



## Tabapuã breed in Northeastern Brazil: genetic progress and population structure<sup>1</sup>

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**ABSTRACT** - The objective of this study was to evaluate the history of the Tabapuã breed in Northeastern Brazil by determining its population structure and genetic progress. Pedigree information from animals born in the period between 1965 and 2006 and weight-adjusted data at 205 (W205), 365 (W365) and 550 (W550) days of age for bovines born between 1975 and 2006 were used. The (co)variance components and genetic value were estimated using the application MTDFREML. Also, the software ENDOG was used for pedigree analysis and parameter estimation based on the probabilities of gene origin, inbreeding and average generation interval. The heritability coefficients for direct genetic effects were  $0.21 \pm 0.03$ ,  $0.26 \pm 0.04$  and  $0.36 \pm 0.05$  for W205, W365 and W550, respectively. During the first 20 years studied, the observed effective size was small. The generation intervals by gametic pathway were:  $7.7 \pm 3.4$  (sire-son),  $7.8 \pm 3.7$  (sire-daughter),  $6.9 \pm 3.3$  (dam-son),  $6.8 \pm 3.1$  (dam-daughter), and mean interval of  $7.3 \pm 3.4$  years. The studied population showed moderate heritability coefficients, whereas the genetic gains based on the studied traits may be higher than those estimated by genetic tendencies. Reduced generation interval, increased effective size and continuous mating control of relatives are important strategies for the genetic progress of the Tabapuã breed in the region.

Key Words: genetic gain, generation interval, inbreeding effective size

### Introduction

Breeding programs are deemed fundamental to improve the productive traits of cattle; however, it is necessary to monitor the results achieved by selection in order to pursue alternatives to improve genetic gains.

Such monitoring can be done through evaluation of genetic changes over time, aiming to verify the genetic progress achieved and helping in adjustments, whenever necessary (Euclides Filho et al., 2000).

The study of genetic tendency is a measure for assessing changes caused by a selection process, regarding specific traits, over the years (Holanda et al., 2004); in addition, this study indicates the hits and misses of the adopted selection methods and helps determine the continuity - or not - of selection strategies.

Likewise, knowledge of the different factors that potentially interfere in the selection process and genetic progress, such as effective size, generation interval and genetics are of great importance for the feasibility of breeding programs (Malhado et al., 2008a). Yet, special

attention should be given to the structure of populations under selection so as to preserve variability and allow greater responses to selection.

The use of information contained in pedigrees is of great importance for studies of population structures, as this is a low-cost technique as compared with other techniques, as for instance, the use of molecular markers (Carneiro et al., 2009).

Furthermore, the study of population structure could make clear the decisions to be taken with respect to different herds and serve as guiding element when it comes to orienting future activities in the scope of breeding programs (Malhado et al., 2008b).

Thus, the major objective of this study was to assess the population structure and genetic progress of weight traits of Tabapuã cattle from Northeastern Brazil.

### Material and Methods

The data utilized refers to the pedigree data of Tabapuã cattle reared in Northeastern Brazil and born between 1965

and 2006. The database comes from the weight gain control of Associação Brasileira de Criadores de Zebu (Brazilian Association of Zebu Breeders - ABCZ). Amongst the growth traits evaluated, the weight of animals raised on pasture and born after 1975 at the 205 (W205), 365 (W365) and 550 (W550) days of life was evaluated. There were 16,461 animals for W205, in 155 farms; 11,580 animals for W365, in 137 farms; and 9,546 animals for W550, in 126 farms, totaling 168 ranches (Alagoas = 11, Bahia = 99, Ceará = 2, Maranhão = 20, Paraíba = 7, Pernambuco = 7, Piauí = 5, Rio Grande do Norte = 3, Sergipe = 14) and 23,345 animals in the  $-A^{-1}$  relationship matrix.

For the purpose of estimating genetic parameters, contemporary groups (CG) consisting of animals of the same sex, farm, time and year of birth were formed, excluding those with less than four animals.

Estimates of (co)variances and prediction components of genetic values were obtained using the Multiple Trait Derivative Free Restricted Maximum Likelihood, through single-trait animal models; the application Multiple Trait Derivative Free Restricted Maximum Likelihood (MTDFREML) developed by Boldman et al. (1995) was utilized.

The models used for the three traits included random genetic effects (direct and maternal), maternal permanent environmental effects, covariate age of cow at calving (linear and quadratic effects), and the fixed effect of contemporary group, including (co)variance between direct and maternal genetic effects.

