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Estimation of the genetic parameters for feed efficiency and carcass traits in Nellore bulls using a genomic matrix

Estimativa de parâmetros genéticos de características de eficiência alimentar e de carcaça de touros Nelore, com uso de matriz genômica

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Highlights

The Bayesian approach enabled more accurate estimates of genetic parameters.
Efficiency and carcass traits have additive variation, making them selectable.
Direct selection is better than indirect for feed efficiency and carcass traits.

Abstract

The selection of animals that are more efficient in feed utilization without compromising carcass quality is important for breeding programs, and genomic and pedigree information can be used to enhance the estimates of genetic values. In this context, this project aims to evaluate the genetic traits of residual feed intake (RFI), dry matter intake (DMI), ribeye area (REA), rib subcutaneous fat thickness (RFT), and rump subcutaneous fat thickness (RFT8) in Nellore bulls participating in the Nelore Qualitas® breeding program, utilizing a genomic matrix. The RFI and DMI data used in this study were collected during feed efficiency tests conducted between 2010 and 2023, involving 1,618 bulls with an average age of 643 ± 41 days, housed in individual and group pens. Technicians from commercial companies performed

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ultrasound scans to measure REA, RFT, and RFT8. Univariate and bivariate animal models, based on a Bayesian approach, were applied to estimate genetic parameters for the traits, using a single-step genomic best linear unbiased prediction (GBLUP). Systematic effects of contemporary groups (pen and year), the linear covariate of age at the beginning of the test, and additive and residual effects were considered. Heritability estimates ranged from moderate to high, with values of 0.27 ± 0.05 (RFI), 0.30 ± 0.05 (DMI), 0.39 ± 0.05 (REA), 0.37 ± 0.04 (RFT), and 0.58 ± 0.05 (RFT8). Genetic correlations between RFI and carcass traits were low, ranging from -0.30 to 0.17, whereas a strong positive correlation was observed between RFI and DMI (0.77 ± 0.06). DMI showed low genetic correlations with carcass traits, ranging from -0.02 to 0.20, and a moderate to high correlation was found between RFT and RFT8 (0.66 ± 0.06) and between RFI and DMI (0.77 ± 0.06). Including feed efficiency and carcass traits in selection programs is feasible and important for improving both carcass quality and the profitability of production systems, as indicated by the heritability estimates.

Key words: Correlation. Heritability. Zebu cattle.

Resumo

A seleção de animais mais eficientes no uso de alimentos sem alterar a qualidade de carcaça é importante para os programas de melhoramento genético, podendo utilizar informações genômicas e de pedigree para aprimorar as estimativas de valores genéticos. Nesse contexto, o presente estudo tem como objetivo estimar parâmetros genéticos para as características consumo alimentar residual (CAR), consumo de matéria seca (CMS), área de olho do lombo (AOL) e espessuras de gordura subcutânea do lombo (EGS) e da garupa (EGS8) em animais Nelore participantes do Programa de Melhoramento Nelore Qualitas® utilizando matriz genômica. Os dados de CAR e CMS utilizados no estudo foram coletados em testes de eficiência alimentar nos anos de 2010 a 2023, em 1618 touros, com idade média de 643 ± 41 dias, em baias individuais e coletivas. A técnica de ultrassonografia foi realizada por técnicos de empresas comerciais, mensurando AOL, EGS e EGS8 dos animais dos testes. Modelo animal em análises uni e bivariadas, com abordagem bayesiana, foi aplicado para estimar os componentes de (co)variâncias e obter os parâmetros genéticos das características, utilizando o método single step genomic best linear unbiased prediction (GBLUP). Foram considerados os efeitos fixos de grupo de contemporâneos (baia e ano do teste), a covariável linear da idade do touro no início do teste, além dos efeitos aditivo e residual. As estimativas de herdabilidade variaram de moderadas a altas, com valores de 0,27 ± 0,05 (CAR), 0,30 ± 0,05 (CMS), 0,39 ± 0,05 (AOL), 0,37 ± 0,04 (EGS) e 0,58 ± 0,05 (EGS8). As correlações genéticas entre CAR e características de carcaça foram baixas, variando de -0,30 a 0,17, enquanto uma forte correlação positiva foi observada entre CAR e CMS (0,77 ± 0,06). O CMS apresentou correlações genéticas baixas com as características de carcaça, variando de -0,02 a 0,20 e uma correlação genética moderada/alta foi encontrada entre EGS_EGS8 (0,66 ± 0,06) e entre CAR_CMS (0,77 ± 0,06). A inclusão de características de eficiência e carcaça são passíveis de seleção e importantes para melhorar a qualidade da carcaça e a rentabilidade dos sistemas produtivos.

