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Genetic relationships among traits related to reproduction and growth of Nelore females

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ABSTRACT

The objective of the study presented here was to analyze the genetic relationships among heifer pregnancy (HP), age at first calving (AFC), stayability (STAY), average annual productivity of the cow, in kilograms of weaned calf per cow per year (PRODAM), postweaning weight gain (PWG), and hip height (HH) of Nelore females from 12 Brazilian herds. (Co) variance components were obtained by six-trait animal model using Gibbs sampling. The posterior mean of the heritability estimates were 0.37, 0.18, 0.19, 0.16, 0.21, and 0.37 for HP, AFC, STAY, PRODAM, PWG, and HH, respectively. In general, the genetic correlations were strong between traits related to reproduction, for example, −0.85 between HP and AFC, and 0.94 between STAY and PRODAM. Weak genetic correlations were obtained between reproductive and growth traits (absolute values ranging from 0.02 to 0.30). Although weak, the genetic correlations between PWG and reproductive traits were favorable, whereas the genetic correlations between HH and reproductive traits were close to zero and slightly unfavorable for HP, AFC, and STAY. An increase of HH is therefore expected to have little or no negative effect on the reproductive performance of females. The posterior mean of genetic correlation between PWG and HH was moderate (0.50). On the basis of the heritability, genetic correlation estimates, and time to obtain data, HP and PRODAM seems to show the best potential as selection criteria to improve the productive and reproductive performance of Nelore females. In principle, it is possible to select for increased PWG without compromising the reproduction of Nelore females. However, selection for PWG may result in an increase of female HH as a correlated response, a fact that could increase management costs in advanced generations of selection. In the light of the results, all traits studied here can be used as selection criteria and there is no strong evidence of genetic antagonism among traits related to reproduction and growth of Nelore females.

1. Introduction

Reproductive traits are important for beef cattle production systems across the world. Female sexual precocity and fertility are related to the profitability of the production system because these traits are determinant for the number of females exposed to breeding, number of weaned calves, and replacement rate, among others. Therefore, any trait associated with reproductive traits should be included in selection plans because, logically, it may have some economic implications [1,2].

Few beef cattle breeding programs have given emphasis on selection for reproductive traits, particularly in tropical environments. The fact that tropical production systems are mainly on the basis of extensive pasture makes the

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collection of animal data difficult. In many cases, the only reproductive information of a cow is available when it calves. As an alternative to the lack of reproductive information, scrotal circumference has been widely used as a selection criterion in breeding programs in an attempt to obtain a possible correlated response in male and female reproductive traits [3,4]. The use of scrotal circumference as an indicator trait of male and female reproduction is reasonable because the physiological mechanisms underlying reproduction are similar in males and females [5]. Therefore, the existence of shared genes that regulate the expression of these traits in both sexes should permit success of this type of selection. In contrast, some studies on beef cattle have demonstrated that the genetic relationship between scrotal circumference and female reproductive traits is not as strong as previously believed (between 0 and 0.20) [3,6,7]. Golden et al. [8] argued that the use of estimated progeny differences (EPDs) for an indicator trait such as scrotal circumference is irrational when the EPD for a female reproductive trait is available. The availability of EPDs for reproductive traits measured directly in females is therefore a relevant issue.

The three most common females traits used as selection criteria in beef cattle raised in tropical environment are heifer pregnancy [9], stayability [10,11], and average annual productivity of the cow [12–14]. Little is known about the genetic relationship between these specific traits and growth traits in beef cattle (*Bos indicus*) raised under tropical conditions. According to some investigators, there is no strong evidence that selection for growth traits will compromise the reproductive performance of *B. indicus* animals [15–17]. However, other authors reported that, although weak, the genetic correlation between some of these traits in *Bos indicus* is unfavorable [18–20].

In view of the importance of female reproductive traits, the objective of the present study was to analyze the genetic relationships among heifer pregnancy (HP), age at first calving (AFC), stayability (STAY), average annual productivity of the cow (PRODAM), postweaning weight gain (PWG), and hip height (HH) of Nelore females.

