., 2023).

The corresponding Spearman correlation between RFI and DMI was 0.33, indicating moderate agreement in animal ranking. This result suggests that animals genetically classified as having lower RFI values tend to rank favorably for reduced feed consumption, supporting the potential use of RFI as a selection criterion to improve biological efficiency and reduce feeding costs.

The genetic correlation between RFI and average daily gain (ADG) was positive and moderate (0.42), whereas the Spearman correlation among EBVs was higher (0.65). This indicates that animals with greater genetic potential for growth tended to present higher RFI values. Similar positive relationships between RFI and growth traits have been described in Nellore cattle, although the magnitude of these associations varies among populations and experimental conditions (Santana et al., 2014; Moraes et al., 2019; Brunes et al., 2023). These differences may be associated with variation in age at evaluation, duration of performance tests, nutritional conditions, and the methodology used to estimate expected feed intake.

The positive association between RFI and ADG indicates a potential biological trade-off between growth intensity and feed efficiency. Animals with higher growth potential generally require greater nutrient availability to support tissue deposition, which may increase feed intake and influence residual intake. Therefore, selection for lower RFI should not be conducted independently of growth performance, and balanced selection indices integrating efficiency and production traits are required.

In contrast, RFI showed a low negative additive genetic correlation with body weight (BW) (− 0.17), with a corresponding Spearman correlation of − 0.28. The limited magnitude of this association indicates that RFI was largely independent of genetic differences in body size. This result agrees with previous studies

showing weak relationships between RFI and BW when feed intake is adjusted for metabolic body weight and growth rate (Arthur and Herd, 2008; Herd and Arthur, 2009; Moraes et al., 2019). This relative independence represents an important advantage of RFI compared with ratio-based efficiency measures because it allows identification of efficient animals without simply selecting smaller individuals.

The association between RFI and ribeye area (REA) was negative and moderate (− 0.27), with a similar Spearman correlation (− 0.29). This relationship indicates that animals genetically superior for feed efficiency tended to present greater genetic merit for muscularity. Similar findings have been reported in Nellore cattle, suggesting that selection for improved feed efficiency does not necessarily compromise carcass development (Moraes et al., 2019; Brunes et al., 2023). This result is particularly relevant because maintaining carcass value while improving feed efficiency remains one of the main challenges in beef cattle breeding programs.

The genetic correlation between RFI and subcutaneous fat thickness (SFT) was low and negative (− 0.11), whereas the Spearman correlation was − 0.21. These results indicate limited genetic association between feed efficiency and fat deposition. Therefore, selection for lower RFI is unlikely to substantially alter subcutaneous fat deposition when carcass traits are considered within balanced selection objectives (Santana et al., 2014; Moraes et al., 2019).

Dry matter intake presented positive additive genetic correlations with BW (0.61), ADG (0.36), REA (0.27), and SFT (0.19), indicating that animals with greater genetic propensity for feed intake also tended to present greater genetic potential for growth and carcass development. The strongest relationship between DMI and BW is biologically expected because larger animals have greater maintenance requirements (Arthur and Herd, 2008).

Body weight showed a strong positive genetic association with REA (0.71) and a moderate association with SFT (0.42), confirming the close relationship between body size and carcass development. The high Spearman correlation between BW and REA (0.84) indicates strong consistency in animal ranking, suggesting that selection for body weight may result in correlated responses in muscularity. Similar relationships have been reported in Nellore cattle (Moraes et al., 2019).

Overall, the genetic correlations indicate that RFI represents a useful efficiency trait because it captures genetic variation related to feed utilization while maintaining partial independence from body size and carcass traits. However, the positive association between RFI and ADG demonstrates that efficiency improvement must be considered together with growth objectives to avoid unfavorable responses. The distribution of mean estimated breeding values across RFI deciles and their relationships with the other evaluated traits are presented in Fig. 2.

The comparison between animals classified according to extreme RFI breeding values revealed distinct genetic profiles associated with feed efficiency selection (Fig. 3). The contrast between the lowest RFI decile (D1; genetically more efficient animals) and the highest RFI decile (D10; genetically less efficient

animals), expressed as the difference in predicted breeding values (ΔEBV = EBV_D1 − EBV_D10), quantified the expected correlated genetic responses associated with selection for feed efficiency.

