Estimates of genetic parameters for carcass, growth and reproductive traits in Nellore cattle

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ABSTRACT

The objective of this study was to estimate genetic parameters for female mature weight (FMW), age at first calving (AFC), weight gain from birth to 120 days (WG_B_120), from 210 to 365 days (WG_210_365), rib eye area (REA), back fat thickness (BF), rump fat (RF) and body weight at scanning date (BWS) using single and multiple-trait animal models by the REML method from Nellore cattle data. The estimates of heritability ranged from 0.163 ± 0.011 for WG_210_365 to 0.309 ± 0.028 for RF using the single-trait model and from 0.163 ± 0.010 for WG_210_365 to 0.382 ± 0.025 for BWS using the multiple-trait model. The estimates of genetic correlations ranged from -0.35 ± 0.08 between AFC with BF to 0.69 ± 0.04 between WG_B_120 with BWS. Selection for weights gains, REA, and BWS can improve FMW.

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1. Introduction

Beef cattle breeding programs require knowledge of genetic relations between productive efficiency with reproductive performance of females due to the economic importance and maintenance costs of the cows in the herd, respectively (Talhari et al., 2003). According to Short et al. (1994), the major advantages of impregnating young heifers were lesser time of investment return and increase in the cow's reproductive life, and in the number of calves.

Body weight and weight gain are associated with the economic efficiency of any beef cattle production system. Estimates of heritability of moderate magnitude for these traits were reported by Boligon et al. (2010a), Martínez-González et al. (2010) and Regatieri et al. (2012), which indicated that a considerable proportion of the variation in these traits was explained by the additive action of the genes, and there were positive genetic correlation between them. It may result in genetic progress for body weight and weight gain when one of them was selected.

Positive genetic correlation between sexual maturity with body weight in young and adult ages of the animals were found in literature (Bullock et al., 1993; Castro-Pereira et al., 2007; Jenkins et al., 1991). Selection for high body weight at young ages can improve body weight at sexual maturity and reproductive performance of the cows due to favorable genetic association with these traits, measured at different ages of the animals (Silva et al., 2000).

Carcass traits such as meat production and subcutaneous fat are also of economic importance and must also be taken into account in genetic breeding programs to determine the return on investment in beef cattle production system. Rib eye area relates to the quantity of muscle, carcass yield and, especially, the proportion of prime

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cuts (Magnabosco et al., 2006). Back fat thickness measured on the *Longissimus dorsi* muscle is an efficient indicator of carcass finish and it is important for the Nellore beef cattle meat industry because it acts as thermal insulation during the carcass chilling process avoiding lose of meat quality (Guedes, 2005). Study rump fat is important especially in relation to animals raised on pasture, since at the age when the ultrasound images are made, it is seen to develop earlier than rib fat does and measurements on this trait are more accurate and presented higher repeatability than do back fat thickness measurements (Costa and Yokoo, 2004).

It is recommended to estimate the genetic parameters simultaneously for all economic important traits (i.e., reproduction, growth and carcass traits). The objective of this study was to estimate genetic parameters for female mature weight, age at first calving, weight gain from birth to 120 days, weight gain from 210 to 365 days, rib eye area, back fat thickness, rump fat and body weight at scanning date from Nellore cattle data.

2. Material and methods

2.1. Animals and data

Records of 133,801 Nellore animals, born between 1998 and 2008, belonging to 23 farms participating in Nellore Cattle Breeding Program of the Association of Breeders and Researchers, Ribeirão Preto, São Paulo, Brazil, were used for the analyses. They were reared on pasture without supplementation. Calves were weaned at 6–8 months of age. The reproductive management consisted of a breeding season of 90–130 days using artificial insemination or controlled natural breeding. See Gunski et al. (2001) for more details about the reproductive management. Body weights and male scrotal circumferences were measured at birth and every 3 months up to at least the age of 18 months.

Total genetic merit is an empirical selection index, developed by the Nellore Brazil program, was used for selecting sires and dams that were genetically superior (Lôbo et al., 2008). This index includes estimates of breeding values for the following traits (with their respective weighting factors in brackets): maternal ability (0.20), pre-weaning weight gain (0.20), post-weaning weight gain (0.20), one-year weight gain (0.20) and scrotal circumference at 365 days of age (0.10) and 450 days of age (0.10).

