Genetic associations among average annual productivity, growth traits, and stayability: A parallel between Nelore and composite beef cattle

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ABSTRACT: This study was conducted to examine the relationship among average annual productivity of the cow (PRODAM), yearling weight (YW), postweaning BW gain (PWG), scrotal circumference (SC), and stayability in the herd for at least 6 yr (STAY) of Nelore and composite beef cattle. Measurements were taken on animals born between 1980 and 2010 on 70 farms located in 7 Brazilian states. Estimates of heritability and genetic and environmental correlations were obtained by Bayesian approach with 5-trait animal models. Genetic trends were estimated by regressing means of estimated breeding values by year of birth. The heritability estimates were between 0.14 and 0.47. Estimates of genetic correlation among female traits (PRODAM and STAY) and growth traits ranged from –0.02 to 0.30. Estimates of genetic correlations ranged from 0.23 to 0.94 among growth traits indicating that selection for these traits could be successful in tropical breeding programs. Genetic correlations among all traits were favorable and simultaneous selection for growth, productivity, and stayability is therefore possible. Genetic correlation between PRODAM and STAY was 0.99 and 0.85 for Nelore and composite cattle, respectively. Therefore, PRODAM and STAY might be influenced by many of the same genes. The inclusion of PRODAM instead of STAY as a selection criterion seems to be more advantageous for tropical breeding programs because the generation interval required to obtain accurate estimates of genetic merit for PRODAM is shorter. Average annual genetic changes were greater in Nelore than in composite cattle. This was not unexpected because the breeding program of composite cattle included a large number of farms, different production environments, and genetic level of the herds and breeds. Thus, the selection process has become more difficult in this population.

Key words: beef cattle, correlation, genetic trend, longevity, threshold model, tropical breeding program

INTRODUCTION

In most beef cattle production systems, the length of the productive life of a cow, the number of calves produced per cow per unit time, and kilograms weaned calf are economically important factors. Herds in which cows remain for a longer period of time and calve regularly require a lower portion of primiparous females than herds in which cows have a greater chance of not getting pregnant and therefore being culled earlier (Garrick, 2006).

In addition, cows are also culled from a herd when they consistently wean light calves (Eler et al., 2008). The length of time a cow stays in the herd is therefore not only related to sexual precocity and cow fertility but also to calf weaning weight. Therefore, Lôbo (1996) proposed an index to evaluate the production efficiency of beef cattle herds. This index takes into account the quantity of weaned calves (kg) and the length of time necessary for their production. Eler et al.
(2008) proposed a similar index, called average annual productivity of the cow (PRODAM).

Another trait related to cow reproduction and production that has been evaluated in some beef cattle breeding programs is stayability in the herd for at least 6 yr (STAY; Silva et al., 2003). The use of an index including cow productivity instead of STAY might be advantageous because a productivity index permits the evaluation of the genetic merit of females with only 1 or few calvings as well as the evaluation of young bulls. Despite the possible advantages of using a productivity index as a selection criterion, little is known about the genetic association of such index with growth traits and with STAY itself.

In view of the importance of these traits for beef cattle production systems, the nature of the relationship and the potential benefits of these traits to be included as a selection criterion are of primary interest. Therefore, the objective of the present study was to determine the genetic correlation among PRODAM, yearling weight (YW), postweaning BW gain (PWG), scrotal circumference (SC), and STAY in Nelore and composite beef cattle from Brazil.

MATERIAL AND METHODS

Animal Care and Use Committee approval was not obtained for this study because the data were obtained from existing databases.

Data from the Genetic Breeding Program of Agro-Pecuária CFM Ltda. (Brazilian Nelore) and Montana Tropical Composite Breeding Program CFM-Leachman Pecuária Ltda. (Brazilian composite beef cattle), which have been stored and analyzed from 1994 by the Animal Breeding and Biotechnology Group, College of Animal Science and Food Engineering, Pirassununga, State of São Paulo, were used in this study.

Nelore Data

The animals were born between 1980 and 2010 on 12 farms located in the states of São Paulo, Mato Grosso do Sul, and Bahia (Table 1). The farms included in this study belong to the same company, which uses 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. Calves born between the end of August and December remained with their dams up to 7 mo of age on high-quality pasture. The breeding season, 90 d for heifers and 60 d for cows, ranged from October to January, depending on the beginning of the rainy season. Heifers were either inseminated, approximately 40%, or multisire natural serviced, approximately 60%. The cow-to-bull ratio was about 35:1.