Animals classified in D1 presented lower EBVs for DMI compared with D10 animals (ΔEBV = − 0.41), confirming that selection for lower RFI is associated with reduced genetic propensity for feed consumption. This response agrees with the positive genetic correlation between RFI and DMI (0.58), indicating that part of the genetic variation affecting RFI is related to voluntary feed intake. However, the magnitude of this difference demonstrates that RFI selection does not simply identify animals with lower intake, but animals that consume less than expected after accounting for production requirements and metabolic body size.

A contrasting response was observed for ADG, with efficient animals presenting lower EBVs than inefficient animals (ΔEBV = − 0.65). This result provides practical evidence of the positive association previously observed between RFI and ADG. Although lower RFI is desirable from an efficiency perspective, the reduction in genetic merit for growth rate indicates that selection exclusively focused on RFI may limit improvement in weight gain. Therefore, simultaneous optimization of feed efficiency and growth requires multi-trait selection strategies.

Interestingly, despite the lower ADG observed in efficient animals, D1 animals presented greater EBVs for BW compared with D10 animals (ΔEBV = + 0.80). This result indicates that improved feed efficiency was not associated with reduced genetic potential for body size. The difference between BW and ADG responses highlights the distinction between accumulated body size and growth rate during the evaluation period, suggesting differences in nutrient partitioning among animals with contrasting efficiency profiles.

A favorable response was observed for REA, with efficient animals showing greater EBVs than inefficient animals (ΔEBV = + 0.71). This result confirms the negative genetic association between RFI and REA and indicates that selection for improved feed efficiency may be compatible with increased muscularity. From a breeding perspective, this is particularly relevant because carcass quality represents an important component of economic value in beef cattle production.

Subcutaneous fat thickness showed a positive but smaller difference between groups (ΔEBV = + 0.38). Considering the low genetic association between RFI and SFT, the expected response in fat deposition due to RFI selection is likely limited and should be interpreted within the context of the overall breeding objective.

The divergence observed between extreme RFI groups provides an applied interpretation of the genetic parameters estimated in this study. While heritability estimates demonstrate the existence of exploitable genetic variation and correlations describe relationships among traits, the D1 versus D10 comparison illustrates the magnitude and direction of expected genetic changes under practical selection scenarios. Therefore, RFI can be incorporated into Nellore breeding programs as a selection criterion for improving

biological efficiency, provided that efficiency, growth, and carcass traits are simultaneously considered to achieve balanced genetic progress.

4. Conclusions

he evaluated traits showed exploitable additive genetic variation in Nellore cattle, with greater genetic control observed for body weight and carcass traits, and moderate genetic control for dry matter intake and residual feed intake. The magnitude of additive genetic variation estimated for RFI indicates that this trait can be effectively incorporated into selection programs aiming to improve feed efficiency.

Selection for lower RFI was associated with reduced genetic propensity for dry matter intake and favorable changes in carcass composition, particularly greater genetic merit for ribeye area. The comparison between extreme RFI breeding-value groups further demonstrated that animals genetically superior for feed efficiency presented distinct genetic profiles, characterized by lower DMI, higher BW and REA, but reduced genetic merit for average daily gain. These results indicate that improvement in feed efficiency through RFI selection should not be pursued independently from growth objectives.

R esidual feed intake represents a valuable selection criterion for improving biological efficiency in Nellore cattle; however, its incorporation into breeding programs should be performed through multi-trait selection strategies that simultaneously consider feed intake, growth performance, and carcass attributes to achieve balanced genetic progress.

Declarations

Statement of Animal Rights

No approval from research ethics committees was required to achieve the objectives of this study because the experimental work was conducted from a consolidated database.

Conflict of Interest

The authors declare that they have no conflict of interest.

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Data Availability

The data that support the findings of this study were provided by the Geneplus-Embrapa Program and Embrapa. Restrictions apply to the availability of these data, which were used under institutional agreement for the current study and are not publicly available.