2.2. Traits

The traits used in the analyses were female mature weight (FMW), age at first calving (AFC), weight gain from birth to 120 days (WG_B_120), weight gain from 210 to 365 days (WG_210_365), rib eye area (REA), back fat thickness (BF), rump fat (RF) and body weight at scanning date (BWS). The mean and standard deviation of age at scanning date was 559.21 ± 59.04 days, ranging from 450 to 790 days of age. The mature weight, weight gains and body weight at scanning date were expressed in kilogram. AFC were measured in months. REA were expressed in square centimeters and BF and RF were measured in millimeters. Only animals with both parents known were used in the analysis. The birth season was defined as the rainy season (animals born between October and March) and dry season (animals born between April and September).

The REA and BF were obtained from cross-sectional images of the *longissimus* muscle (LM) between the 12th and 13th ribs. Back fat thickness was estimated at the 3/4 position from the chine bone end of the LM using the cross-sectional REA image. Further, RF was measured over the intersection between the *gluteus medium* and *biceps femoris* muscles located between the hooks and pin bones.

The ultrasound images were collected and interpreted in accordance with the methodology recommended by the UGC. Further details about the RTU measurements can be found in Yokoo et al. (2008) and Yokoo et al. (2010). Female mature weight (FMW) was the body weight from 4 to 12 years of age related to maintenance costs and growth rate of the cows. The body weights were standardized to body weight at birth, at 120 days, at 210 days, at 365 days and FMW. The WG_B_120 were calculated by the difference between body weight at 120 days of age and body weight at birth and the WG_210_365 by the difference between body weight at 365 days and body weight at 210 days.

Table 1
Effects that composed the contemporary group for each trait.

Trait	Management group (farm+heard)				Sex	Year	Season
	At 120 days	At 210 days	At 365 days	At 450 days			
FMW	$P=0.85$	$P=0.51$	$P=0.06$	$P<0.05^*$	–	$P<0.01^{**}$	$P<0.01^{**}$
AFC	$P=0.07$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	–	$P<0.01^{**}$	$P<0.01^{**}$
WG_B_120	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$
WG_210_365	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$
REA	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$
BF	$P=0.83$	$P=1.00$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$
RF	$P<0.05^*$	$P=0.99$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$
BWS	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$	$P<0.01^{**}$

FMW=female mature weight; AFC=age at first calving; WG_B_120=weight gain from birth to 120 days; WG_210_365=weight gain from 210 to 365 days; REA=rib eye area; BF=back fat thickness; RF=rump fat thickness; BWS=body weight at scanning date (days).
* Significant at 5%.
** Highly significant at 1%.

2.3. Statistical analysis

Least-squares analyses were performed by the GLM procedure of the SAS Software (SAS 9.2, SAS Institute, Cary, NC, USA), to define the fixed effects of the mixed models. The fixed effect of contemporary groups (CG) was defined concatenating season and year of birth of the animals, sex, and management group of animals (defined as number of farm and heard at 120, 210, 365 and 450 days). The fixed effect of CG was significant ($P < 0.05$) for all traits and it was formed in a different manner for each trait (Table 1).

If the range of ages in a CG was higher than 60 days for AOL, BF, RF and BWS, the CG was subdivided into 60-day intervals, a practice commonly referred to as 'age slicing', limiting the difference in ages among animals which were directly compared (Meyer, 2005). 'Age slicing' limited the range of ages of animals which were directly compared with each other. The covariate age of dam at calving (linear and quadratic effects) was included into the model for AFC, WG_B_120, WG_210_365, REA, BF, RF and BWUS ($P < 0.05$) and the covariate age of animal at scanning (linear and quadratic effects) was included only for REA, BF, RF and BWS ($P < 0.05$). The assumptions of variance analysis on each trait were checked and records with standardized residuals above 3.5 or below −3.5 standard deviations were excluded.

2.4. Estimates of genetic parameters

The estimates of (co)variance components were obtained by using the restricted maximum likelihood method (REML), in a single and multiple-trait animal model, using the WOMBAT program (Meyer, 2007). The general animal model included contemporary group and covariates as fixed effects and the additive genetic and residual as random effects.

The maternal genetic effect for all the traits, except for BF and RF, was included in the single-trait animal model. Permanent environmental random effect was added only for WG_B_120. But the structure of the data allowed estimating the variance components for maternal and permanent environment only for WG_B_120 in multi-trait animal model.

The single-trait analyses were kept in this study to present the variance components of the maternal and permanent environment effects of the traits. In the results and discussion section only the estimates of heritability from multi-trait animal model was used to compare with the results from literature, as the goal of this study was not to make comparisons between the estimates of genetic parameters using different models.