Composite Beef Cattle Data

Data from animals including purebred, crossbred, and composite beef cattle born between 1980 and 2010 on 58 farms located in municipalities of the Brazilian states of Goiás, Minas Gerais, Mato Grosso do Sul, Mato Grosso, Pará, Rio Grande do Sul, and São Paulo were used (Table 1).

In the formation of the composite cattle used in this study the breeds were regrouped according to their genetic similarity and general performance into 4 large and general biological types, which are identified by the abbreviation NABC: group N (Bos indicus)
represented by Zebu breeds and breeds of African origin, group A (*Bos taurus*) represented by breeds adapted to tropical climates, group B (*Bos taurus*) represented by European breeds of British origin, and group C (*Bos taurus*) represented by European breeds of continental origin (Ferraz et al., 1999). In this population, an animal (composite beef cattle) should be composed of at least 3 different breeds, 12.5% adapted breed to the tropical environment and 25% of Zebu breed (group N) plus breeds adapted to tropical climates (group A). The maximum acceptable values are 37.5% group N, 87.5% group A, 100% group N plus A, and 75% for groups B, C and B plus C. Further information about the formation of the present composite beef cattle can be found in Santana et al. (2012a).

The animals were kept on pasture with or without supplements in the dry season (April to September). In general, the pastures were composed of *Brachiaria brizantha*. Especially in the Pantanal (Midwest) and Pampa (southern Brazil), the native pasture plays an important role in animal feeding. All farms provided mineral supplements and some protein. About 60% of cows were inseminated and 40% were placed in lots with a group of bulls. The cow-to-bull ratio was 30:1 or 25:1. Calves were born between September and December and remained with their dams until they were 7 mo old.

**Traits**

To obtain PRODAM, calf weaning weights were first adjusted using the PROC MIXED procedure (SAS Inst. Inc., Cary, NC) in a model that included the fixed effect of contemporary group (herd, year of birth, sex, and management group), age of calf at recording (linear effect), age of dam at calving (linear and quadratic effects), individual and maternal breed composition (only for composite cattle), and individual and maternal heterozygosis (linear effect; only for composite cattle) as covariates and the random effect of sire. 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 from the beginning of reproductive life were included in this file. The PRODAM was calculated by the equation

\[
PRODAM_i = \frac{\left(\sum_{j=1}^{n} WW_{ij}\right) x 365}{ACC_i - 365},
\]

where \(PRODAM_i\) is the average annual productivity in kilograms weaned calf per cow per year, \(\sum_{j=1}^{n} WW_{ij}\) 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 \(ACC_i\) 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 mo, with a minimum breeding age of 18 mo.

In recent years, heifers started to be exposed to bulls at 14 mo of age (range: 12 to 16 mo). An Eq. [2]

\[
PRODAM_i = \frac{\left(\sum_{j=1}^{n} WW_{ij}\right) x 365}{ACC_i - 365}
\]

similar to Eq. [1] was used to calculate PRODAM for these heifers with value 365 in the denominator referring to the calving target at 24 mo, with a minimum breeding age of 12 mo.

Using Eq. [1] and [2], PRODAM can be defined as the weight (kg) of weaned calves produced annually by a cow during the time she stays in the herd, subtracting a fixed period of 550 or 365 d depending on the age at which the cow started reproduction (conventional age of 2 yr or exposed to breeding at 1 yr of age and calved).

The PWG in Nelore was defined as BW gain from weaning (205 d) to 550 d of age (i.e., BW gain over a period of 345 d). In composite cattle, the PWG was defined as BW gain from weaning (205 d) to 420 d of age (i.e., BW gain over 215 d). Therefore, YW in Nelore was measured at about 550 d of age and for composite cattle was measured at about 420 d of age. Scrotal circumference was measured with an appropriate metric tape at yearling age (around 550 or 420 d of age). Measurements for PWG and YW were taken on male and female progeny. The STAY was defined as successful (coded 1) when a cow calved every year up to the age of 6 yr given that she had the opportunity to breed. Otherwise STAY was coded 0.

As proposed by Harville and Mee (1984), records for the binary trait STAY of contemporary groups in which all scores were the same (i.e., groups without variability) were eliminated. In addition, for all traits, records of animals in contemporary groups with fewer than 10 animals, contemporary groups with all progeny of a single sire, and sires with fewer than 5 progeny records, records of animals with unknown sire or dam and data exceeding 3.5 SD above or below the overall mean of the trait were excluded (Table 1).

