Feed Efficiency in Nellore Cattle (*Bos Indicus*): Impact of Molecular Breeding Value Estimation Methods in the Accuracy of Breeding Values Estimates

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ABSTRACT: Data from individually controlled feed consumption of 640 Nellore young bulls (DMI), average daily gain (ADG), feed conversion rate (FCR), residual feed intake (RFI) and residual intake and body weight gain (RIG), genotyped in Illumina Bovine SNP50 v2 DNA Analysis BeadChip were used. After quality control, 28,231 DNA markers were considered informative and were submitted to six approaches for estimation of molecular breeding values: Bayes A, Bayes B, Bayes C, Bayes Cπ, GBLUP and Single Step. Accuracies of genome-assisted expected progeny differences were compared with accuracies estimated from single traits REML BLUP analyses and the increment is reported in this paper. Very intense impacts of using molecular information were observed in genotyped animals, and their sires and dams, with genotyped young bulls estimates reaching accuracies as high as the ones of bulls with 45 or more progeny.

Keywords: *Bos indicus*; Beef cattle; Feed efficiency; Genome assisted EBV

Introduction

There is a global concern about the environmental impact of livestock production and competition for food, grain and supplements that can be used for humans and cattle. Beef cattle growth and feed efficiency are economically relevant traits for several beef production systems, as food is one of the most important components of costs, especially for feedlots, a growing tendency on intensive beef industry. Nellore is the most important beef breed in the Brazilian herd (Ferraz & Felicio (2010)), and, as the country is one of the major players in beef international market, several studies of feed efficiency and on genomics applied to economically important traits are being developed in Brazil and Latin America, on *Bos indicus* cattle (Pinto et al. (2011); Rezende et al. (2012); Silva et al., (2012); Montaldo et al., (2012); Gomes et al., (2013); Alexandre et al., (2014); Almeida et al., (2014a,b); Grion et al., (2014)). However, to date, there is no consensus about the most adequate model for evaluation of feed efficiency in *Bos indicus.*

The objective of this study was to evaluate the effect of incorporation of genomic information on the accuracy of Expected Progeny Differences (EPD), of five traits related to feed efficiency in Nellore cattle.

Materials and Methods

Data and trait definition. Records of 640 Nellore (*Bos indicus*) males, born between 2005 and 2011, with age of 611.5±100.4 days and 388.9±45.7 kg were used in 11 experiments of individual control of feed intake, realized from 2007 to 2012 with days in feed from 70 to 90 days. Measured traits were: Dry matter intake (DMI) for each animal, adjusted to dry matter; Average daily gain (ADG). The feed efficiency traits, feed conversion ratio (FCR), residual feed intake (RFI) and residual intake and body weight gain (RIG) were calculated using DMI and ADG.

Models for trait calculations. FCR was calculated by ratio of DMI by ADG, while RFI and RIG represent the residues (ε_1 and ε_2) of regression equations that estimated DMI and ADG, respectively. Contemporary groups (CG) considered as the different experiments. The sexual condition (steers and young bulls) was included as a covariate in the statistical models. The models for estimating these traits were:

$$DMI = \beta_0 + \beta_1 ADG + \beta_2 MBW^{0.75} + \beta_3 SC + \beta_4 CG + \varepsilon_1$$

$$ADG = \beta_0 + \beta_1 DMI + \beta_2 MBW^{0.75} + \beta_3 SC + \beta_4 CG + \varepsilon_2$$

The parameters (β) estimated based on the PROC MIXED procedure of the SAS software.

RIG was calculated by:

$$RIG = RG + (-1RFI)$$

Adjustment of phenotypes: Records were adjusted to fixed effects, estimated on single trait analyses performed by MTDFREML (Boldman et al., 1995) under animal model. Fixed effects fitted were contemporary group, age and weight at the begging of the experiment were taken into account as quadratic covariates, considering 1055 phenotyped animals, from which only 640 were genotyped. This strategy was used to better estimate fixed effects.

Allele substitution effect and estimation of molecular breeding values (MBV). These values were estimated by GWAS methodologies Bayes A, Bayes B, Bayes C and Bayes Cπ, using the software GenSel (e-BIGS, Fernando & Garrick (2013); Garrick & Fernando (2013); in Gondro et al. (2013), chapters 10 & 11, available at http://bigs.ansci.iastate.edu/). The analysis considering GBLUP and Single Step were performed using BLUPF90 (Misztal et al. (2009), available at http://nce.ads.uga.edu/~ignacy/ newprograms.html).