Estimates of genetic, phenotypic and environmental trends regarding the evaluated traits were obtained by weighted linear regression of the mean of the dependent variable (genetic values, observed weight values and contemporary groups solution) over the year of birth of the calf; for this purpose, the software SAS (Statistical Analysis System, version 9.1) was used.

Also, the software ENDOG was used for pedigree analysis and parameter estimation based on the probabilities of gene origin, inbreeding and average generation interval (Gutiérrez & Goyache, 2005).

The effective size of the population ( $Ne$ ) was estimated per year, as a function of the number of adult males and females able to mate, according to the following equation:

$$Ne = \frac{(4Nm \times Nf)}{(Nm + Nf)}, \text{ in which } Nm \text{ and } Nf \text{ stand for the number of males and females used in breeding, respectively.}$$

The increase in inbreeding ( $\Delta F$ ) was calculated using the classical formula:

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}, \text{ in which } F_t \text{ stands for the mean inbreeding}$$

coefficient estimated in the current generation; and  $F_{t-1}$  indicates the average inbreeding coefficient estimated in the previous generation.

The average generation interval was calculated based on the four gametic pathways: sire-son, sire-daughter, dam-son and dam-daughter.

The effective number of founders representing the number of animals with an equal contribution to produce the same genetic variability observed in the studied population was calculated to evaluate the concentration of animals and original genes, according to the formula (Boichard et al., 1997):  $fe = \frac{1}{\sum_{k=1}^f q_k^2}$ , in which  $q_k$  refers to the probability of the gene to originate from founder  $k$ .

The effective number of ancestors represents the minimum number of animals (founders or not) needed to explain the total genetic diversity of the population (Gutiérrez & Goyache, 2005). It is calculated similarly to the effective number of founders:  $f_a = \frac{1}{\sum_{j=1}^a q_j^2}$ , in

which  $q_j$  stands for the marginal contribution of an ancestor  $j$  (not necessarily founder); i.e., the genetic contribution of an ancestor, which cannot be explained by a previously selected ancestor.

The average relatedness coefficient (AR) simultaneously calculates inbreeding and individual coancestry (Gutiérrez et al., 2003). This parameter was calculated using an algorithm so as to obtain a vector  $c'$  defined as:

$$c' = (1/n) 1' A [1]$$

In which  $A$  is the numerator of relationship matrix of  $n \times n$  size. On the other hand, the numerator relationship matrix can be achieved from the matrix  $P$ , in which  $P_{ij}$  equals to 1 if  $j$  is the father of  $i$ , and equals to 0, if it is not the father; therefore, the animal parents are defined (Quaas, 1976) by:

$$A = (I - \frac{1}{2} P) - 1 D (I - \frac{1}{2} P') - 1 [2]$$

In which  $I$  stands for the identity matrix and  $D$  refers to a diagonal matrix with elements other than zero, obtained by:

$$d_{ii} = 1 - \frac{1}{4} a_{jj} - \frac{1}{4} a_{kk};$$

$d_{ii} = 1$ , if none of the parents are known;  $d_{ii} = \frac{3}{4}$ , if one parent is known;  $d_{ii} = \frac{1}{2}$ , if both parents are known,  $j$  and  $k$  are the parents of individual  $i$ .

$$\text{From [2], } A (I - \frac{1}{2} P') = (I - \frac{1}{2} P) - 1 D [3]$$

By pre-multiplying both sides of [3] by  $(1/n) 1'$ , the result is:

$$(1/n) 1' A (I - \frac{1}{2} P') = (1/n) 1' (I - \frac{1}{2} P) - 1 D$$

$$\text{and using [1]: } c' (I - \frac{1}{2} P') = (1/n) 1' (I - \frac{1}{2} P) - 1 D$$

By multiplying  $c'$  between parentheses and isolating  $c'$ :

$$c' = (1/n) 1' (I - \frac{1}{2} P) - 1 D + \frac{1}{2} c' P' [4]$$

Wright's F-statistics ( $F_{it}$ ,  $F_{st}$  and  $F_{is}$ ) (1978) were also obtained using the software ENDOG (Gutiérrez & Goyache, 2005).  $F_{it}$  stands for the mean inbreeding coefficient of the population;  $F_{st}$  denotes the expected mean inbreeding coefficient estimated in hypothetical populations produced via random mating of parents in each period; finally,  $F_{is}$  expresses the chance deviation obtained from the current matings. When  $F_{is}$  is greater than zero, the real inbreeding exceeds the expected level for random matings, indicating that more closely related animals have mated; hence, the population was divided into subpopulations. When  $F_{is}$  is lower than zero, either inbreeding is avoided or mating between subpopulations predominates.