**Model and Parameter Estimation**

The statistical model for PRODAM included the fixed effect of contemporary group (farm and year of birth). The model for YW, PWG, and SC included the respective fixed effects of contemporary group (farm, year of birth, sex (only YW and PWG), and postweaning management group) and covariates age of animal at recording (linear effect) 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 her progeny until the ages specified. In addition, for composite cattle, the models included the following effects based on NABC definition: individual and maternal breed composition and individual and maternal heterozygosis as linear covariates. Direct additive genetic effects were included as random effects for all traits. The effect of weaning management group (WMG) was included as random effect for YW, PWG, and SC.

A management practice adopted in the herds of the present study leads in some situations to the formation of postweaning management groups that include animals from various WMG. During the formation of postweaning contemporary groups, the inclusion of WMG as a fixed effect results in numerous postweaning contemporary groups with few observations. For the estimation of genetic parameters, animals belonging to contemporary groups with few observations were excluded. However, exclusion of contemporary groups with small numbers cannot be applied to the prediction of breeding values because there is interest in predicting breeding values for all animals or at least for young bulls to be commercialized and for replacement heifers. Therefore, to overcome this problem and to obtain postweaning contemporary groups with a larger number of observations, the WMG was assumed to be an uncorrelated random effect. Additional information about this procedure can be found in Santana et al. (2012b).

The (co)variance components were obtained by 5-trait analysis using a Bayesian approach. Analysis was performed with the THRGIBBS1F90 program (Misztal et al., 2002). The previous distributions for the (co)variance components were noninformative inverse Wishart distribution for all random effects. Analysis consisted of a single chain of 250,000 cycles, with a conservative burn-in period of 25,000 cycles and a thinning interval of 25 cycles. Thus, 9,000 samples were effectively used to estimate the parameters and their respective highest posterior density intervals (HPD; i.e., the shortest possible interval enclosing 95% of the posterior mass).

The 5-trait animal model can be described as follows:

\[ y = X\beta + Z_a u_a + Z_{wmg} u_{wmg} + e, \]

in which \( y \) is the vector of observations, \( X \) is the incidence matrix that associates the fixed effects with vector \( \beta \) of the parameters, \( Z_a \) and \( Z_{wmg} \) are matrices that associate direct 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 residual covariance between SC and STAY and between SC and PRODAM was set to 0. Stayability was analyzed using this threshold model:

\[ f(y_i | t_i) = \prod_{r=1}^{n_i} \left[ I(t_i < t_r)I(y_i = 0) + I(t_i > t_r)I(y_i = 1) \right], \]

in which \( y_i \) is the \( i \)th phenotypic observation (categories 0 or 1), \( n_i \) is the total number of data for the trait studied, \( t_r \) is the underlying liability of observation \( i \), and \( t_i \) is the threshold that defines the response category for the trait. A probit model was used for STAY and a multivariate normal (MVN) distribution was assumed for PRODAM, YW, PWG, and SC:

\[ y | \beta, u_a, u_{wmg}, R \sim MVN(\begin{bmatrix} X\beta + Z_a u_a + Z_{wmg} u_{wmg} \end{bmatrix}, R \otimes I), \]

in which \( R \) is the residual (co)variance matrix, \( \otimes \) is the Kronecker product, and \( I \) is an identity matrix of appropriate order. Genetic trends were estimated by regressing weighted means of expected breeding values of animals by birth year (1996 to 2010).

**RESULTS AND DISCUSSION**

**Heritability**

The heritability estimates obtained for the traits studied were of moderate to high magnitude (Table 2). The heritability in the present study for PRODAM in Nelore (0.23) was greater than those reported in the literature for cow productivity defined as kilograms weaned calf over a certain period of time in studies with Nelore (0.10 to 0.16; Schwengber et al., 2001; Azevêdo et al., 2005; Eler et al., 2008). Studies reporting heritability for PRODAM in composite beef cattle are scarce. Martínez et al. (2004) found estimates of heritability ranging from 0.16 to 0.21 for number of calves born, number of calves weaned, and cumulative weaning weight by 6 yr after first calving in Hereford cows. Baldi et al. (2008) reported low estimates of heritability for kilograms of calves weaned up to 10 yr of age and during total herd life in Canchim (62.5% Zebu and 37.5% Charolais) cows of 0.10 and 0.13, respectively. The selection for PRODAM would be possible in a breeding program and could be relatively effective as a result of the moderate estimates of heritability obtained in Nelore cattle. However, the lower estimate of heritability for PRODAM in composite cattle (0.14) does not support this expectation.

