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Across-country correlations of feed efficiency traits in beef cattle

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Introduction

Selection for improved feed efficiency in beef cattle has the potential to improve the sustainability of food production systems globally. Feed costs can account for up to 70% of total production expenses, making efficient conversion of feed into body mass a major economic driver (Arthur *et al*., 2001; Berry and Crowley, 2013). Improved feed efficiency also reduces methane emissions and nutrient excretion, contributing to environmentally sustainable production (Basarab *et al*., 2013). However, improved feed efficiency in one production system may not translate to other production systems due to differences in feed composition, management practices, and environmental conditions. These differences pose a challenge for international breeding programs if the top bulls based on phenotypes in one production system do not provide improved feed efficiency across globally diverse production environments.

In 2025, Brazil surpassed the United States of America as the world's largest beef producer, driven by increased productivity, expanded feedlot finishing, improved genetics, and strong export demand. Despite both countries having high production, they have very different production systems: US production is characterized by high-energy feed, intense feedlot finishing, and younger slaughter age compared to low-moderate-energy feed, short-term feedlot finishing, and older slaughter ages in Brazil. Additionally, the use of growth hormones is widespread in the United States but prohibited in Brazil. Given these differences, sires of progeny with superior feed efficiency in the intensive production systems of the United States may not produce the most feed-efficient progeny in Brazil.

Feed efficiency is challenging and expensive to measure in beef cattle due to the need for specialized equipment for individual animal intake recording and controlled feeding environments. It is also biologically complex, impacted by maintenance energy requirements, diet, rumen microbiota, and animal behavior and physiology. One of the most widely used indicators of feed efficiency is residual feed intake (RFI), calculated as average daily dry matter intake (DMI) corrected for metabolic mid-weight (MMW), average daily gain (ADG), and sex. Because RFI is phenotypically independent of growth and body size, it has emerged as a popular measure of feed efficiency (Koch *et al*., 1963). Animals with lower RFI consume less feed than expected for their level of production and maintenance, making RFI a convenient trait for tracking feed efficiency.

The objective of this study was to estimate genetic parameters for feed efficiency traits in beef cattle from the United States and Brazil, evaluating potential regional differences in sire rankings. Leveraging a valuable dataset in which each sire had multiple progeny in each country, we assessed genetic parameters and sire rankings to inform data-driven strategies for international selection.

Materials & Methods

Data description. Phenotypic performance records and pedigree information were obtained from Angus-influenced beef cattle populations evaluated in the United States and Brazil. Animals evaluated in Brazil were from Angus × Nellore F1 crossbred population (ABS XBlack). After removing sires with fewer than two offspring recorded in each region, the final dataset comprised 1,369 animals from the United States and 588 animals from Brazil, representing progeny of 27 common sires. The distribution of progeny per sire differed

between regions, with an average of 50.8 (±63.9) progeny per sire in the USA and 21.8 (±21.0) progeny per sire in Brazil. This structure enabled estimation of across-country genetic parameters using shared sire information. All animals underwent approximately 45 days of feed intake testing at multiple facilities in the United States and Brazil, following standardized protocols. Feed efficiency traits evaluated in this study included ADG, DMI, and RFI measured in kilograms. Phenotypic records exceeding the mean ±3 standard deviations and contemporary groups containing fewer than two observations were excluded from the analysis.

Statistical analyses. Residual feed intake was calculated across the full dataset as the residual from a multiple regression model of DMI on metabolic body weight, ADG, and sex.

$$RFI = DMI - (\beta_0 + \beta_1 MMW + \beta_2 ADG + \beta_3 sex) \quad (1)$$

where RFI is residual feed intake, DMI is dry matter intake, MMW is metabolic mid-weight calculated as body weight raised to the power of 0.75, ADG is average daily weight gain, and sex is fitted as fixed effects. In this model, β_0 represents the intercept, whereas β_1, β_2, and β_3 are regression coefficients associated with MMW, ADG and sex, respectively.

Univariate PBLUP (pedigree based best linear unbiased mixed model) were applied to estimate heritabilities for each country separately:

$$\boldsymbol{y} = \boldsymbol{Xb} + \boldsymbol{Zs} + \boldsymbol{e} \quad (2)$$

Where $\boldsymbol{y}$ is the vector of phenotypic observations; $\boldsymbol{b}$ is the vector of fixed effects; $\boldsymbol{s}$ is the vector of random sire effects; and $\boldsymbol{e}$ is the vector of random residuals**.** $\boldsymbol{X}$ and $\boldsymbol{Z}$ are the incidence matrices relating observations to fixed and random effects, respectively. The fixed effects included contemporary group (the combination of farm of origin, feedlot, pen and on-test date), sex, and the covariate of age. The random sire effect follows a multivariate normal distribution $\boldsymbol{s} \sim \mathrm{N}(0, \boldsymbol{A}\sigma_s^2)$ where $\boldsymbol{A}$ is the numerator relationship matrix derived from a 3-generation pedigree for sires. Heritability was calculated as:

$$h^2 = \frac{4\sigma_s^2}{\sigma_p^2} \quad (3)$$

Where σ_s^2 is sire additive genetic variance, and σ_p^2 is phenotypic variance.