2. Materials and methods

2.1. Data

Data from the Genetic Breeding Program of Agro-Pecuária CFM Ltda., stored and analyzed since 1984 by the Animal Breeding and Biotechnology Group, College of Animal Science and Food Engineering, Pirassununga, State of São Paulo, were used in this study. Data from 59,292 Nelore females, daughters of 972 sires and 30,931 dams, born between 1980 and 2010 on 12 farms located in the states of São Paulo, Mato Grosso do Sul, and Bahia, were used (Table 1). The farms included in this study belong to the same company, which uses the basic standard procedures of data collection and storage. The animals were kept on high-quality pasture (40% *Brachiaria brizantha*, 50% *Panicum maximum*, and 10% others) and received only salt and mineral supplementation. The breeding season, 90 days for heifers and 60 days for cows, ranged from October to January, depending on the beginning of the rainy season. Around 40% of the females were artificially inseminated and the remaining animals were placed randomly in lots with a group of bulls or in some cases in lots with a single bull. The cow-to-bull ratio was about 35:1. Calves remained with their dams on high-quality pasture up to 7 months of age.

2.2. Traits

2.2.1. Heifer pregnancy

About 60 days after the end of the breeding season, the heifers (exposed to a bull at around 14 months of age) from three farms were submitted to transrectal palpation or ultrasound for the diagnosis of pregnancy. Heifer pregnancy was analyzed as a categorical trait, with a value of 1 (success) being assigned to heifers that were diagnosed pregnant and a value of 0 (failure) being assigned to those that were not pregnant at that time.

2.2.2. Age at first calving

Age at first calving was calculated as the difference in months between the dam date of birth and the date of birth of her first registered calf.

2.2.3. Stayability

Stayability was defined as successful (coded 1) when a cow stayed in the herd up to the age of 6 years, given that it had the opportunity to breed (had a calf or a positive pregnancy diagnosis). Otherwise, STAY was coded 0. According to the management system of the company, a cow is kept in the herd until 6 years of age if it is productive, that is, calves every year. Cows that do not calve regularly or that wean very light-weight calves are culled systematically.

2.2.4. Average annual productivity of the cow

The PRODAM is defined as the amount (in kg) of weaned calf per cow per unit of time. To obtain PRODAM [14], calf weaning weights were first adjusted using the PROC MIXED procedure [21], in a model that included the fixed effect of contemporary group (herd, year of birth, sex, and management group of the calf), age of calf at recording (linear effect) and age of dam at calving (linear and quadratic effects) as covariates, and the random effect of sire of the calf. A data file of the cows was created, which included the PRODAM of each cow computed based on the adjusted weaning weight of the calf. Only cows that have been recorded since the beginning of reproductive life were included in this file. The following equation was used for the calculation of PRODAM:

$$PRODAM_i = \frac{\left(\sum_{j=1}^{n} WW_{ij}\right) * 365}{ACC_n - 550} \quad (1)$$

where $PRODAM_i$ is the average productivity in kilograms of weaned calf per cow per year; $\sum_i^n WW_{ij}$ is the sum of adjusted weaning weights of all calves of each cow; WW_{ij} is the adjusted weaning weight of calf j of cow i, and ACC_n is the age of the cow (in days) at the last calving. The value 365 in the numerator corresponds to an annual production basis, and the value 550 in the denominator refers to the first calving target at 30 months, with a minimum breeding age of 18 months.

As only part of this population was exposed to bull at around 14 months of age, an equation (2) similar to (1) was used to calculate PRODAM for these heifers, with the value 365 in the denominator referring to the calving target at 24 months, with a minimum breeding age of 12 months. Using equations (1) and (2), PRODAM can be defined as the weight (in kg) of weaned calves produced annually by a cow during the time it stays in the herd, subtracting a fixed period of 550 or 365 days depending on the age at which the cow started reproduction (conventional age of 2 years, or exposed to breeding at 1 year of age and calved).