Palavras-chave: Correlação genética. Herdabilidade. Zebuíno.

Introduction

Cattle industry in Brazil holds a crucial position within the national economy, notable for possessing the world's largest commercial beef herd, totaling 234 million head (Instituto Brasileiro de Geografia e Estatística [IBGE], 2023), and by its leading role in global meat exports. The beef herd predominantly consists of zebuine animals, notably the Nellore breed, recognized for their high adaptability to tropical climates. Nevertheless, the industry encounters low off-take rates, escalating costs, and growing sustainability demands (Neves et al., 2023). To address these issues, breeding programs initiatives have aimed to enhance production efficiency and carcass quality, reinforcing Brazil's standing in the international marketplace (Menezes et al., 2022).

Feed efficiency traits can be measured through dry matter intake (DMI) and residual feed intake (RFI). Enhancing feed efficiency offers economic and sustainable advantages, rendering it one of the most esteemed traits in genetic breeding programs (Nichele et al., 2015). In addition, carcass attributes such as ribeye area (REA), rib subcutaneous fat thickness (RFT), and rump subcutaneous fat thickness (RFT8) have been employed as selection criteria owing to their strong correlation with both the yield of commercial cuts and meat quality (Kruk et al., 2024).

Genetic breeding programs include phenotypic and pedigree data to estimate the genetic values of animals for various traits of interest. However, measuring and predicting traits associated with carcass quality or feed efficiency in young animals remains challenging (Fernandes et al., 2016; Meuwissen et al., 2016). This challenge can be addressed through techniques such as carcass ultrasonography, feed efficiency testing, and the application of genomic data. Bayesian methods have been developed to integrate genomic information into genetic evaluations, with variations depending on the prior distributions employed (De Los Campos et al., 2013). Among these methods, ssGBLUP is notable; it combines the pedigree relationship matrix (A) and the genomic relationship matrix (G) into the so-called H matrix, thereby enabling joint evaluation of genotyped and non-genotyped animals based on their kinship relationships (Legarra et al., 2009; Aguilar et al., 2010; VanRaden, 2008).

The selection of animals that are most efficient in feed utilization, without compromising carcass traits, is of the upmost importantance for genetic breeding programs. In addition to traditional selection, combining genomic and pedigree information allows for more accurate prediction of genomic breeding values. In this context, the present study uses this genomic matrix to estimate genetic parameters for traits related to feed efficiency and carcass quality in Nellore bulls participating in performance tests.

Materials and Methods

Ethics committee

The project received approval from the Animal Use Ethics Committee (CEUA) of the Faculty of Veterinary Medicine and Animal Science, UNESP, Botucatu/SP, under protocol number 0474/2023- CEUA.