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Figures

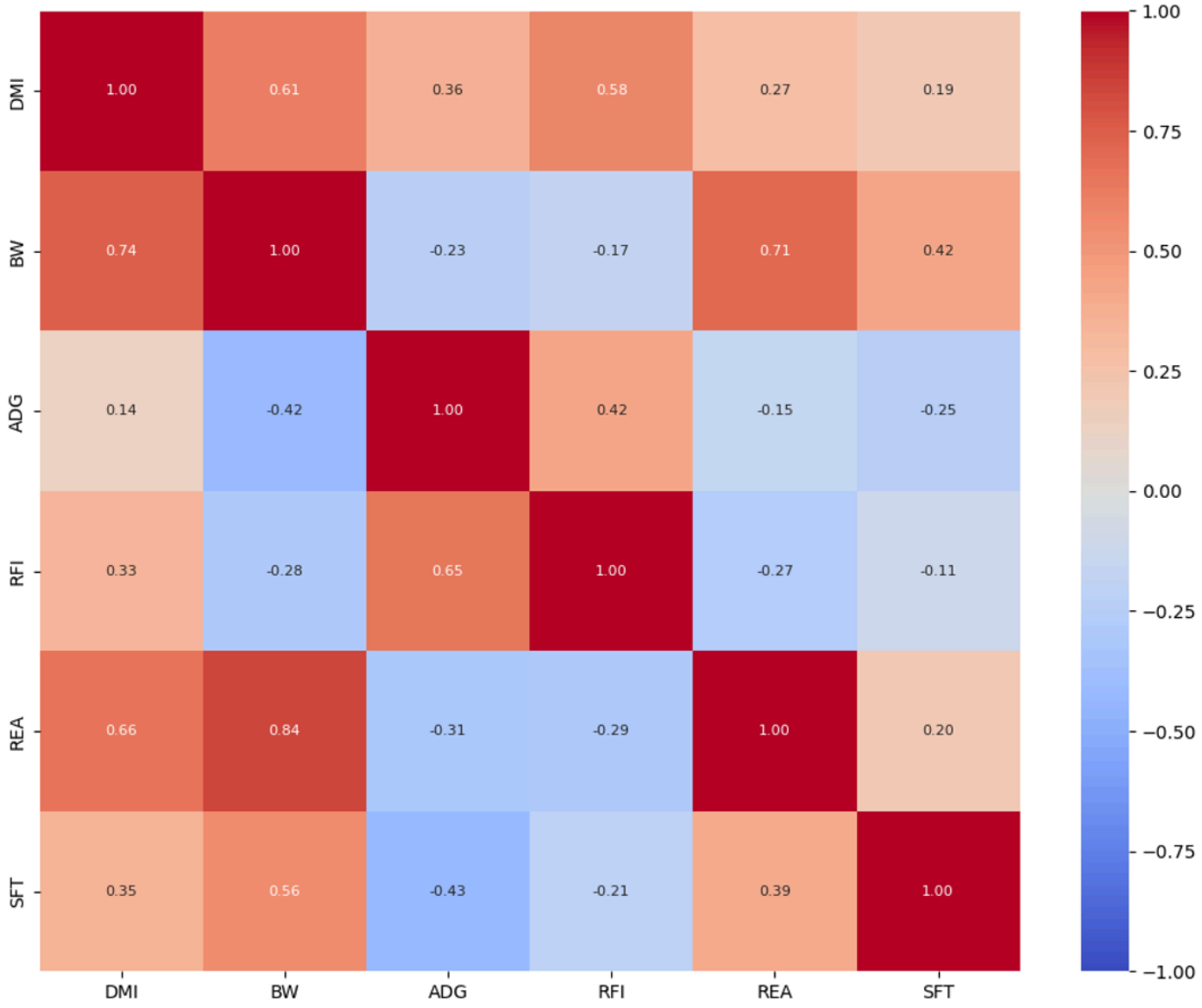


Figure 1

Additive genetic correlations above the diagonal and Spearman rank correlations among predicted breeding values below the diagonal for the following traits: DMI (dry matter intake), BW (body weight), ADG (average daily gain), RFI (residual feed intake), REA (ribeye area), and SFT (subcutaneous fat thickness).