2.2.5. Postweaning weight gain

This trait was defined as weight gain (in kg) from weaning (205 days) to 550 days of age, that is, weight gain over a period of 345 days.

2.2.6. Hip height

Hip height was measured at 18 months of age with a metric tape as the distance (in cm) from the ground to hip.

2.3. Data selection

As only part of the females of the present population had the opportunity to be exposed to bull at around 14 months of age, the information of AFC used in the present study were restricted to females who participated in the standard breeding season at around 24 months of age. Records for the binary traits HP and STAY of contemporary groups in which all scores were the same, that is, groups without variability, were eliminated. In addition, for all traits, records of animals in contemporary groups with fewer than 10 animals, records of animals with unknown sire or dam, and data exceeding 3.5 SDs above or below the overall mean of the trait (except for HP and STAY) were excluded (Table 1).

2.4. Model and analysis

The model for HP, AFC, PWG, and HH included the respective fixed effects of contemporary group (farm, year of birth, postweaning management group) and covariates age of animal at recording (linear effect, except for AFC) and age of dam at calving (linear and quadratic effects). For PWG, the model included the age of animal at weaning and age of animal at yearling as linear covariates. The contemporary groups for STAY were formed by combining the farm code, birth year of the cow, and farm of birth of each of its progeny. The effect of weaning management group (WMG) was included as random effect for HP, AFC, PWG, and HH as proposed by Santana et al. [22]. The statistical model for PRODAM included the fixed effect of contemporary group (farm and year of birth of the cow).

The (co)variance components were obtained by six-trait analysis using Gibbs sampling. Analysis was performed with the THRGIBBS1F90 program [23]. Because traits HP and AFC were measured on different animals, in this case, the residual covariance was set to zero. The prior distributions for the (co)variance components were inverse Wishart distributions. Analysis consisted of a single chain of 500,000 cycles, with a conservative burn-in period of 50,000 cycles and a thinning interval of 25 cycles. Thus, 18,000 samples were effectively used to estimate the parameters and their respective mean, and highest posterior density intervals. The six-trait animal model can be described as follows:

$$y = X\beta + Z_a u_a + Z_{wmg} u_{wmg} + e \, , \tag{2}$$

where y is the vector of observations, X is the incidence matrix that associates the fixed effects with vector β of the parameters, Z_a and Z_{wmg} are matrices that associate additive genetic and WMG effects with the respective vectors ($u_a$and u_{wmg}), and e is the vector of residual effects. The WMG effects were assumed to be uncorrelated.

The following threshold model [24] was used to analyze HP and STAY:

$$f\left(y_i \middle| l_i\right) = \prod_{i=1}^{n_i} 1\left(l_i < t_i\right) 1\left(y_i = 0\right) + 1\left(l_i > t_i\right) 1\left(y_i = 1\right), \tag{3}$$

where y_i is the ith phenotypic observation (categories 0 or 1), n_i is the total number of data for the trait studied, 1(.) is an indicator function that takes value 1 if the condition specified is true, otherwise the value is 0, l_i is the underlying liability of observation i, and t_i is the threshold that

Table 1
Description of the data set for heifer pregnancy (HP), age at first calving (AFC), average annual productivity (PRODAM), stayability (STAY) in the herd for at least 6 years, postweaning weight gain (PWG), and hip height (HH) in Nelore females.

Item	Trait					
	HP (0 or 1)	AFC (mo)	STAY (0 or 1)	PRODAM (kg)	PWG (kg)	HH (cm)
Number of animals in the pedigree	55,659	32,757	66,523	58,562	77,988	60,492
Number of sires with progeny record	468	688	888	910	806	558
Mean number of progeny records per sire	44.63	18.73	41.34	34.45	42.93	46.99
Number of dams with progeny record	18,367	10,717	24,028	22,040	22,703	16,943
Mean number of progeny records per dam	1.57	1.20	1.53	1.42	1.51	1.54
Animals with records	28,887	12,883	36,708	31,349	44,000	31,395
Mean of the trait	—	35.24	—	135.86	102.47	133.34
Standard deviation	—	2.83	—	28.89	26.28	5.61
Number of contemporary group (CG)	83	225	221	115	360	230
Mean number of animals per CG	348.03	57.26	166.09	272.60	122.22	136.50
% Success	16.1	—	28.9	—	—	—