The covariance between direct and maternal genetic effects was set to zero as suggested by Albuquerque and Meyer (2001), Benyshek et al. (1988), and Meyer (1997). The relationship matrix included 136,980 animals born between 1998 and 2008. The convergence criterion for carrying out the analyses was 10^{-5}.

The matrix representation of the general animal model is:

$$y = Xb + Z_1a + Z_2m + Z_3p + e$$

where y is the vector of observations; b, vector of fixed effects; a, vector of direct additive genetic effects; m, vector of maternal additive genetic effects; p, vector of maternal permanent environmental effects; and e, vector of residual random errors associated with the observations. X, Z_1, Z_2 and Z_3 are the incidence matrices related to b, a, m and p to y. It is assumed that $E[y] = Xb$, $\text{Var}(a) = A \otimes \Sigma a$, $\text{Var}(m) = A \otimes \Sigma m$, $\text{Var}(p) = I_{N_m} \otimes \Sigma p$ and $\text{Var}(e) = I_N \otimes \Sigma e$, which Σa is the matrix of direct additive genetic (co)variances between traits; Σm is the maternal additive genetic covariance matrix; Σp, maternal permanent environmental covariance matrix; Σe, residual covariance matrix; A, relationship matrix; I, identity matrix, N_m, number of dam of animals with records, N, number of animals with records and $\otimes$, the direct product between matrices. It is assumed that m and p were not correlated.

3. Results and discussion

The descriptive statistics for the studied traits are in Table 2 and the covariance components and estimates of heritability are in Tables 3 and 4 for single and multi-trait animal model, respectively. The estimate of heritability for FMW was 0.32 ± 0.041 using multi-trait model indicating that this trait had moderate proportion of additive genetic variation and it could respond to selection. Pedrosa et al. (2010) reported estimates of heritability of 0.43 for mature weight from Nellore females of different herds. Kaps et al. (1999) studied mature weight in Angus cattle and reported estimates of heritability ranged from 0.44 to 0.53 suggesting the inclusion of mature weight in economic selection indexes to evaluate what biotypes are compatible with the production

Table 2
Number of records (n), mean, standard deviation (SD), coefficient of variation (CV), minimum and maximum values and total of contemporary groups (CG) for each studied trait in Nellore cattle.

Traits (unit)	n	Mean	SD	CV (%)	Minimum	Maximum	CG
FMW (kg)	3796	484.13	66.33	13.70	280.00	765.00	120
AFC (months)	16,323	35.40	4.97	14.04	21.00	49.00	737
WG_B_120 (kg)	62,212	94.12	18.47	19.63	24.00	186.00	2558
WG_210_365 (kg)	49,267	55.47	26.06	46.97	1.00	247.00	673
REA (cm²)	11,335	52.75	10.18	19.31	21.86	100.87	77
BF (mm)	12,484	2.48	1.11	44.82	0.40	13.72	393
RF (mm)	12,522	3.18	1.66	52.21	0.40	14.22	59
BWS (kg)	9611	342.77	54.13	15.79	193.00	582.00	9

FMW=female mature weight; AFC=age at first calving; WG_B_120=weight gain from birth to 120 days; WG_210_365=weight gain from 210 to 365 days; REA=rib eye area; BF=back fat thickness; RF=rump fat thickness; BWS=body weight at scanning date (days).

Table 3
Estimates of (co)variance components and genetic parameters for carcass traits, age of first calving and growth traits with single-trait animal model.

Parameters[a]	Traits[b]							
	FMW	AFC	WG_B_120	WG_210_365	REA	BF	RF	BWS
σ_a^2	914.66	2.692	44.88	48.786	15.07	0.109	0.29	355.22
σ_e^2	2150.90	13.420	122.74	248.44	32.72	0.367	0.64	816.33
σ_m^2	52.44	0.162	15.58	2.201	1.487	–	–	20.309
σ_p^2	–	–	27.72	–	–	–	–	–
h_a^2	0.293 ± 0.051	0.165 ± 0.020	0.213 ± 0.012	0.163 ± 0.011	0.306 ± 0.028	0.228 ± 0.024	0.309 ± 0.028	0.298 ± 0.034
h_m^2	0.017 ± 0.022	0.010 ± 0.008	0.074 ± 0.008	0.007 ± 0.003	0.030 ± 0.011	–	–	0.017 ± 0.012
p^2	–	–	0.131 ± 0.007	–	–	–	–	–

[a] σ_a^2 = direct additive genetic variance; σ_e^2 = environmental variance; σ_m^2 = maternal additive genetic variance; σ_p^2 = variance due to maternal permanent environmental effects; h_a^2 = heritability of direct effects and standard error; h_m^2 = heritability of maternal effects and standard error and p^2 = maternal permanent environmental as proportions of phenotypic variances.
[b] FMW = female mature weight; AFC = age at first calving; WG_B_120 = weight gain from birth to 120 days; WG_210_365 = weight gain from 210 to 365 days; REA = rib eye area; BF = back fat thickness; RF = rump fat thickness; BWS = body weight at scanning date (days).