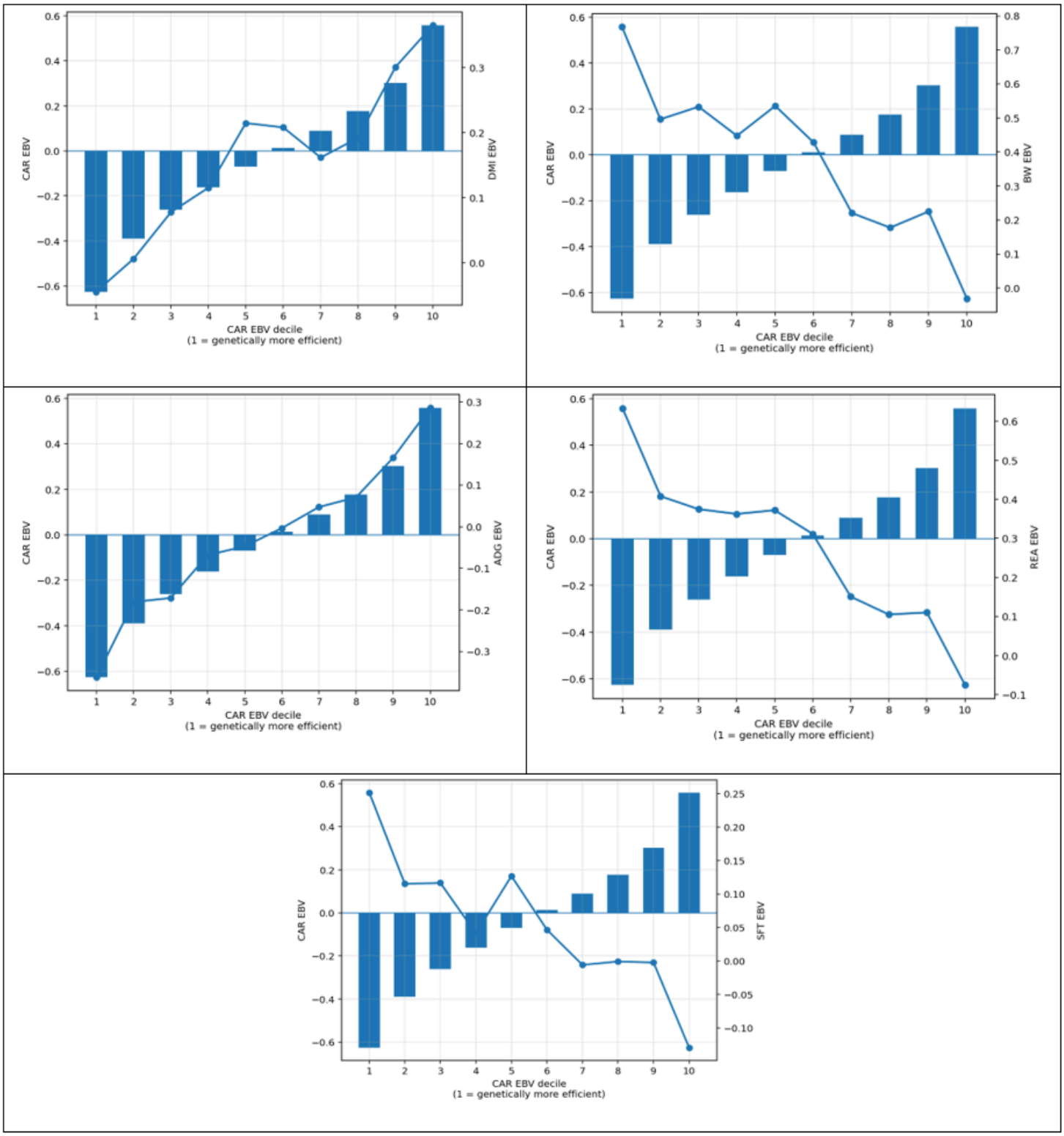


Figure 2

Distribution of mean predicted breeding values for residual feed intake (RFI; blue bars, left axis) across RFI deciles and their relationship with the mean predicted breeding values of the other evaluated traits (blue line, right axis). Deciles were defined according to predicted breeding values for RFI, from genetically more efficient animals with lower RFI to less efficient animals with higher RFI.