Table 2
Posterior means [95% highest posterior density intervals] of variance components, heritability, and weaning management group (WMG) as a proportion of the phenotypic variance (WMG^2) obtained for heifer pregnancy (HP), age at first calving (AFC), average annual productivity (PRODAM), stayability (STAY) in the herd for at least 6 years, postweaning weight gain (PWG), and hip height (HH) in Nelore females by multitrait analysis.

Trait	Additive genetic variance	WMG	Residual variance	Heritability	WMG^2
HP (0 or 1)	0.77 [0.63; 0.95]	0.32 [0.25; 0.39]	1.00 [1.00; 1.00]	0.37 [0.33; 0.42]	0.15 [0.13; 0.18]
AFC (mo)	0.96 [0.75; 1.16]	0.31 [0.22; 0.48]	4.19 [3.99; 4.38]	0.18 [0.14; 0.21]	0.06 [0.04; 0.09]
STAY (0 or 1)	0.24 [0.20; 0.29]	—	1.00 [1.00; 1.00]	0.19 [0.16; 0.22]	—
PRODAM (kg)	119.47 [102.20; 138.80]	—	615.12 [597.9; 631.8]	0.16 [0.14; 0.19]	—
PWG (kg)	70.77 [63.70; 78.21]	56.04 [49.43; 63.40]	202.58 [196.8; 208.4]	0.21 [0.19; 0.23]	0.17 [0.15; 0.19]
HH (cm)	4.53 [4.07; 4.96]	0.92 [0.74; 1.38]	6.81 [6.50; 7.13]	0.37 [0.34; 0.40]	0.08 [0.06; 0.11]

defines the response category for the trait. A probit model was used for HP and STAY and a normal distribution was assumed for AFC, PRODAM, PWG, and HH:

$$y|\beta, u_a, u_{wmg}, R \sim MVN(X\beta + Z_a u_a + Z_{wmg} u_{wmg}, R \otimes I), \quad (4)$$

where R is the residual (co)variance matrix; $\otimes$ is the Kronecker product and I is an identity matrix of appropriate order.

3. Results

The estimates of variance components and genetic parameters are shown in Table 2. In general, the posterior mean heritability estimates were of moderate magnitude, indicating that all traits studied can be used as selection criteria, especially HP and HH (0.37). The effect of WMG as a proportion of phenotypic variance was higher for HP and HH, demonstrating the importance of this effect for the expression of these traits.

The posterior means of genetic correlations between the traits studied ranged from low to high (Table 3). In general, the genetic correlations were strong between traits related to reproduction, for example, −0.85 between HP and AFC, and 0.94 between STAY and PRODAM. Weak genetic correlations were obtained between reproductive and growth traits (−0.28 to 0.32). Although weak, the genetic correlations between PWG and reproductive traits were favorable, whereas the genetic correlations between HH and reproductive traits were close to zero and slightly unfavorable for HP, AFC, and STAY. The genetic correlation between PWG and HH was moderate (0.50). The residual correlations were close to zero (−0.04 to 0.15) for all traits studied (Table 3).

4. Discussion

The posterior mean of heritability estimate for HP obtained in the present study (Table 2) was lower than that reported by Eler et al. [9] (0.57) and Van Melis et al. [25] (0.53) for Nelore cattle. However, these authors used a model that did not include WMG as an additional random effect in the analysis of HP. Silva et al. [26] reported a heritability of 0.45 for HP (16 months) of Nelore cattle, indicating that this trait would respond satisfactorily to selection. Johnston et al. [27] obtained heritability estimate for age at detection of the first CL or corpus albicans in Brahman of 0.57. The heritability for HP estimated in this study was similar to that reported by Santana et al. [17] (0.42) for Nelore using an model that included WMG as a random effect. Heifer pregnancy is a trait that has been selected in several Nelore herds in Brazil. Based on the heritability estimate obtained, HP has the potential for expansion as a selection criterion in tropical breeding programs. In addition, WMG exerted an important effect on HP and should be included in the genetic evaluation of this trait in the population studied.