Animals and management

The data were collected from information regarding animals participating in different feed efficiency trials promoted by the Nelore Qualitas® genetic breeding program from 2010 to 2023. The tests from 2010 and 2015 were carried out at the Beef Cattle Experimental Confinement, located at the School of Veterinary Medicine and Animal Science at the Federal University of Goiás (CEBC/EVZ/UFG), in Goiânia-GO, at an altitude of 771 meters, with coordinates of latitude 16º36′ and longitude 49º15′. The region features a humid temperate climate characterized by dry winters and hot summers, with an average temperature of 23.4°C (Cardoso et al., 2014), using an individual pen system. From 2016 to 2022, the tests were conducted at the Center for Innovation in Genetics and Animal Nutrition (CIGNA), situated at the Lageado Experimental Farm which is affiliated with the Faculty of Veterinary Medicine and Animal Science (FMVZ) of São Paulo State University "Júlio de Mesquita Filho," campus Botucatu, São Paulo, at an altitude of 786 meters. The location is positioned at 22º53′ south latitude and 48º25′ west longitude, where collective pens outfitted with electronic troughs from Intergado® (Intergado Ltda, Minas Gerais, Brazil) were utilized. In 2023, the test was carried out at the Humberto de Freitas Technological Center, located at Central Bela Vista in Botucatu, at an altitude of 1000 meters, with geographic coordinates of approximately -23° 0′ south latitude and -48° 25′ west longitude, and characterized by a warm-humid temperate climate with average temperatures exceeding 22°C, using a collective pen system.

The phenotypic data originated from 1,618 Nellore bulls, with an average age of 643.10 ± 41.89 days. The animals were adapted to the diet and facilities for approximately 21 days, followed by a testing period of about 56 days, during which they had *ad libitum* access to the diet and water, resulting in a total confinement duration of 77 days. The DMI (kg day^{-1}) was determined during the individual feed efficiency test by calculating the difference between the total diet supplied and the residual in the trough, multiplied by the percentage of dry matter (DM, %) of the total diet to facilitate automatic recording of individual daily feed intake. The variable DMI was calculated by averaging each animal's daily DMI over the duration of the test period. The RFI (kg DM day^{-1}) was derived through phenotypic regression of daily weight gain (DWG) and metabolic live weight (MLW) on DMI, employing the PROC REG procedure from the Statistical Analysis System® v.9.3 (SAS Institute, 2011), in accordance with Koch et al. (1963). For tests commencing in 2016, the effect of the pen was incorporated into the data of Nelore Qualitas®. The regression model was as follows:

$$\mathbf{DMI}\boldsymbol{i} = \boldsymbol{\beta 0} + \boldsymbol{\beta 1}(\boldsymbol{D}\mathbf{WG}) + \boldsymbol{\beta 2}\ (\mathbf{MLW}) + \mathbf{RFI}\boldsymbol{i}$$

where **DMI**$\boldsymbol{i}$ = Predicted dry matter intake for each animal $\boldsymbol{i}$; $\boldsymbol{\beta 0}$ = Regression intercept; $\boldsymbol{\beta 1}$ = Partial regression coefficient on **DMG**; $\boldsymbol{\beta 2}$ = Partial regression coefficient on **MLW**; **RFI**$\boldsymbol{i}$ = Residual feed intake of animal $\boldsymbol{i}$.

At the end of each test, in vivo carcass traits, ribeye area (REA, cm²), rib subcutaneous fat thickness (RFT, mm), and rump subcutaneous fat thickness (RFT8, mm) were assessed using ultrasound imaging techniques. The measurements of REA and

RFT were obtained in a transverse orientation relative to the animal's vertebral column, over the *Longissimus thoracis* muscle, situated between the 12th and 13th ribs on the right side of the animal. The RFT8 measurement was taken at the intersection between the *gluteus medius* and *biceps femoris* muscles. Data integrity was maintained by excluding missing values, as carcass characteristic measurements were not conducted in certain years.

Genetic parameters

The BLUPF90+ family program, through GIBBSF90+ (Misztal et al., 2014), was used to obtain the components of (co) variance within univariate and bivariate analyses utilizing a Bayesian methodology. The model can be expressed in matrix notation as follows:

$$y = \mathbf{X}b + \mathbf{Z}a + e$$

where y is a vector of observations for feed efficiency and carcass traits, b is a vector of fixed environmental effects (Contemporary Group (CG); Evaluation Year and Pen) and a linear covariate of age at the start of the test, a is the vector of random additive effects of the animals, **X** and **Z** are incidence matrices that relate the records to their respective effects, and e is the vector of residual random effects.

