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Genetic assessment of resilience indicators derived from dry matter intake, and feeding behavior using random regression models in beef cattle

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Introduction

Resilience to environmental challenges is a key attribute for productivity, animal welfare, and the sustainability of beef cattle production systems in tropical regions, particularly under climate change and increasing nutritional and health pressures (Berghof *et al*., 2019). In this context, the ability of animals to maintain stable performance and behavioral patterns in the face of environmental challenges becomes strategic for both production and genetic improvement (Gorssen *et al*., 2023). Animal resilience is defined as the ability to tolerate or rapidly recover from environmental challenges while maintaining biological functioning close to the expected trajectory (Rodrigues *et al*., 2024). Advances in precision livestock technologies have enabled the continuous collection of feed intake and feeding behavior data, which reflect sensitive responses to environmental stressors and allow a more detailed assessment of animal resilience capacity. Therefore, resilience indicators derived from residuals of predictive models applied to longitudinal data, such as residual variance and first-order autocorrelation, have been proposed to quantify the magnitude of environmental impact and the persistence of responses over time. Despite the potential of these indicators, studies evaluating their genetic variability and their relationships with performance traits in beef cattle remain limited, particularly when derived from feed intake and feeding behavior data. Hence, the objectives of this study were to derive resilience indicators from the residuals of random regression models applied to feed intake and feeding behavior traits, and to estimate heritability (h^2) and genetic correlations (r_g) using genomic information between these resilience indicators and feeding behavior, intake, and performance traits.

Materials & Methods

Phenotypic and genomic data. Data used in this study were obtained from Nellore experimental breeding program conducted by the Institute of Animal Science, Beef Cattle Research Center (Sertãozinho, SP, Brazil). Data was obtained from an existing database, and therefore, approval from the Ethics Committee was not required. The phenotypic dataset comprised records collected between 2013 and 2024, totaling 1,353 growing Nellore males. During the post-weaning period, animals were evaluated under a feedlot system and received an ad libitum diet formulated to meet the nutritional requirements of the category. Individual feed intake was recorded using GrowSafe® electronic feeding systems, allowing the collection of daily measurements of dry matter intake (DMI), total feeding time (FT), and number of feeding events (FE), resulting in 77,784 feeding behavior records. In addition, performance traits were considered, including average daily gain (ADG) and body weight adjusted to 378 days of age (W378). The pedigree comprised 13,351 individuals, and the genomic dataset included 3,860 genotyped animals with 383,856 SNP markers after quality control (removal of SNP and/or samples with Call Rate < 0.90, MAF < 0.05, Mendelian conflicts > 1.0%, and extreme deviations from Hardy-Weinberg Equilibrium P-value < 1×10^{-8}).

Derivation of resilience indicators. Longitudinal trajectories of DMI, FT, and FE were modeled using random regression models based on Legendre orthogonal polynomials describing the days of the feed efficiency test, with third-order polynomials fitted for DMI and fourth-order polynomials for FT and FE. The (co)variance components for the random regression models were estimated considering the ssGBLUP method and the AIREML algorithm. Based on the residuals obtained from the random regression models, resilience indicators were calculated for DMI, FT, and FE, including the natural logarithm of the residual variance (LnVar) and the first-order autocorrelation of deviations (r_{auto}).

Statistical analyses for genetic evaluation. The (co)variance components were estimated in a ssGBLUP framework considering the AIREML algorithm in the blupf90+ software (Misztal *et al*., 2014). Univariate analyses were conducted to estimate variance components and heritabilities of the evaluated traits, while bivariate analyses were performed to estimate genetic correlations between resilience indicators, feeding behavior traits, and performance traits. The systematic effects included the contemporary groups (concatenation of birth year and selection line), birth month (September-November), and cow age (in years) as both linear and quadratic covariates. Random effects included direct additive genetic effects for all traits, and for the resilience indicators; maternal genetic and maternal permanent environmental effects were also considered. Only for W378 and ADG, age at yearling (in days) was also included as a covariate.