Table 4
Estimates of (co)variance components and genetic parameters for carcass traits, age of first calving and growth traits with multi-trait animal model.

Parameters[a]	Traits[b]							
	FMW	AFC	WG_B_120	WG_210_365	REA	BF	RF	BWS
σ_a^2	1050.80	2.73	50.40	48.82	17.34	0.11	0.30	507.57
σ_e^2	2234.30	13.56	122.45	249.93	33.14	0.38	0.66	820.99
σ_m^2	–	–	13.60	–	–	–	–	
σ_p^2	–	–	24.00	–	–	–	–	
h_a^2	0.320 ± 0.041	0.168 ± 0.018	0.239 ± 0.013	0.163 ± 0.010	0.343 ± 0.025	0.230 ± 0.022	0.31 ± 0.026	0.382 ± 0.025
h_m^2	–	–	0.065 ± 0.007	–	–	–	–	
p^2	–	–	0.114 ± 0.007	–	–	–	–	

[a] σ_a^2 = direct additive genetic variance; σ_e^2 = environmental variance; σ_m^2 = maternal additive genetic variance; σ_p^2 = variance due to maternal permanent environmental effects; h_a^2 = heritability of direct effects and standard error; h_m^2 = heritability of maternal effects and standard error and p^2 = maternal permanent environmental as proportions of phenotypic variances.
[b] FMW = female mature weight; AFC = age at first calving; WG_B_120 = weight gain from birth to 120 days; WG_210_365 = weight gain from 210 to 365 days; REA = rib eye area; BF = back fat thickness; RF = rump fat thickness; BWS = body weight at scanning date (days).

system, once direct selection for mature weight could change female size and, consequently, nutritional requirements.

The estimates of heritability for WG_B_120 and WG_210_365 were 0.239 ± 0.013 and 0.163 ± 0.010, respectively. Boligon et al. (2010b) reported estimates of heritability of 0.23 ± 0.03 and 0.25 ± 0.03 for average gains from weaning to yearling and yearling to after yearling, respectively. Paneto et al. (2002) reported estimates of heritability of 0.16 for average gains from weaning to yearling and of 0.21 and yearling to after yearling. In this study, the heritability estimates for weight gain in different ages were of moderate magnitude, indicating that these traits could respond to selection, improving genetically the weight gain for the corresponding period.

In this study, the heritability estimates for AFC (0.168 ± 0.018) was close to those reported by Boligon et al. (2010b), Guindolin et al. (2010) and Talhari et al. (2003) of 0.13, 0.18 and 0.14, respectively. This result indicated that this trait had low proportion of additive genetic variance to total of the traits and could respond slowly to the selection process.

The heritability estimates were 0.343 ± 0.025, 0.230 ± 0.022, 0.31 ± 0.026 and 0.382 ± 0.025 for REA, BF, RF and BWS, respectively, indicating that these traits could respond to selection. If the purpose is to change the subcutaneous fat, faster genetic changes could be reached with the use of RF than the BF, because the first one had higher estimate of heritability compared with the second trait. Yokoo et al. (2010) reported heritability of 0.29 ± 0.07 for REA, 0.50 ± 0.09 for BF and 0.39 ± 0.09 for RF from Nellore cattle. Zuin et al. (2012) found heritability of 0.29 ± 0.03, 0.21 ± 0.02 and 0.23 ± 0.03 for REA transformed as $REA^{0.4}$, BF transformed as $\log_{10}(BF)$ and RF transformed as $\log_{10}(RF)$, respectively. Guindolin et al. (2010) reported that back fat thickness and *longissimus* muscle area had heritability's estimates of 0.51 and 0.48, respectively.

The estimate of heritability for maternal genetic effect of weight gain from birth to 120 days was 0.065 ± 0.007 using multi-trait model. This indicated that this effect needed to be taken into account in the genetic analyses to obtain more accurate estimates of breeding values. Estimates of maternal heritability ranged from 0.007 ± 0.003 for WG_210_365 to 0.074 ± 0.008 for WG_B_120 in the single-trait analyses. It is possible using single-trait model including maternal genetic and maternal permanent environment effects to obtain more

Table 5

Estimates of direct additive genetic correlations (above the diagonal) and residuals correlations (below the diagonal) for the traits analyzed[a].