The analysis involved a single chain comprising 60,000 samples set for Gibbs sampling. The initial 20,000 samples were discarded, representing approximately one-third of the total, and subsequent samples were collected every 10 cycles, resulting in 4,000 samples utilized for inference. Convergence was evaluated using the POSTGIBBSF90 program (Misztal et al., 2014), through visual inspection of the chains, assessment of the effective sample size, and applying the Geweke diagnostic (Smith, 2007). Convergence was indicated by statistical values falling between -1.96 and 1.96. The posterior means, standard deviations, 95% credible intervals of the (co)variance components, heritabilities, and genetic and phenotypic correlations were derived from the chains that demonstrated convergence.

Genomic information

Genomic data from 7,876 animals, participants in Qualitas' feed efficiency tests, were utilized, encompassing seven distinct commercial SNP panels (Table 1). The genotypic information from 609 Nellore bulls, genotyped with the high-density panel of 770,000 markers (Illumina Inc., San Diego, CA), was employed as a reference to impute genotypes across five panels with varying SNP densities (~74,000; ~70,000; ~56,000; ~54,000; and ~29,000), culminating in a dataset containing 468.158 SNPs (excluding sex chromosomes and following quality control procedures) for all animals. For imputation, the FImpute v.2.2 software (Sargolzaei et al., 2014) was utilized, with consideration given to the animals' pedigree information. Only autosomal chromosomes and markers with established genomic positions were incorporated into the analyses.

Table 1
Number of SNPs shared with the BovineHD panel (SNPs_cHD), across different SNP panels

Painel	N_SNP	N_SNP_29	SNPs_HD	N_A
Illumina® BovineHD	777.962	735.965		609
GSGT Version 1.9.4 90K Ind_Full_A_PublicMasked	74.677	69.981	69.778	121
GSGT Version 2.0.4 ZBN_20006795X372004_A1	74.653	70.974	66.738	837
Zoetis_BR_MD_ZBM	70.092	66.723	66.608	128
Zoetis_BR_MD_ZM2	56.169	53.803	53.692	346
GSGT Version 2.0.4 GGP_Indicus_50K_A1	54.791	51.976	51.410	5.100
Zoetis_BR_LD_ZL5	29.842	27.843	27.756	735

N_SNP = number of SNPs; **_29**: located up to chromosome 29; **_HD** = SNPs in BovineHD; **N_A** = number of genotyped animals.

A quality control process for the genotypes was implemented across all genotype panels in accordance with the following exclusion criteria: 1) call rate below 0.9 (for both individual animals and SNPs), 2) minor allele frequency (MAF) under 0.01, 3) maximum discrepancy between observed and expected frequencies exceeding 0.15 (indicating deviation from Hardy-Weinberg equilibrium), and 4) pedigree inconsistencies.

Genomic information was integrated into the analytical models utilizing the ssGBLUP method, as Misztal et al. (2009) and Legarra et al. (2009) has suggested.

Results and Discussion

The descriptive statistics concerning feed efficiency and carcass traits are presented in Table 2. The mean values for these traits are consistent with those documented by Ceacero et al. (2016), Grigoletto et al. (2017), and Buzanskas et al. (2017), all of whom conducted studies involving Nellore cattle.

The estimates of variance components and heritabilities derived from the univariate analyses for feed efficiency and carcass traits in Nellore cattle (Table 3) showed moderate to high values.

Table 2
Description of the database analyzed with age, efficiency, and carcass traits

Variable	NOBS	Mean	SD	Max	Min
RFI	1618	0.00	0.02	4.10	-3.71
DMI	1618	10.86	0.03	16.97	6.87
REA	1604	82.72	0.27	122.74	51.42
RFT	1485	5.32	0.05	14.98	1.20
RFT8	1364	7.28	0.06	16.57	1.78

NOBS = Number of records (n); **SD** = Standard Deviation; **Max** = Maximum; **Min** = Minimum; **RFI** = Residual Feed Intake; **RFI** = Residual Feed Intake; **DMI** = Dry Matter Intake; **REA** = Longissimus dorsi area; **RFT** = Subcutaneous fat thickness of the loin; **RFT8** = Subcutaneous fat thickness at the rump.