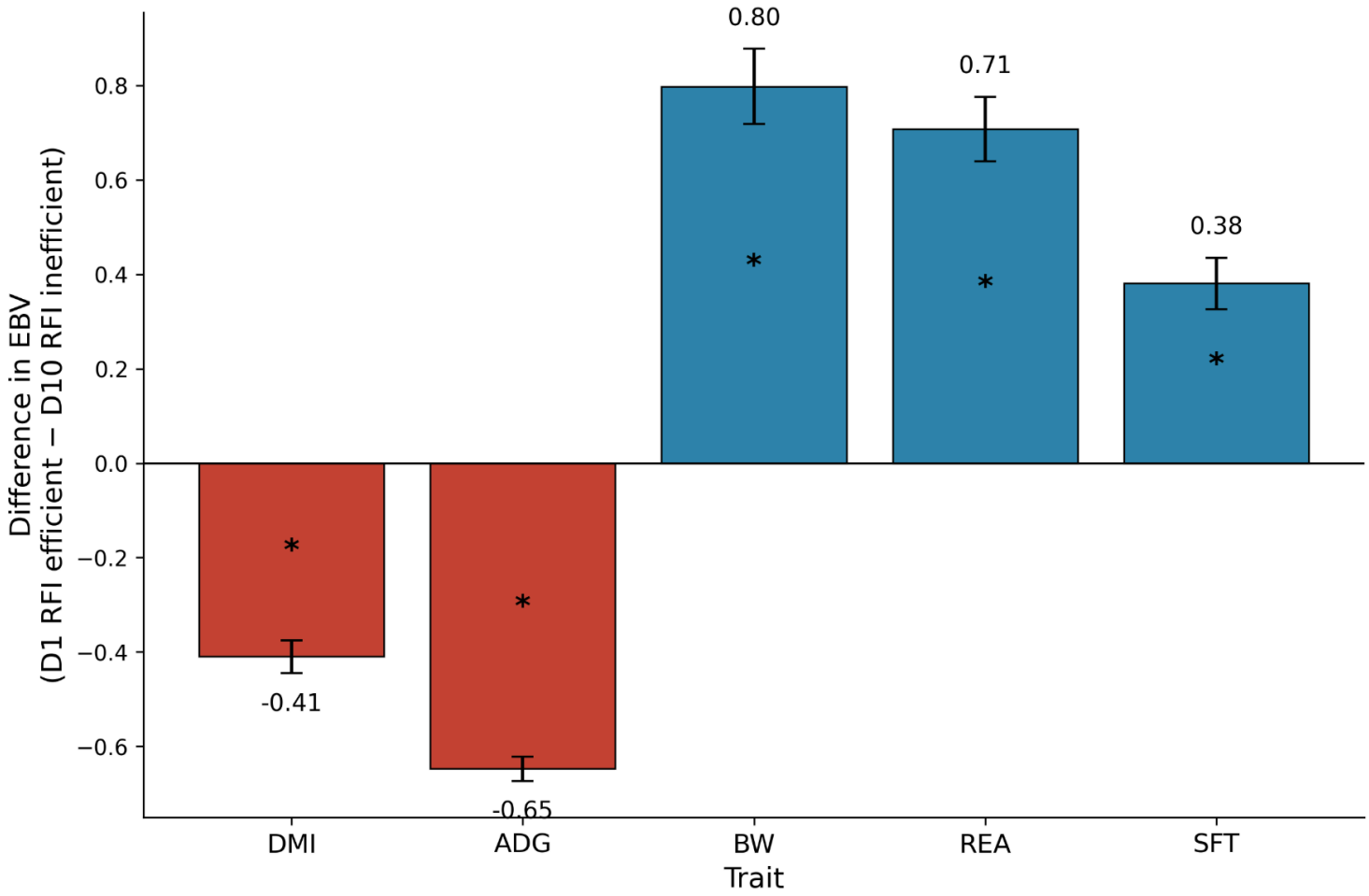


Figure 3

Expected correlated genetic responses in feed intake, growth, and carcass traits between animals with contrasting residual feed intake breeding values. Differences represent the contrast between the lowest RFI decile (D1; genetically more efficient animals) and the highest RFI decile (D10; genetically less efficient animals).