	FMW	AFC	WG_B_120	WG_210_365	REA	BF	RF	BWS
FMW	–	0.11 ± 0.10	0.59 ± 0.07	0.36 ± 0.10	0.32 ± 0.09	0.19 ± 0.10	0.11 ± 0.09	0.63 ± 0.08
AFC	-0.03 ± 0.03	–	-0.02 ± 0.06	-0.34 ± 0.07	-0.25 ± 0.08	-0.35 ± 0.08	-0.19 ± 0.08	-0.21 ± 0.07
WG_B_120	0.30 ± 0.03	-0.13 ± 0.02	–	-0.09 ± 0.01	0.41 ± 0.05	0.08 ± 0.06	-0.01 ± 0.06	0.69 ± 0.04
WG_210_365	0.14 ± 0.04	-0.07 ± 0.02	-0.09 ± 0.01	–	0.33 ± 0.06	0.36 ± 0.08	0.26 ± 0.07	0.53 ± 0.05
REA	0.08 ± 0.07	-0.11 ± 0.04	0.29 ± 0.02	0.25 ± 0.02	–	0.19 ± 0.06	0.18 ± 0.06	0.68 ± 0.03
BF	-0.02 ± 0.05	-0.10 ± 0.03	0.09 ± 0.02	0.11 ± 0.02	0.27 ± 0.02	–	0.65 ± 0.04	0.11 ± 0.06
RF	-0.09 ± 0.06	-0.14 ± 0.03	0.07 ± 0.02	0.12 ± 0.02	0.25 ± 0.02	0.57 ± 0.01	–	0.08 ± 0.06
BWS	0.20 ± 0.07	-0.13 ± 0.04	0.44 ± 0.02	0.40 ± 0.02	0.61 ± 0.02	0.29 ± 0.02	0.30 ± 0.02	–

[a]FMW=female mature weight; AFC=age of first calving; WG_B_120=weight gain from birth to 120 days; WG_210_365=weight gain from 210 to 365 days; REA=rib eye area; BF=back fat thickness; RF=rump fat thickness; BWS=body weight at scanning date (days).

accurate estimates of breeding values when the structure of the data does not allow estimating the variance components of these effects in a multi-trait model. But it must to take into account that the maternal heritability had lower magnitude for all traits compared with WG_B_120 (0.074 ± 0.008; Table 3), and the estimates of standard errors were of the same magnitude of estimates of maternal heritability, indicating that this effect may be close to zero and may not cause a lot of differences for predicting the breeding values when it is not taken into account in the model, except for WG_B_120.

The genetic correlation between FMW and AFC (Table 5) was 0.11 ± 0.10 indicating that selection on AFC could cause little genetic changes on mature weight. On the other hand, Boligon et al. (2010b) reported low and negative genetic correlations between age at first calving and body weight at two (-0.20), and five (-0.14) years of age. Boligon and Albuquerque (2011) also reported low and negative genetic correlation between these two traits (-0.12 ± 0.05) estimated by Bayesian method. These differences in genetic correlations could be by differences in the data structure and in statistical modeling.

The genetic correlations between FMW with WG_B_120 and between FMW with WG_210_365 were positive and of moderate magnitude, indicating that animals with greater weight gains tends to present higher mature weight (Table 5). Thus, the selection based on weight gains could increase the weight of mature animals, which is not always desired. Boligon et al. (2010b) reported lower genetic correlations between female mature weight with average weight gains from weaning to yearling (0.30) and from yearling to after yearling (0.32), in Nellore cattle, when compared with this study. Regatieri et al. (2012) found genetic correlation between mature weight with weight gain from birth to weaning and with weight gain from weaning to yearling of 0.47 ± 0.03 and 0.58 ± 0.02 in Nellore cattle, respectively.

The genetic correlation between the carcass termination traits (REA, BF and RF) with FMW were 0.32 ± 0.09, 0.19 ± 0.10 and 0.11 ± 0.09, respectively, indicating that selection for carcass traits, especially for REA, would increase the mature weight. Yokoo et al. (2010) showed moderate and positive genetic correlations of body weight at different ages (120, 210, 365, 450, and 550 days of age) with longissimus muscle area and close to zero with subcutaneous fat traits (BF and RF) in Nellore cattle. No previous genetic correlations between FMW and carcass

traits measured by real-time ultrasound were found in the literature. The genetic correlation between FMW and BWS was 0.63 ± 0.08 indicating that selection for this trait could change genetically the body weight at maturity.