Table 1. Variance components used in single-trait REML animal model analysis

Trait	Genetic variance	Residual variance	Heritabilty
DMI	0.262	0.499	0.34
ADG	0.029	0.068	0.42
FCR	0.160	3.800	0.04
RFI	0.085	0.560	0.13
RIG	0.106	0.855	0.11

DMI - Dry matter intake; ADG - Average daily gain; FCR – feed conversion rate; RFI - residual feed intake, RIG - residual intake and body weight gain

Table 2. Variance components used in Bayes A, Bayes B, Bayes C and Bayes Cπ, GBLUP and Single Step analysis

Trait	Method (Bayes)	Genetic variance	Residual variance	Genomic h^2	Π (%)
DMI	A	0.712	0.861	0.453	
	B	0.635	0.935	0.404	1.5
	C	0.623	0.940	0.399	1.5
	Cπ	0.641	0.915	0.411	61.2
ADG	A	0.019	0.063	0.237	
	B	0.018	0.064	0.217	1.5
	C	0.021	0.061	0.258	1.5
	Cπ	0.016	0.066	0.190	75.1
FCR	A	0.421	2.448	0.147	
	B	0.436	2.416	0.153	1.5
	C	0.436	2.416	0.153	1.5
	Cπ	0.347	2.517	0.121	91.4
RFI	A	0.107	0.695	0.133	
	B	0.092	0.707	0.116	1.5
	C	0.119	0.690	0.147	1.5
	Cπ	0.023	0.762	0.030	99.4
RIG	A	0.135	1.054	0.114	
	B	0.135	1.054	0.114	1.5
	C	0.149	1.042	0.125	1.5
	Cπ	0.027	1.140	0.023	99.9

DMI - Dry matter intake; ADG - Average daily gain; FCR – feed conversion rate; RFI - residual feed intake, RIG - residual intake and body weight gain

Bayesian analysis were performed in with 41,000 iterations and burn-in of the first 1,000. The variance components used for single-trait analysis are presented in Table 1. The prior genetic and residual variances were estimated using Bayes C, with π = 0,015. These genetic parameters used in the six approaches for estimating MBV, in Table 2 and the variance components for two-trait analysis in Table 3. Similar varcomp were used for GBLUP and Single Step analysis.

The ghats generated by each method were considered as MBV for each animals and used, for Bayes A. B, C and Cπ, as a second trait in two-trait analysis under REML animal model (MTDFREML, Boldman et al., 1995), being the first trait the phenotypes for DMI, ADG, FCR, RFI and RIG, in proper models. Accuracies were considered the correlation between the estimate and the "true" value ($r_{T,I}$). Accuracies from the two-trait analysis, that generated genome assisted EPD, were compared to the single trait analysis using the traits and proper models, which generated normal EPD and their accuracies for each animal in the pedigree. Those comparisons were made for 3 classes of animals: young bulls, genotyped, sires and dams.

The concept equivalent progeny number was calculated as a quadratic regression of accuracy for a given bull, on its progeny number.

Table 3. Variance components used in two traits REML analysis, considering molecular breeding values from Bayes A, Bayes B, Bayes C and Bayes Cπ analysis and second traits

Trait	Method	Genetic variance of MBV	Residual variance of MBV	h^2 of MBV	Genetic correlation
DMI	Bayes A	0.142	0.060	0.70	0.86
	Bayes B	0.143	0.021	0.87	0.97
	Bayes C	0.129	0.222	0.85	0.96
	Bayes Cπ	0.138	0.022	0.86	0.99
ADG	Bayes A	0.003	0.001	0.71	0.85
	Bayes B	0.003	0.001	0.69	0.82
	Bayes C	0.005	0.001	0.84	0.98
	Bayes Cπ	0.002	0.001	0.62	0.76
FCR	Bayes A	0.045	0.010	0.82	0.45
	Bayes B	0.040	0.023	0.63	0.95
	Bayes C	0.059	0.007	0.90	0.90
	Bayes Cπ	0.026	0.023	0.53	0.96
RFI	Bayes A	0.009	0.005	0.63	0.98
	Bayes B	0.022	0.009	0.70	0.84
	Bayes C	0.010	0.006	0.60	0.97
	Bayes Cπ	0.007	0.004	0.62	0.97
RIG	Bayes A	0.007	0.005	0.60	0.66
	Bayes B	0.006	0.003	0.68	0.83
	Bayes C	0.010	0.004	0.72	0.99
	Bayes Cπ	0.001	0.001	0.60	0.62