The heritability estimates for YW in Table 2 were moderate in both populations studied here (0.36 to 0.41). Therefore, YW is expected to respond favorably to direct selection. Similar estimates were reported by Van Melis et al. (2003) and Shiotsuki et al. (2009) in Nelore cattle,
0.36 and 0.34, respectively. Fordyce et al. (1996) in a study with Brahman-Shorthorn and Sahiwal-Shorthorn beef cattle in Australia reported estimates of 0.23, 0.20, and 0.36 for BW at 12, 18, and 24 mo of age, respectively. Moser et al. (1998) found a heritability estimate of 0.40 for YW in Brangus cattle.

The heritability for PWG in Nelore (0.21) was similar to that reported by Eler et al. (2000), Van Melis et al. (2003), and Santana et al. (2012b) for Nelore cattle (0.15 to 0.29). The heritability estimate obtained for PWG in composite cattle (0.21) was slightly greater than those reported for some Bos taurus × Bos indicus or Bos taurus populations raised in a (sub)tropical environment. Santana et al. (2010) in a study with composite cattle raised in Brazilian states of Mato Grosso do Sul and São Paulo found estimates of heritability that ranged from 0.06 to 0.18 for PWG. Prayaga and Henshall (2005) found estimates ranging from 0.15 to 0.16 for ADG from weaning to final BW of 524 d of age of crossbred beef cattle in Australia. Cardoso et al. (2004) reported heritability estimate of 0.20 for PWG in Brazilian Angus. Burrow (2012) reported a study based on Brahman and tropical composites in northern Australia that showed a significant difference in daily BW gain depending on environmental conditions. Therefore, the differences between estimates obtained here and in the literature were probably due to large variations in the environment to which the animals were raised as they belonged to herds from different regions of Brazil. The moderate heritability estimates for PWG suggest that selection can improve growth in both populations studied here.

The heritability for SC in Table 2 was high for Nelore (0.47) and moderate for composite cattle (0.30), indicating that this trait responds favorably to selection. Estimates ranging from 0.46 to 0.57 have been reported for Nelore by Pereira et al. (2001), Eler et al. (2004), and Santana et al. (2012b). In general, there is a large difference between estimates of heritability for SC of composite populations reared in tropical and temperate environments and also between purebred and composite cattle reared in a tropical environment. Burrow (2001) reported heritability of 0.46 for SC in Australian composite cattle. Mwansa et al. (2000) reported heritability estimate of 0.65 for SC measured at 12 mo of age in Canadian composite cattle. In contrast, Buzanskas et al. (2010) found a heritability of 0.24 for SC at 420 d of age in Brazilian Canchim cattle and Santana et al. (2010) reported heritability estimates ranging from 0.21 to 0.32 in a study with composite cattle from Brazil. Therefore, breed–environment-specific parameters are required for genetic evaluations as highlighted by Burrow (2012) and Santana et al. (2012a).

The heritability estimates obtained for STAY in Table 2 indicates that this trait can be included as a selection criterion to increase the productive life of Nelore and composite cows (0.16 to 0.27). Studying Nelore cattle, Van Melis et al. (2007) reported heritabilities of 0.25, 0.22, and 0.28 for STAY at 5, 6, and 7 yr of age, respectively. Silva et al. (2003) estimated a heritability of 0.20 for STAY in Nelore animals and suggested that selection for this trait may reduce heifer replacement costs because the culling of cows should decline over time. Maiwashe et al. (2009) with a similar definition of STAY reported estimates of heritability of 0.20, 0.20, 0.20, 0.18, and 0.20 for STAY at 4, 5, 6, 7, and 8 yr of age in South African Angus.

**Weaning Management Group**

The WMG accounted for a significant portion of the phenotypic variance observed in YW and PWG of Nelore (0.06 and 0.14) and composite cattle (0.08 and 0.14), indicating that this effect is relevant for the genetic evaluation of PWG in animals of this population (Table 2). In contrast, the effect of WMG on SC was close to 0 and is therefore less important for genetic evaluations. Santana et al. (2012b) in a study with Nelore cattle reported estimates of 0.14 and 0.03 for WMG in PWG and SC, respectively. The inclusion of WMG as uncorrelated random effect resulted in more consistent contemporary groups that were formed by a larger number of animals. This procedure may favor the correct genetic evaluation of animals in both populations studied here.