The genetic association between AFC with WG_B_120 was close to zero and between AFC with WG_210_365 was -0.34 ± 0.07 (Table 5), indicating that additive genes for weight gain between 210 and 365 days could be connected somehow to those responsible for sexual precocity of the animal. So, animals that gained more weight between 210 and 365 days may be more sexually precocious. But AFC and WG_210_365 had little influence of the additive genes due to the low heritability estimates (Table 4) and, consequently, it could be more difficult to obtain genetic gains for these traits by the selection process. The genetic association between WG_B_120 with WG_210_365 was low (Table 5), indicating the action of different additives genes at different stages of animal weight gain.

The genetic correlation between AFC with subcutaneous fat traits (BF and RF) was negative and of low to moderate magnitude (Table 5). Higher subcutaneous fat deposition could indicating earlier finishing and could result in animals more sexually precocious, but further study about this subject must be done. But according to Shiotsuki et al. (2009) the selection for improve visual scores of conformation, finishing, and muscling will result in small or no response in heifer pregnancy at 16 month. Guindolin et al. (2010) reported that age at first calving, back fat thickness and longissimus muscle area had heritability estimates of 0.14, 0.51 and 0.48, respectively. According to these authors, AFC had negative genetic correlation with back fat thickness, longissimus muscle area and body weight at 210 days (-0.37, -0.63 and -0.51 respectively), indicating that is possible to improve meat and fat deposition and consequently decrease the age at first calving.

The genetic correlations between AFC with REA and between AFC with BWS were negative and of low magnitude (Table 5). Selection based on BWS is indicated if it was desirably to diminish the AFC and increase REA or BWS because this trait had higher estimate of heritability compared with REA and AFC (Table 4). Genetic correlations between REA with WG_B_120, WG_210_365, BF, RF and BWS were 0.41 ± 0.05, 0.33 ± 0.06, 0.19 ± 0.06, 0.18 ± 0.06 and 0.68 ± 0.03, respectively (Table 5). So, animals that gained more weight at these evaluated ages or those ones that had greater body weight at scanning date tended to

have larger rib eye area. The genetic correlations between BWS with REA and with weight gains ranged from 0.53 ± 0.05 to 0.69 ± 0.04 and between BWS with BF and with RF were 0.11 ± 0.06 and 0.08 ± 0.06, indicating that selection for BWS could improve REA and weight gains. But the BF and RF could respond slowly to the selection process by selecting BWS because of the low genetic correlation between these traits and low heritability of BF and RF.

Some Nellore cattle breeding programs aim to improve the BF and RF. The weight gains and the REA should be selected in a weighted manner to increase subcutaneous fat, measured by BF and RF in a uniform manner and not in excess. It is important to increase the amount of subcutaneous fat in proportion to the increase in the amount of meat on the carcass to ensure the meat tenderness. According to Guedes (2005) and Yokoo et al. (2008) the beef quality in Brazil depends on some factors as the uniform subcutaneous fat distribution over the carcass surface acting as thermal insulation to protect the carcass from excessively rapid cooling, avoiding shrinkage of muscle fibers and consequent toughening of the meat. Lack of fat may also cause excessive water loss, which leads not only to weight loss but also to darkening of the meat during the chilling period (Felício, 1998). According to Pereira et al. (2009) Nellore cows presented good performance for final body weight, carcass yield and fat thickness, which is favorable for the production of early animals favoring AFC.

Bertrand et al. (2001) made a review on carcass traits measured by ultrasound in cattle and reported that traits measured by ultrasound were moderately to highly relate to the same traits measured in finished slaughtered animals. Devit and Wilton (2001) reported high and positive estimates of genetic correlation between bull ultrasound measurements and steer carcass measurements suggesting that genetic improvement for steer carcass traits could be achieved by using yearling bull ultrasound measurements as selection criteria. Moser et al. (1998) suggested that ultrasound measurements of breeding animals may be used in programs of genetic evaluation to reduce the time and expense required to obtain useful estimates of genetic merit for carcass traits.

4. Conclusion

Selection for weight gains, rib eye area and body weight at scanning date can increase female mature weight. But, animals must be select in such way that it does not increase excessively the accumulation of subcutaneous fat.

Mature weight can be taking into account in Nellore breeding programs to reduce or maintain the cows' size. Body weight at scanning date can be take into account because its genetic correlation with weight gains and rib eye area can be sufficient to cause genetic changes in these two traits.

Conflict of interest statement

We declare that there is no conflict of interest in the publication of this paper.