Results and Discussion

Phenotypic aspects and heritability estimates. Table 1 presents the descriptive statistics and heritability estimates for performance traits, feed intake traits, and resilience indicators. Body weight adjusted to 378 days of age (W378) showed a mean of 350.52 ± 58.23 kg and a heritability of 0.36 ± 0.04, while average daily gain (ADG) averaged 0.96 ± 0.25 kg/day, with an estimated heritability of 0.28 ± 0.04. Regarding feed intake, dry matter intake (DMI) averaged 5.59 ± 1.13 kg/day (h^2 = 0.26 ± 0.04), and total feeding time (FT) averaged 59.54 ± 15.41 min/day, with a heritability of 0.42 ± 0.05. Resilience indicators exhibited substantial variability. Mean LnVar values ranged from 0.20 ± 0.42 for DMI to 5.46 ± 0.60 for FT and 5.09 ± 0.47 for FE, with heritability estimates varying between 0.16 ± 0.05 and 0.34 ± 0.05. In contrast, rauto showed mean values ranging from 0.05 ± 0.16 to 0.10 ± 0.17, with low heritability estimates, between 0.01 ± 0.02 and 0.03 ± 0.03.

Heritability estimates for resilience indicators highlight differences in the degree of genetic control among the evaluated metrics. Overall, LnVar-based indicators showed low to moderate heritabilities. Estimates within this range are consistent with previous reports, including 0.15 in dairy cattle (Poppe *et al*., 2020), approximately 0.12 in growing pigs (Gorssen *et al*., 2023), and higher estimates ranging from 0.22 to 0.42 in beef cattle (Rodrigues *et al*., 2025). Collectively, these results indicate that LnVar captures a genetic component associated with animals' sensitivity to environmental variation, regardless of the longitudinal metric considered, reinforcing its applicability as a resilience indicator across different types of repeated individual records.

In contrast, r_{auto}-based indicators exhibited low or near-zero heritability estimates, suggesting limited genetic influence on the speed of recovery following environmental perturbations. Similar estimates have been reported across species, with values around 0.04 in dairy cattle (Poppe *et al*., 2020) and estimates of 0.06 in pigs and 0.03 in sheep (Gorssen *et al*., 2023; Smith *et al*., 2025), indicating a strong influence of environmental and management factors on this resilience indicator. Nevertheless, r_{auto} provides complementary information to LnVar by capturing a distinct dimension of resilience related to the temporal persistence of deviations.

Table 1. Descriptive statistics and genetic parameter estimates for resilience indicators derived from feeding behavior traits. Number of observations (N), mean and standard deviation (Mean ± SD), observed range (Range), heritability and standard error (h^2 ± SE), additive genetic variance (σ^2_a), and residual variance (σ^2_e) are reported in the original units of each trait.

Trait[1]	N	Mean ± SD	Range	σ^2_a	σ^2_e	h^2 ± SE
W378 (kg)	1353	350.52 ± 58.23	125.71 - 512.29	657.81	1140.20	0.36 ± 0.04
ADG (kg/d)	1353	0.961 ± 0.249	-0.214 - 1.661	10280	26364	0.28 ± 0.04
DMI (kg/d)	1353	5.590 ± 1.134	2.21 - 11.00	0.260	0.760	0.26 ± 0.04
FT (min)	1353	59.54 ± 15.41	18.55 - 135.89	80.35	109.06	0.42 ± 0.05
FE	1353	79.80 ± 26.24	22.72 - 183.50	106.70	211.40	0.33 ± 0.05
DMI_{LnVar}	1353	0.196 ± 0.415	-1.271 - 1.544	0.02	0.08	0.24 ± 0.04
DMI_{rauto}	1353	0.087 ± 0.169	-0.468 - 0.750	0.001	0.03	0.03 ± 0.03
FT_{LnVar}	1353	5.463 ± 0.596	3.236 - 7.211	0.05	0.10	0.34 ± 0.05
FT_{rauto}	1353	0.101 ± 0.170	-0.416 - 0.641	0.001	0.02	0.01 ± 0.02
FE_{LnVar}	1353	5.091 ± 0.466	2.978 - 6.445	0.02	0.12	0.16 ± 0.04
FE_{rauto}	1353	0.048 ± 0.157	-0.479 - 0.548	0.001	0.02	0.02 ± 0.03

[1] W378: yearling weight adjusted to 378 days; ADG: average daily gain; DMI: daily dry matter intake; FT: total daily feeding time; FE: number of daily feeding events; DMI_{LnVar}: natural logarithm of the residual variance of daily dry matter intake; DMI_{rauto}: first-order autocorrelation of the residuals of dry matter intake; FT_{LnVar}: natural logarithm of the residual variance of feeding time; FT_{rauto}: first-order autocorrelation of the residuals of feeding time; FE_{LnVar}: natural logarithm of the residual variance of the number of feeding events; FE_{rauto}: first-order autocorrelation of the residuals of the number of feeding events.