**Genetic Correlation**

The genetic correlation between PRODAM and YW and between PRODAM and PWG was favorable but of low magnitude (Table 3). These estimates indicate that selection for PRODAM will be inefficient to increase YW
and PWG in short-term selection. Unfortunately, a lack of research exists about previous estimates of genetic correlation between these traits. In Canchim cattle, Baldi et al. (2008) found genetic correlations close to 0 of cow weight at first breeding and at first calving with kilograms weaned calf during the time the cow stays in the herd and kilograms of weaned calf produced by cows up to 10 yr of age. In contrast, Gianlorenço et al. (2003) obtained a genetic correlation of 0.61 between bull BW at 12 mo of age and the number and kilograms weaned calf produced by females up to 10 yr of age in Canchim animals. Also studying Canchim cattle, Mello et al. (2006) found genetic correlations of cow weight at weaning and at 12 mo of age with kilograms weaned calf produced to up to 10 yr of age of 0.37 and 0.39, respectively. Archer et al. (1998) showed that selection for greater growth rates does not compromise female reproduction in Angus cattle.

The genetic correlation between PRODAM and SC was moderate and favorable in composite cattle (0.30; Table 3). Similarly, Gianlorenço et al. (2003) estimated a genetic correlation of 0.41 between kilograms weaned calf produced by cows up to 10 yr of age and SC at 12 mo, indicating that selection to increase male SC should result in more kilograms of weaned calf. Selection designed to increase PRODAM in composite population may result in an increase of SC as a correlated response. However, this statement is not supported by the low genetic correlation obtained in Nelore cattle. Eler et al. (2004) and Van Melis et al. (2010) showed that selection of Nelore animals for SC would be not very effective to improve female reproductive and productive traits.

Strong positive correlation was observed between PRODAM and STAY and therefore, these traits should be influenced by many of the same genes. The traits that make up PRODAM have genes that have an effect on them and those same genes that have an effect on reproduction and/or other traits that affect STAY. Studying a Canchim herd, Baldi et al. (2008) estimated a genetic correlation of 0.91 between kilograms calf weaned up to 10 yr of age and length of time the cow remained in the herd. Logically, cows that are more productive tend to remain in the herd for a longer period of time. The genetic correlation between PRODAM and STAY indicate that it would not be necessary to include both traits as a selection criterion. Despite the low heritability estimate obtained for PRODAM in composite cattle, the selection for PRODAM seems to be more advantageous because its measurement is less time consuming than that of STAY (6 yr of age). Mawaiwa et al. (2009) emphasized that the long generation interval required to obtain accurate estimates of genetic merit may slow genetic progress for stayability at older ages. According to Eler et al. (2008), the use of PRODAM as a selection criterion would permit the evaluation of younger cows and bulls. Selection for PRODAM has various benefits for the production system because it is an index that comprises important female traits such as age at calving, reproductive regularity, and stayability as well as calf weight at weaning (Schwenger et al., 2001). Mercadante et al. (2000) alerted to the fact that the formulas available to evaluate cow productivity should be used with caution because they include numerous traits of different heritability and economic importance. According to Smith (1983), although the individual effects of traits of low heritability or economic value are small, their cumulative effects may become expressive when these traits are combined in an index. The author concluded that the efficiency of selection highly depends on which trait dominates the index and on the genetic correlation between the traits included in the index.

The genetic correlations among YW, PWG, and SC were greater in composite cattle than in Nelore. This finding may be due to longer selection for these traits in parental breeds (Bos taurus) of composite cattle studied here. In Nelore cattle, Pereira et al. (2001) obtained an estimate of genetic correlation between YW and SC and between PWG and SC of 0.25 and 0.12, respectively.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Nelore</th>
<th>Composite beef cattle</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRODAM–YW</td>
<td>0.12</td>
<td>0.01</td>
</tr>
<tr>
<td>PRODAM–PWG</td>
<td>0.10</td>
<td>0.00</td>
</tr>
<tr>
<td>PRODAM–STAY</td>
<td>0.11</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Table 3. Posterior mean, SD, and 95% highest posterior density interval (HPD) of genetic and environmental correlations between average annual productivity (PRODAM), yearling weight (YW), postweaning BW gain (PWG), scrotal circumference (SC), and stayability at 6 yr (STAY) in Brazilian Nelore and composite beef cattle.
Santana et al. (2012b) reported a genetic correlation between PWG and SC of 0.19 for Nelore. Burrow (2001) found estimates ranging from 0.40 to 0.68 for weight recorded at about 18 mo of age with daily live weight gain during different periods in composite cattle from Australia. Prayaga and Henshall (2005) reported a genetic correlation of 0.73 between yearling weight and ADG in crossbred beef cattle from Australia. Therefore, selection for any growth trait is expected to have favorable correlated response in the other, mainly for composite cattle. According to Kriese et al. (1991) this was not unexpected because some of the same genes are involved in expression of all these growth traits.