Table 3
Estimates of variance component and heritability in univariate models of feed efficiency and carcass traits of Nellore bulls

Trait	Variable	Mean	SD	CI	ESS	Geweke
FEED EFFICIENCY						
RFI	σ^2_a	16.32	3.34	9.59 to 22.52	43.0	-0.37
	σ^2_e	43.86	3.01	37.94 to 49.56	75.2	0.28
	h^2	0.27	0.05	0.17 to 0.36	42.8	-0.37
DMI	σ^2_a	35.44	6.49	22.65 to 47.41	46.3	-0.32
	σ^2_e	81.66	5.65	71.03 to 92.87	83.4	0.23
	h^2	0.30	0.05	0.20 to 0.39	46.7	-0.32
CARCASS						
REA	σ^2_a	27.08	4.20	19.77 to 36.18	71.3	0.08
	σ^2_e	40.92	3.28	34.36 to 47.28	113.9	-0.08
	h^2	0.39	0.05	0.29 to 0.50	73.6	0.08
RFT	σ^2_a	100.90	14.78	71.79 to 127.20	97.5	-0.03
	σ^2_e	171.17	12.31	147.40 to 194.80	167.6	0.04
	h^2	0.37	0.04	0.27 to 0.45	101.1	-0.04
RFT8	σ^2_a	259.81	31.78	202.30 to 321.60	129.9	-0.16
	σ^2_e	180.86	21.03	141.10 to 222.00	172.1	0.15
	h^2	0.58	0.05	0.47 a 0.68	133.4	-0.16

Variable = Component; **SD** = Standard Deviation; **CI** = Credibility Interval (95%); **ESS** = Effective Sample Size; **σ^2_a** = Additive Variance; **σ^2_e** = Residual Variance; **h^2** = Heritability; **RFI** = Residual Feed Intake; **DMI** = Dry Matter Intake; **REA** = Longissimus dorsi area; **RFT** = Subcutaneous fat thickness of the loin; **RFT8** = Subcutaneous fat thickness at the rump.

The heritability estimate for RFI was regarded as moderate (0.27 ± 0.05) and aligns with the values reported by Polizel et al. (2018), Ceacero et al. (2016), Grigoletto et al. (2017), and Silva et al. (2016), who reported values of 0.28, 0.24, 0.30, and 0.23, respectively.

The estimate for DMI (0.30 ± 0.05) was lower than the results reported by Silva et al. (2016), Polizel et al. (2018), and Novo et al. (2021). These observed variations in this characteristic may be attributed to methodological differences, such as the inclusion or exclusion of genomics, breed differences (Novo et al., 2021), or the age of the animals (Polizel et al., 2018; Silva et al., 2016). According to Freetly et al. (2020), the regulation of intake in growing cattle can be influenced by multiple factors, including but not limited to diet composition.

The heritability estimates for REA (0.39±0.05), regarded as moderate, align with findings by Pires et al. (2017), Kluska et al. (2018), Ceacero et al. (2016), and Silveira et al. (2019). Regarding RFT, the estimated value (0.37±0.04) is consistent with values reported by Moraes et al. (2019), Ceacero et al. (2016), and Silveira et al. (2019). In Senepol heifers, Novo et al. (2021) reported heritability of 0.45 for RFT, this increase in the estimate may be attributed to higher additive variances within the population (Martínez et al., 2016). The heritability estimate for RFT8 (0.58±0.05) agrees with the findings of Moraes et al. (2019) and Silveira et al. (2019), suggesting the potential for rapid genetic gain through direct selection of this trait relative to others.

The genetic and phenotypic correlations estimated through bivariate analyses between feed efficiency traits and carcass traits are presented in Table 4. Understanding the genetic correlation between two traits, including their magnitude and direction, is essential for developing effective genetic breeding programs (Moraes et al., 2019). Such knowledge assists in formulating selection strategies and in the appropriate selection of criteria (Ceacero et al., 2016).