A bivariate sire model was fitted using phenotypic records from the United States and Brazil to estimate genetic and residual covariance components. The residual covariance between regions was fixed at zero due to the absence of animals evaluated in both environments. Genetic correlations were calculated as the estimated genetic covariance divided by the square root of the product of the corresponding genetic variances. All genetic parameter estimates were obtained using ASREML.

Results & Discussion

Estimations of heritability in feed efficiency traits from the United States and Brazil are presented in Table 1. Heritability for all evaluated traits were generally lower in the Brazilian population compared with the United States population. For ADG, the estimated heritability was 0.11 in Brazil and 0.20 in the United States. Similarly, heritability estimates for DMI were 0.11 in Brazil and 0.52 in the United States. RFI also exhibited lower heritability in Brazil relative to the United States. Moderate heritability estimates in the US population are consistent with previous reports (Arthur *et al*., 2001; Nkrumah *et al*., 2007). Lower heritability observed in the Brazilian population may reflect greater environmental variation, differences in management systems, genetic diversities in dam breeds, or smaller sample size.

Table 1. Estimation of genetic parameters for ADG, DMI and RFI.

	USA	Brazil		
Trait	$h^2 \pm$ SE	$h^2 \pm$ SE	Cor_p	$Cor_g \pm$ SE
ADG	0.20 ± 0.15	0.11 ± 0.12	0.025	-0.83 ± 0.84
DMI	0.52 ± 0.23	0.11 ± 0.10	-0.31	-0.22 ± 0.74
RFI	0.12 ± 0.11	0.05 ± 0.08	0.063	-0.91 ± 0.55

h^2= heritability; SE=standard error; Cor_p=phenotypic correlation; Cor_g =genetic correlation.

Phenotypic correlations based on progeny performance of the 27 common sires were low and positive across regions (Table 1), indicating limited consistency in sire performance between regions, which may reflect the presence of genotype-by-environment (G×E) interactions, as suggested in previous studies (Hayes *et al*., 2003; Mulder *et al*., 2006). In contrast, genetic correlations between the United States and Brazil were strongly negative for all traits and were associated with large standard errors (Table 1). The negative genetic correlation estimates observed between regions suggests the potential for sire re-ranking across production environments, indicating that genetic performance expressed in one country may not be fully transferable to another. Similar patterns have been reported for growth and fertility traits in international cattle populations (Weigel *et al*., 2001; Santana *et al*., 2016), and RFI and DMI have been shown to be sensitive to heat stress in cattle (Nascimento *et al*., 2025), supporting the possibility of G×E interactions. Differences in environmental conditions, including climate, diet composition, management practices, health protocols and production systems, may influence the expression of genetic components in feed efficiency traits. However, given the relatively large standard errors associated with the estimates, additional data and further investigation are needed to characterize significance of these G×E effects.

With the globalization of cattle genetics, elite sires are increasingly used across multiple countries and production systems to accelerate genetic gain and improve economic efficiency. While this strategy offers opportunities to disseminate superior genetics, G×E interactions may lead to re-ranking of sires across regions, potentially reducing the effectiveness of international breeding programs (Falconer and Mackay, 1996; Hayes *et al*., 2003). The use of sires across countries should be accompanied by careful evaluation of genetic correlations between environments. Selection strategies may benefit from incorporating region-specific performance data, multi-environment genetic evaluations, or environment-specific expected progeny differences (EPD) to account for potential G×E effects. Improving connectedness among populations through shared reference sires and expanded progeny testing across environments may further enhance the accuracy of across-country evaluations. Understanding genetic correlations of economically important traits across countries is therefore essential for designing effective selection strategies and breeding programs.

Conclusions

Improving feed efficiency is a critical strategy for enhancing both the sustainability and profitability of beef production systems. The results of this study indicate differences in the genetic architecture of feed efficiency traits between beef cattle populations evaluated in the United States and Brazil. Heritability estimates were generally, but not significantly, lower in the Brazilian population, and negative genetic correlations across regions indicated potential reranking of sires, although these estimates were associated with large standard errors. Collectively, these findings highlight the complexity of implementing universal genetic evaluations for feed efficiency traits across countries. Measuring progeny feed efficiency within each production environment may improve the accuracy of sires' EPD estimation, and the use of region-specific sire EPDs should be considered when making breeding decisions to support accurate selection and optimize genetic progress.

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