References

Albuquerque, L.G., Meyer, K., 2001. Estimates of direct and maternal genetics effects for weights from birth to 600 days of age in Nellore cattle. J. Anim. Breed. Genet. 118, 83–92.

Benyshek, L.L., Johnson, M.H., Little, D.E., Bertrand, J.K., Kriese, L.A., 1988. Application of an animal model in the United States beef cattle industry. J. Dairy Sci. 71, 35–53.

Bertrand, J.K., Green, R.D., Herring, W.O., Moser, D.W., 2001. Genetic evaluation for beef carcass traits. J. Anim. Sci. 79, 190–200.

Boligon, A.A., Albuquerque, L.G., 2011. Genetic parameters and relationships of heifer pregnancy and age at first calving with weight gain, yearling and mature weight in Nellore cattle. Livest. Sci. 141, 12–16.

Boligon, A.A., Mercadante, M.E.Z., Forni, S., Lôbo, R.B., Albuquerque, L.G., 2010a. Covariance functions for weights from birth to maturity in Nellore cows. J. Anim. Sci. 88, 849–859.

Boligon, A.A., Albuquerque, L.G., Mercadante, M.E.Z., Lôbo, R.B., 2010b. Study of relations among age at first calving, average weight gains and weights from weaning to maturity in Nellore cattle. Rev. Bras. Zootec. 39, 746–751.

Bullock, K.D., Bertrand, J.K., Benyshek, L.L., 1993. Genetic and environmental parameters for mature weight and other growth measures in Polled Hereford cattle. J. Anim. Sci. 71, 1737–1741.

Castro-Pereira, V.M., Alencar, M.M., Barbosa, R.T., 2007. Estimates of genetic parameters and of direct and correlated responses to selection for growth and reproductive traits in a Canchim cattle herd. R. Bras. Zootec. 36, 1029–1036.

Costa, G.Z., Yokoo, M.J., 2004. Ultra-sonografia no Melhoramento de Carcaça. Brangus News 1, 24–27.

Devit, C.J.B., Wilton, J.W., 2001. Genetic correlation estimates between ultrasound measurements on yearling bulls and carcass measurements on finished steers. J. Anim. Sci. 79, 2790–2797.

Felício, P.E., 1998. Desdobramento da qualidade da carne bovina. Hig. Aliment. 2, 16–22.

Guedes, C.F., 2005. Desempenho produtivo e características de carcaça das progênies de touros representativos da raça Nelore e de diferentes grupos genéticos. M.Sc. Thesis. Universidade de São Paulo, Pirassununga. ⟨http://www.teses.usp.br/teses/disponiveis/74/74131/tde-19042006-125755/publico/2977000.pdf⟩ (accessed 13.06.12).

Guindolin, D.G.F., Grupioni, N.V., Chud, T.C.S., Urbinati, I., Lôbo, R.B., Bezerra, L.A.F., Paz, C.C.P., Munari, D.P., 2010. Genetic association for growth, reproductive and carcass traits in Guzera Beef Cattle. In: Proceedings of 9th World Congress on Genetics Applied to Livestock Production. Leipzig, Germany. ⟨http://www.kongressband.de/wcgalp2010/assets/pdf/0640.pdf⟩ (accessed 07.01.12).

Gunski, R.J., Garnero, A.V., Bezerra, L.A.F., Corrado, M.P., Lôbo, R.B., 2001. Idade ao primeiro parto, período de gestação e peso ao nascimento na raça Nelore. Ciênc. Agron. 32, 46–52.

Jenkins, T.G., Kasps, M., Cundif, L.V., Ferrell, C.L., 1991. Evaluations of between- and within-breed variation in measures of weight–age relationships. J. Anim. Sci. 69, 3118–3128.

Kaps, M., Herring, W.O., Lamberson, W.R., 1999. Genetic and environmental parameters for mature weight in Angus cattle. J. Anim. Sci. 77, 569–574.

Lôbo, R.B., Bezerra, L.A.F., Faria, C.U., Magnabosco, C.U., Albuquerque, L.G., Bergmann, J.A.G., Sainz, R.D., Oliveira, H.N., 2008. Avaliação Genética de Touros da Raça Nelore: Sumário 2008, 14th ed ANCP, Ribeirão Preto.

Magnabosco, C.U., Sainz, R.D., Faria, C.U., Yokoo, M.J., Manicardi, F., Barbosa, V., Guedes, C., Leme, P.R., Pereira, A., Araújo, F.R.C., Sanches, A.C., Lôbo, R.B., 2006. Avaliação genética e critérios de seleção para características de carcaça em Zebuínos: Relevância econômica para mercados globalizados. In: Simpósio de Produção de Gado de Corte, vol. 5, Viçosa, Brazil.