Table 4
Genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal), along with their respective estimated standard deviations in bivariate models between feed efficiency and carcass traits in Nellore bulls

	FEED EFFICIENCY		CARCASS		
	RFI	DMI	REA	RFT	RFT8
RFI		0.77 ± 0.06	-0.30 ± 0.11	0.13 ± 0.14	0.17 ± 0.12
DMI	0.24 ± 0.04		-0.02 ± 0.11	0.20 ± 0.12	0.17 ± 0.11
REA	-0.10 ± 0.03	-0.02 ± 0.04		0.02 ± 0.13	-0.25 ± 0.10
RFT	0.05 ± 0.05	0.07 ± 0.05	0.01 ± 0.05		0.66 ± 0.06
RFT8	0.07 ± 0.05	0.07 ± 0.04	-0.12 ± 0.05	0.31 ± 0.04	

RFI = Residual Feed Intake; **DMI** = Dry Matter Intake; **REA** = Longissimus dorsi area; **RFT** = Subcutaneous fat thickness of the loin; **RFT8** = Subcutaneous fat thickness at the rump.

The estimates of the correlations of RFI with carcass traits REA, RFT, and RFT8 were -0.30±0.11, 0.13±0.14, and 0.17±0.12, respectively, and are considered low. Ceacero et al. (2016) in young Nellore bulls estimated values for RFI and REA (0.00±0.16), RFI and RFT (0.37±0.17), and RFI and RFT8 (0.30±0.16), showing similar correlations to the present study. These results suggest a limited potential for achieving genetic progress in carcass traits through indirect selection via RFI, due to the negative genetic correlation between RFI and REA. While it is advantageous as it favors animals with higher REA and increased efficiency (negative values), it is of low magnitude. In the case of fat thickness (RFT and RFT8), the values considering the standard deviation are negligible.

The estimates of correlations between DMI and carcass traits REA, RFT, and RFT8 were -0.02±0.11, 0.20±0.12, and 0.17±0.11, respectively, indicating very low correlations. Novo et al. (2021), in studies with Senepol heifers, found results of 0.51 (DMI and REA) and 0.18 (DMI and RFT), while more recent research with Guzerá animals by Pereira et al. (2023) found results of 0.31 for DMI and REA, 0.29 for REA and RFT, and 0.05 for DMI and RFT8. The impact of DMI on carcass traits is moderate, indicating that a reduction in feed intake does not significantly compromise muscle deposition but is correlated with fat deposition in the animals.

The genetic correlation between REA and RFT, and between REA and RFT8, were 0.02 ± 0.13 and -0.25 ± 0.10, respectively, indicative of low correlations. Consequently, indirect selection for any of these traits is unlikely to result in significant gains or losses. Previous literature indicates a low genetic correlation between REA and RFT, with Yokoo et al. (2015) reporting values of 0.22 and 0.19, and Ceacero et al. (2016) reporting values of 0.09 and 0.18, respectively. These observed variations may be attributed to genetic differences and the distinct environmental conditions under which the animals were reared.

The traits RFT, RFT8, and RFI and DMI exhibited strong correlations, with values of 0.66±0.06 and 0.77±0.06, respectively. Similar correlations for RFT and RFT8 have been documented previously by Yokoo et al. (2015) (0.67) and Ceacero et al. (2016) (0.79). Additionally, Novo et al. (2021) and Polizel et al. (2018) observed significant correlations for RFI and DMI, amounting to 0.71 and 0.61, respectively. These findings suggest a potential for rapid genetic gain through the indirect selection of these traits.

Conclusion

The estimates of heritability, which range from moderate to high for RFI and DMI, indicate that these traits are potential targets for direct selection. The genetic correlation between RFI and DMI and RFT and RFT8 confirms the presence of common genes that govern these traits. Conversely, the low correlations between feed efficiency and carcass traits suggest that selecting RFI or DMI does not adversely affect carcass traits, thereby enhancing productivity and profitability within meat production systems by selecting efficient animals.

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