For AFC, the posterior mean of heritability estimate (Table 2) was similar to that reported by Pereira et al. [18] for AFC of Nelore heifers exposed to bulls at 14 months of age (0.18) and higher than AFC of heifers exposed to bulls at 26 months of age (0.02). In addition, there was a difference in the variation of these traits as demonstrated by the SD and coefficient of variation for heifers exposed at 14 (132.9 days and 13.13%) or 26 (49.77 days and 4.53%) months of age. Pereira et al. [18] emphasized that older females are better prepared for breeding than younger females, a fact impairing the detection of genetic differences in reproductive performance between older females. Grossi

Table 3
Posterior means [95% highest posterior density intervals] of genetic (above the diagonal), and residual (below the diagonal) correlations for heifer pregnancy (HP), age at first calving (AFC), average annual productivity (PRODAM), stayability (STAY) in the herd for at least 6 years, postweaning weight gain (PWG), and hip height (HH) in Nelore females by multitrait analysis.

Trait	HP	AFC	STAY	PRODAM	PWG	HH
HP	—	−0.85 [−0.91;−0.74]	0.73 [0.65; 0.79]	0.67 [0.58; 0.74]	0.31 [0.21; 0.40]	−0.10 [−0.19; −0.01]
AFC	0	—	−0.60 [−0.70; −0.49]	−0.57 [−0.67; −0.46]	−0.28 [−0.40; −0.16]	0.04 [−0.07; 0.14]
STAY	0.03 [0.01; 0.04]	−0.03 [−0.04;−0.02]	—	0.94 [0.92; 0.96]	0.23 [0.14; 0.32]	−0.05 [−0.13; 0.05]
PRODAM	0.03 [0.01; 0.04]	−0.02 [−0.03; −0.01]	0.15 [0.14; 0.17]	—	0.32 [0.24; 0.41]	0.25 [0.17; 0.34]
PWG	0.05 [0.03; 0.07]	−0.04 [−0.06; −0.03]	0.04 [0.02; 0.06]	0.08 [0.06; 0.09]	—	0.50 [0.44; 0.56]
HH	0.00 [−0.01; 0.02]	−0.01 [−0.03; 0.02]	0.01 [−0.01; 0.02]	0.01 [0.00; 0.03]	0.13 [0.11; 0.15]	—

et al. [28] reported a heritability of 0.07 for AFC (mean of 36 months of age) in Nelore females. Buzanskas et al. [29], studying AFC in Brazilian Canchim cattle, estimated a heritability of 0.04. The mean AFC of the animals studied by Buzanskas et al. [29] was 40.28 months. Johnston et al. [30] reported heritability estimate of 0.52 for the number of days from the end of the calving period (coinciding with the start of mating) to the estimated first ovulation date of 3-year-old Brahman cows. However, this estimate decreased to values of 0.20 and 0.24 in 4- and 5-year-old cows, respectively. Thus, the observation made by Pereira et al. [18] can be applied to the results obtained here. Although the biological phenotype underlying HP and AFC is heifer puberty, a difference in genetic variation was observed in the present study when HP and AFC were compared, with the heritability coefficient for HP being on average 0.19 units higher than that for AFC. The latter trait was measured in the population at 35 months (Table 1), whereas HP was obtained at around 14 months of age. It is therefore desirable that heifers of the population studied have the opportunity to breed earlier, a procedure that could make the genetic improvement of reproductive performance more efficient.