Martínez-González, J.C., García-Esquivel, F.J., Parra-Bracamonte, G.M., Castillo-Juárez, H., Cienfuegos-Rivas, E.G., 2010. Genetic parameters for growth traits in Mexican Nellore cattle. Trop. Anim. Health Prod. 42, 887–892.

Meyer, K., 1997. Estimates of genetic parameters for weaning weight of beef cattle accounting for direct-maternal environmental covariances. Livest. Prod. Sci. 52, 187–199.

Meyer, K., 2005. Genetic principal components for live ultrasound scan traits of Angus cattle. Anim. Sci. 81, 337–345.

Meyer, K., 2007. Wombat—a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). J. Zhejiang Univ. Sci. B 8, 815–821.

Moser, D.W., Bertrand, J.K., Misztal, I., Kriese, L.A., Benyshek, L.L., 1998. Genetic parameter estimates for carcass and yearling ultrasound measurements in Brangus cattle. J. Anim. Sci. 76, 2542–2548.

Paneto, J.C.C., Lemos, D.C., Bezerra, L.A.F., Filho, R.M., Lobo, R.B., 2002. Study of quantitative growth traits from 120 to 550 days of age in Nellore cattle. Rev. Bras. Zootec. 31, 668–674.

Pedrosa, V.B., Eler, J.P., Ferraz, J.B.S., Silva IV, J.A., Ribeiro, S., Silva, M.R., Pinto, L.F.B., 2010. Genetic parameters for mature weight and growth traits in Nelore cattle. Rev. Bras. Saúde Prod. Anim. 11, 104–113.

Pereira, P.M.R.C., Pinto, M.F., Abreu, U.G.P., Lara, J.A.F., 2009. Características de carcaça e qualidade de carne de novilhos superprecoces de três grupos genéticos. Pesqui. Agropecu. Bras. 44, 1520–1527.

Regatieri, I.C., Boligon, A.A., Baldi, F., Albuquerque, L.G., 2012. Genetic correlations between mature cow weight and productive and reproductive traits in Nellore cattle. Genet. Mol. Res. 11, 2979–2986.

Silva, A.M., Alencar, M.M., Freitas, A.R., Barbosa, R.T., Barbosa, P.F., Oliveira, M.C.S., Corrêa, L.A., Novaes, A.P., Tullio, R.R., 2000. Herdabilidades e correlações genéticas para peso e perímetro escrotal de machos e características reprodutivas e de crescimento de fêmeas, na raça Canchim. Rev. Bras. Zootec. 29, 2223–2230.

Shiotsuki, L., Silva II, J.A.V., Tonhati, H., Albuquerque, L.G., 2009. Genetic associations of sexual precocity with growth traits and visual scores of conformation, finishing, and muscling in Nellore cattle. J. Anim. Sci. 87, 1591–1597.

Short, R.E., Staigmiller, R.B., Bellows, R.A., Greer, R.C., 1994. Breeding heifers at one year of age: biological and economic considerations. In: Fields, M.J., Sand, R.S. (Eds.), Factors Affecting Calf Crop, CRC Press, London, pp. 55–68.

Talhari, F.M., Alencar, M.M., Mascioli, A.S., 2003. Genetic correlations among reproductive and growth traits of females, in a Canchim cattle herd. Rev. Bras. Zootec. 32, 880–886.

Yokoo, M.J., Lôbo, R.B., Araujo, F.R.C., Bezerra, L.A.F., Sainz, R.D., Albuquerque, L.G., 2010. Genetic associations between carcass traits measured by real-time ultrasound and scrotal circumference and growth traits in Nellore cattle. J. Anim. Sci. 88, 52–58.

Yokoo, M.J., Albuquerque, L.G., Bezerra, L.A.F., Lôbo, R.B., Araujo, F.R.C., Silva, J.A.V., Sainz, R.D., 2008. Genetic and environmental factors affecting ultrasound measures of longissimus muscle area and back fat thickness in Nellore cattle. Livest. Sci. 117, 147–154.

Zuin, R.G., Buzanskas, M.E., Caetano, S.L., Venturini, G.C., Guidolin, D.G.F., Grossi, D.A., Chud, T.C.S., Paz, C.C.P., Lôbo, R.B., Munari, D.P., 2012. Genetic analysis on growth and carcass traits in Nellore cattle. Meat Sci. 91, 352–357.