Genetic correlations. Table 2 presents estimates of genetic correlations between resilience indicators derived from feed intake and feeding behavior (LnVar and r_{auto}) and performance and feed intake traits. In general, correlations involving LnVar-based indicators were predominantly positive and of moderate to high magnitude with W378, ADG, and DMI. Notably, genetic correlations between DMILnVar and W378, ADG, and DMI were 0.74 ± 0.11, 0.64 ± 0.14, and 0.65 ± 0.11, respectively. In contrast, correlations involving rauto showed high variability and standard errors larger than the estimates, resulting in genetically null associations, despite some point estimates of relatively high magnitude, such as those between FTrauto and W378 (0.84 ± 0.50) and ADG (0.98 ± 0.65).

Table 2. Genetic correlation between resilience derived from feed intake and feeding behavior and performance, feed intake, and feeding behavior traits.

Trait[1]	DMI		FT		FE	
	LnVar	r_{auto}	LnVar	r_{auto}	LnVar	r_{auto}
W378	0,74 (0,11)	0,19 (0,53)	-0,12 (0,05)	0,84 (0,50)	0,22 (0,12)	0,50 (1,30)
ADG	0,64 (0,14)	0,09 (0,46)	-0,06 (0,17)	0,98 (0,65)	0,23 (0,13)	0,44 (1,34)
DMI	0,65 (0,11)	0,18 (0,54)	-0,17 (0,13)	0,49 (0,89)	0,46 (0,12)	0,46 (0,82)
FT	0,02 (0,12)	-0,36 (1,11)	-0,41 (0,14)	-0,22 (0,51)	0,01 (0,18)	-0,20 (0,64)
FE	0,35 (0,12)	0,46 (0,87)	0,54 (0,13)	0,55 (0,76)	0,98 (0,03)	0,88 (1,08)

[1] W378: yearling weight adjusted to 378 days; ADG: average daily gain; DMI: daily dry matter intake; FT: feeding time; FE: feeding events; DMI_{LnVar}: natural logarithm of the residual variance of daily dry matter intake; DMI_{rauto}: first-order autocorrelation of the residuals of daily dry matter intake; FT_{LnVar}: natural logarithm of the residual variance of feeding time; FT_{rauto}: first-order autocorrelation of the residuals of feeding time; FE_{LnVar}: natural logarithm of the residual variance of the number of feeding events; FE_{rauto}: first-order autocorrelation of the residuals of the number of feeding events.

The observed genetic correlations indicate that LnVar-based resilience indicators are largely regulated by the same genes as performance and feed intake traits, suggesting that animals

genetically superior for growth and intake tend to exhibit greater magnitude of fluctuations over time. Similar findings have been reported in the literature, including a strong positive genetic correlation between LnVar and average milk yield across lactation (0.86 ± 0.03) in dairy cattle (Poppe *et al*., 2020), as well as correlations ranging from 0.35 to 0.70 in beef cattle, considering longitudinal indicators associated with female performance during gestation and their effects on offspring performance (Rodrigues *et al*., 2025). These results reinforce the consistency of LnVar as a resilience indicator applicable across different longitudinal traits.
Conversely, genetic correlations involving rauto were less consistent and accompanied by standard errors exceeding the estimates, characterizing genetically null associations. A similar pattern has been observed in previous studies, with low-magnitude correlations between rauto and productive traits, such as in sheep, where first-order autocorrelation of body weight ranged from −0.23 to 0.17 in association with wool production and quality traits (Smith *et al*., 2025), and in pigs, where correlations were close to zero, ranging from −0.09 to 0.03 for feed intake and carcass traits (Gorssen *et al*., 2023). These findings reinforce that rauto is strongly influenced by environmental and management conditions, while its joint interpretation with LnVar allows the capture of complementary dimensions of resilience related to both the intensity and temporal persistence of deviations in longitudinal data.

Conclusions

This study shows that resilience indicators derived from longitudinal feed intake and feeding behavior data have a detectable genetic basis in beef cattle. LnVar presented low to moderate heritability and consistent genetic associations with growth and intake traits. In contrast, rauto showed low heritability and null genetic correlations with performance traits, indicating that likely different sets of genes regulate the capacity of recovery and productivity of beef cattle. Although LnVar was positively correlated with performance traits, greater resilience was not necessarily associated with higher growth, highlighting that resilience and productivity are related but with distinct biological dimensions. Overall, LnVar-based indicators provide a practical framework for incorporating resilience into genetic evaluations using precision feeding data.

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