The posterior mean of heritability estimate for STAY (0.19) was similar to those obtained by Van Melis et al. [11] (0.22) and Silva et al. [10,31] (0.12 and 0.21) for Nelore cattle. The use of STAY as a selection criterion should increase the number of cows that remain in the herd for at least 6 years and that calve regularly. However, Maiwashe et al. [32] pointed out that the generation interval necessary to obtain accurate estimates of genetic merit for STAY is long, a fact that may delay the genetic progress of herds.

In the present study, the posterior mean of heritability estimate for PRODAM (0.16) was close to that of STAY (0.19), indicating that these traits respond similarly to selection in the population studied. The estimate obtained was similar to those reported by Eler et al. [13] (0.15–0.16), Schwengber et al. [12] (0.15), and Grossi et al. [28] (0.14–0.25) who used indices similar to PRODAM. According to Eler et al. [13] and Santana et al. [14], the use of PRODAM rather than STAY as a selection criterion may be more advantageous because the former permits the inclusion of data from females with only one or few calvings, a fact increasing the accuracy of predicting the genetic merit of bulls and young cows. The use of PRODAM as a selection criterion may therefore increase the reproductive and productive efficiency of cows and consequently reduce culling rates in the herds.

Hip height should respond rapidly to selection in the population studied here. The mean heritability estimates for PWG and HH (Table 2) were similar to those reported by Pereira et al. [18] (0.26) and Shiotsuki et al. [19,20] (0.15) for PWG and by Silva et al. [16] (0.30) and Pedrosa et al. [33] (0.35) for HH of Nelore cattle. As observed for HP, WMG is an important effect that should be included in the genetic evaluation of PWG in Nelore cattle. In the present study, WMG explained about 17% of the phenotypic variance, a percentage similar to that reported by Santana et al. [14,17] for PWG in the population studied here (14%), but including the combined data of males and females.

The genetic correlation of −0.85 between HP and AFC (Table 3) indicates that these traits are influenced by many of the same genes. Considering the heritability estimates of the two traits, the genetic correlation and a selection intensity corresponding to selection of 80% females, the direct response in AFC is expected to be 30% less than the correlated response obtained by selection for HP. Taking into account the time necessary for measurement of the traits, the efficiency of direct selection for AFC is still less when compared with HP. Therefore, HP rather than AFC should be chosen as a selection criterion to improve the reproductive performance of Nelore females in the population studied. Silva et al. [26] obtained a genetic correlation of −0.32 between the binary traits HP at 16 months and AFC in Nelore. However, the definition of HP used by these authors differed from that employed here. Silva et al. [26] defined heifers that calved until 31 months of age as success and heifers that did not as failure. Few studies have investigated the genetic relationship between these traits in Zebu cattle raised under tropical conditions.

The genetic correlations between HP and STAY and between AFC and STAY (0.73 and −0.60, respectively) were similar in terms of absolute values. This was also observed for the genetic correlation between HP and PRODAM and between AFC and PRODAM (0.67 and −0.57, respectively). This finding was not unexpected because the genetic correlation between HP and AFC was close to unity. Selection for HP or AFC can contribute to increase STAY and PRODAM of females in this population. Johnston et al. [30] reported that age at puberty had a genetic correlation (0.34) with lactation anestrus in Brahman cattle. Although this is not a strong correlation, it suggests that selection for reduced age at puberty would result in shorter anestrus, which would lead to higher possibility of conception, pregnancy, and, therefore, higher numbers of calves produced. Van Melis et al. [25] and Santana et al. [17] reported a posterior mean of the genetic correlation estimate between HP and STAY of 0.64 and 0.59, respectively, in Nelore. Grossi et al. [28] in a study with Nelore obtained an estimate of −0.33 between AFC and cow productivity index similar to PRODAM. It is therefore expected that Nelore females starting their reproductive live earlier tend to stay in the herd for a longer period of time and to produce more kilograms of weaned calf. The posterior mean of the genetic correlation between STAY and PRODAM was close to unity, indicating that many of the same genes influence both traits. Studying a Canchim beef cattle herd, Baldi et al. [34] estimated a genetic correlation of 0.91 between kilograms of calves weaned up to 10 years of age and length of time the cow stayed in the herd. For PRODAM, young cows with production records are included in the genetic evaluation, whereas for STAY, these cows still have no production records. Therefore, the accuracy of breeding values for PRODAM could be higher than that for STAY in the case of young cows and bulls. The high genetic correlation between these traits and their equal heritability estimate suggest that PRODAM is the best choice as a selection criterion to increase cow productivity and stayability in the herd.