As mentioned earlier, PRODAM and STAY should be influenced by many of the same genes and the genetic correlation between growth traits and STAY was very similar to the correlation between growth traits and PRODAM as expected. Selection for growth traits will result in little or no correlated response for STAY. However, simultaneous selection for these traits is possible. Silva et al. (2006) reported a genetic correlation of 0.19 between SC and STAY for Nelore animals of the same population as that used in the present study. Santana et al. (2012b) found a genetic correlation between SC and STAY for Nelore animals of the same population as that used in the present study. Santana et al. (2012b) found a genetic correlation of 0.17 and 0.19, respectively. Therefore, the joint analysis of growth traits, productivity, and stayability is recommended.

**Environmental Correlation**

In general, the environmental correlations among all traits studied were positive and low (Table 3). The environmental correlations were greater in Nelore cattle than in composite cattle because the rearing environment is more homogeneous for this breed. The population of Nelore cattle studied here belongs to the same company, which uses standard procedures of management. As expected, a greater environmental correlation was obtained between YW and PWG, indicating that environmental effects will act in the same direction on these traits.

**Genetic Trend**

The average breeding value for the traits studied increased over time in both breeds (Table 4). The average annual genetic changes were greater in Nelore than in composite cattle, suggesting greater effectiveness of selection in Nelore breeding program. This was not unexpected because the breeding program of composite cattle includes a large number of farms and different production environments and genetic level of the herds and breeds. Thus, the selection process has become more difficult in this population.

In the composite cattle, the bulls are selected based on an index including standardized estimated progeny differences for birth weight, weaning weight, PWG, SC, and muscle score, weighted –1, 3, 4, 1, and 1, respectively. Consequently, we observed a nonsignificant trend in PRODAM and STAY.

According to the current estimate of average annual genetic change in PRODAM and STAY, the selection for these traits in Nelore cattle has been effective. Lower estimates of genetic changes were obtained previously in the Nelore population studied. Eler et al. (2008) reported an average annual genetic change of 0.26 kg in PRODAM considering animals born until 2002. Silva et al. (2003) reported an average annual genetic change of 0.14% in STAY for animals born until 2001. Van Melis et al. (2007) found an estimate of average annual genetic

Table 4. Estimates of annual genetic changes (±SE) from 1996 to 2010 for average annual productivity (PRODAM), yearling weight (YW), postweaning BW gain (PWG), scrotal circumference (SC), and stayability at 6 yr (STAY) in Brazilian Nelore and composite beef cattle

<table>
<thead>
<tr>
<th>Cattle</th>
<th>PRODAM, kg</th>
<th>YW, kg</th>
<th>PWG, kg</th>
<th>SC, cm</th>
<th>STAY, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nelore</td>
<td>0.66 ± 0.05***</td>
<td>1.16 ± 0.07***</td>
<td>0.78 ± 0.05***</td>
<td>0.07 ± 0.00***</td>
<td>0.60 ± 0.05***</td>
</tr>
<tr>
<td>Composite</td>
<td>0.05 ± 0.04</td>
<td>0.70 ± 0.04***</td>
<td>0.37 ± 0.03***</td>
<td>0.05 ± 0.00***</td>
<td>0.07 ± 0.04</td>
</tr>
</tbody>
</table>

1 Expected breeding value expressed on percent probability.
***Genetic trend significantly different from 0 (P < 0.0001).
change in STAY of 0.34% for animals born until 2003. There are no previous estimates of genetic change for the other traits in the populations studied.

There is an important difference between the genetic parameters of the Nelore and composite cattle, indicating that the genetic evaluation of each of these populations requires particular attention. All traits studied can respond to selection. Furthermore, the genetic correlation among these traits was favorable and simultaneous selection for growth, productivity, and stayability is therefore possible. The joint analysis of growth traits, productivity, and stayability contribute to an increase the accuracy of prediction of genetic merit for PRODAM and STAY. The inclusion of PRODAM instead of STAY as a selection criterion seems to be more advantageous for tropical beef cattle production systems.

**LITERATURE CITED**


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