DMI - Dry matter intake; ADG - Average daily gain; FCR – feed conversion rate; RFI - residual feed intake, RIG - residual intake and body weight gain

Results and Discussion

The impact of the incorporation of genomic information in the accuracy of estimates of breeding values for these very difficult and expensive to measure traits, is presented in Table 4. It is important to express these impacts by class of animals (genotyped young bulls, their sires and dams). Very important enhance of accuracy can be observed for genotyped animals, especially for FCR, RFI and RIG and for MBV estimated by Bayesian methods. Less important increases were observed for DMI and ADG. Young bulls' sires and dams, although not genotyped, obtained large increments on their accuracies when their genomic assisted EPV for FCR, RFI and RIG were estimated, similarly to what happened with genotyped animals. Differences of increment on accuracies can be explained by different assumptions of each method, like variance of markers, number of markers considered important, etc.

The mean accuracy of young bulls, depending on trait and method of estimation of MBV reached values as high as .99 (DMI, Bayes Cπ), .96 (ADG, Bayes B), .95 (FCR, GBLUP), .94 (RFI, Bayes C) and .97 (RIG, Bayes C) equivalent to the accuracy of bulls with, respectively, 30,

23, more than 45 and more than 45 progeny. That reduces the risk of selection decisions, and generation interval, if young bulls are used. Results support the importance of genotyping young animals measured for feed efficiency and the use of molecular breeding values in the estimation of EPD has important impact of accuracies, even in non-genotyped sires and dams. However, as MBV and original phenotypes have a linear combination that increment on accuracy should have been overestimated.

Table 4. Impact on accuracy of EBV, expressed as percentage of increment in relation to single-trait analysis, when using molecular breeding value (MBV) estimated by different methods.

Trait	Method of estimation of MBV	Impact on accuracy Young bulls	Sires	Dams
DMI	Bayes A	20.0	7.4	16.8
	Bayes B	53.2	30.5	50.2
	Bayes C	49.4	27.3	46.2
	Bayes Cp	59.0	34.6	55.5
	GBLUP	0.9	-4.4	-2.8
	Single Step	15.8	7.2	12.7
ADG	Bayes A	10.4	1.9	7.1
	Bayes B	6.7	-0.4	3.2
	Bayes C	41.8	22.5	38.2
	Bayes Cp	2.1	-3.1	-1.5
	GBLUP	2.4	-3.0	-1.1
	Single Step	14.6	4.0	11.1
FCR	Bayes A	62.6	37.0	64.0
	Bayes B	247.0	179.8	255.7
	Bayes C	232.1	168.5	240.5
	Bayes Cp	253.5	184.2	261.7
	GBLUP	257.5	187.5	266.2
	Single Step	229.8	165.2	237.2
RFI	Bayes A	124.4	82.4	124.0
	Bayes B	79.5	48.7	78.9
	Bayes C	120.4	79.7	120.4
	Bayes Cp	118.0	77.8	117.9
	GBLUP	30.7	14.0	28.4
	Single Step	31.7	14.9	29.7
RIG	Bayes A	39.1	22.7	36.5
	Bayes B	144.4	98.1	144.3
	Bayes C	144.5	98.7	144.8
	Bayes Cp	34.0	19.4	31.4
	GBLUP	15.7	6.0	11.3
	Single Step	16.8	6.7	13.0

DMI - Dry matter intake; ADG - Average daily gain; FCR – feed conversion rate; RFI - residual feed intake, RIG - residual intake and body weight gain

Conclusion

The incorporation of molecular information in the estimation of EPD of Nellore cattle can be useful as it produces increments in the level of accuracy of the genomic assisted estimations. This incorporation might decrease risk in selection decisions, and increases genetic gain/year, both by increasing accuracy and decreasing generation interval, when using young replacement genotyped bulls. Further studies, using cross validation need to be implemented.

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