Considering the genetic correlations between PWG and traits related to female reproduction (Table 3), selection for higher PWG does not compromise female reproduction in the population studied and may have some favorable effect on the reproduction of Nelore females in long-term selection. Shiotsuki et al. [19] reported a genetic correlation of 0.09 between PWG and pregnancy of Nelore heifers at 16 months of age. Santana et al. [17] obtained genetic correlation estimates of 0.20 between PWG and HP and between PWG and STAY in Nelore cattle. In the study of Pereira et al. [18], the genetic correlations were −0.08 and −0.03 between PWG and AFC of Nelore heifers exposed to bulls for the first time at around 14 and 26 months of age, respectively. According to these authors, females with a higher postweaning growth rate tend to reach puberty earlier and, consequently, to calve earlier. The different genetic correlation estimates reported in the studies mentioned above are likely due to the use of combined data of males and females, influence of management practices, and nutrition.

The low genetic correlations between HH and reproductive traits suggest that only a small number of the same genes influence these traits (Table 3). Silva et al. [16] reported a low genetic correlation between HH and HP (0.10) in Nelore cattle. In general, the genetic correlations between HH and reproductive traits studied here were unfavorable. Pereira et al. [18] also reported an unfavorable genetic correlation between AFC and HH (0.16). Mercadante et al. [15] compared lines of Nelore cattle (a control line selected for mean yearling weight and a line selected for higher yearling weight) and concluded that selection for body weight promoted high HH responses without compromising the reproductive performance of cows with respect to days to calving and calving success. An increase of HH is therefore expected to have little or no negative effect on the reproductive performance of Nelore females. It is also important to note that in the studies mentioned above [15,17,19], the animals are kept in relatively good management conditions (good quality pastures and mineral supplementation) which could favor the reproduction even for larger and heavier cows and lead to little or no genetic relationship between the growth and reproduction in Nelore cattle. The good nutrition also plays a positive effect on the weight gain of the animals, which consequently favors the earlier achievement of puberty in heifers [35–37] leading to higher pregnancy rates and lower AFC.

The moderate genetic correlation between HH and PWG indicates that selection for an increase of one trait results in an increase of the other. Maiwashe et al. [38] obtained a genetic correlation of 0.40 between shoulder height and average daily gain in a performance test of South African Bonsmara cattle. Cardoso et al. [39] reported a genetic correlation of 0.50 between yearling size and PWG for Brazilian Angus cattle. Riley et al. [40] in a study with Brahman cattle reported a genetic correlation of 0.24 between HH and average daily gain. In the population studied, bulls are selected based on an index that includes standardized EPDs for weaning weight, PWG, scrotal circumference, and muscle score, weighted 20%, 40%, 20%, and 20%, respectively. The greater weight of PWG may increase HH in the population, a fact that could contribute to an increase of management costs of the animals. It is therefore important that HH is monitored constantly in the animals of the Nelore population studied.

The low residual correlations between the traits studied suggest that improvement of environmental conditions for one trait should not favor any of the other traits studied. These results agree with those reported by Shiotsuki et al. [19,20], Van Melis et al. [25], and Santana et al. [17] in studies of growth and reproductive traits of Nelore cattle.

On the basis of the heritability and genetic correlation estimates obtained for the traits studied, HP and PRODAM show the best potential as selection criteria to improve the productive and reproductive performance of Nelore females. These traits can be included in the selection index of this population. In principle, it is possible to select for increased PWG without compromising the reproduction of Nelore females. However, selection for PWG may result in an increase of female HH as a correlated response, a fact that could increase management costs in advanced generations of selection.

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