The main founders and/or ancestors were ordered in a decreasing order, based on their AR and contribution values, respectively, using the SORT procedure of SAS (Statistical Analysis System, version 9.1). For comparison of animal classification in relation to AR and contribution, correlation analysis of classification using the Spearman's rank correlation of PROC CORR in SAS (Statistical Analysis System, version 9.1) was performed.

## Results and Discussion

Means and coefficients of variation (CV) for weights adjusted at 205 (W205), 365 (W365) and 550 (W550) days of life were 173.84±29.61 kg and 17.03%; 232.88±42.64 kg and 18.31%; 302.27±59.56 kg and 19.70%, respectively. These means are above those observed by Ferraz Filho et al. (2002), in a study involving the Tabapuã breed, whose values were 170.30, 222.40 and 286.45 kg for W205, W365 and W550, respectively.

The direct heritability coefficients were 0.21±0.03, 0.26±0.04 and 0.36±0.05 for W205, W365 and W550, respectively (Table 1). These estimates are considered of moderate magnitude and reveal that the selection could be efficient and provide genetic progress over the years, mainly when it comes to weight at 550 days of life.

Values similar to those obtained in this study, concerning the observed trait at W205, were found by Jacinto et al. (2005) and Ribeiro et al. (2007), both reporting estimates of

0.20 for Tabapuã animals. Yet, lower results were reported by Ferraz Filho et al. (2002) (0.16), Campêlo et al. (2004) (0.15) and Guimarães et al. (2003) (0.14) for animals of that breed.

With respect to W365, the direct heritability estimate (0.26) is similar to the value presented by Ferraz Filho et al. (2004) (0.27) for Tabapuã breed and that presented by Pimenta Filho et al. (2001) (0.26), for the Guzerat breed.

The highest direct heritability value (0.36) was estimated for W550. The same value was found by Van Melis et al. (2003) for Nellore cattle. Lower results were reported by Ferraz Filho et al. (2002) (0.13) and Guimarães et al. (2003) (0.20), for the Tabapuã breed.

The estimated values for the coefficients of maternal heritability were low in all three characteristics evaluated (Table 1), suggesting little maternal influence and greater difficulty in genetic gain through selection for the maternal effect, mainly on the characteristics W365 and W550. Higher value of maternal heritability was observed in the characteristic P205, decreasing in subsequent ages, a result that confirms the greater importance of maternal effect in the pre-weaning.

Values close to those found in this study were mentioned in Tabapuã by Ribeiro et al. (2007), who reported values of 0.17, 0.06 and 0.01, and Ferraz Filho et al. (2002), who estimated 0.10, 0.03 and 0.03, for the characteristics W205, W365 and W550, respectively. According to the authors of the latter study, these results reveal that maternal effects had an influence on the weaning weight, but there was little effect on post-weaning weights.

The study of genetic trends allows evaluating the efficiency of selection and monitoring the genetic progress of the herd over the years. For W205, the direct genetic trend (linear regression) was significant ( $P < 0.001$ ) and equal to 0.051 kg/year (Figure 1). Therefore, there was a gain of 2.04 kg during the 40 years of study. In terms of annual genetic change, this represents an increase of 0.03% in the average weaning weight. This trend was lower than that found by Ferraz Filho et al. (2002), who observed a direct genetic gain of 0.134 kg/year for Tabapuã cattle reared in Brazil. Some authors have found positive trends for other

Table 1 - Estimates of (co)variance components and genetic parameters for weights adjusted at 205 (W205), 365 (W365) and 550 (W550) days of life of Tabapuã cattle in Northeastern Brazil

Traits	$\sigma_a^2$	$\sigma_m^2$	$\sigma_{am}$	$\sigma_{ep}^2$	$\sigma_e^2$	$\sigma_p^2$	$h_a^2$	$h_m^2$	$r_{Gam}$
W205	104.89	66.90	-16.28	35.04	313.93	504.49	0.21	0.13	-0.19
W365	227.55	47.08	20.44	56.78	534.66	886.51	0.26	0.05	0.20
W550	558.33	32.89	7.62	43.47	903.34	1545.66	0.36	0.02	0.06

$\sigma_a^2$  - direct additive genetic variance;  $\sigma_m^2$  - additive maternal genetic variance;  $\sigma_{am}$  - genetic covariance between direct and maternal additive effects;  $\sigma_{ep}^2$  - permanent environmental variance;  $\sigma_e^2$  - residual variance;  $\sigma_p^2$  - phenotypic variance;  $h_a^2$  - direct heritability;  $h_m^2$  - maternal heritability;  $r_{Gam}$  - genetic correlation between direct and maternal additive effects.

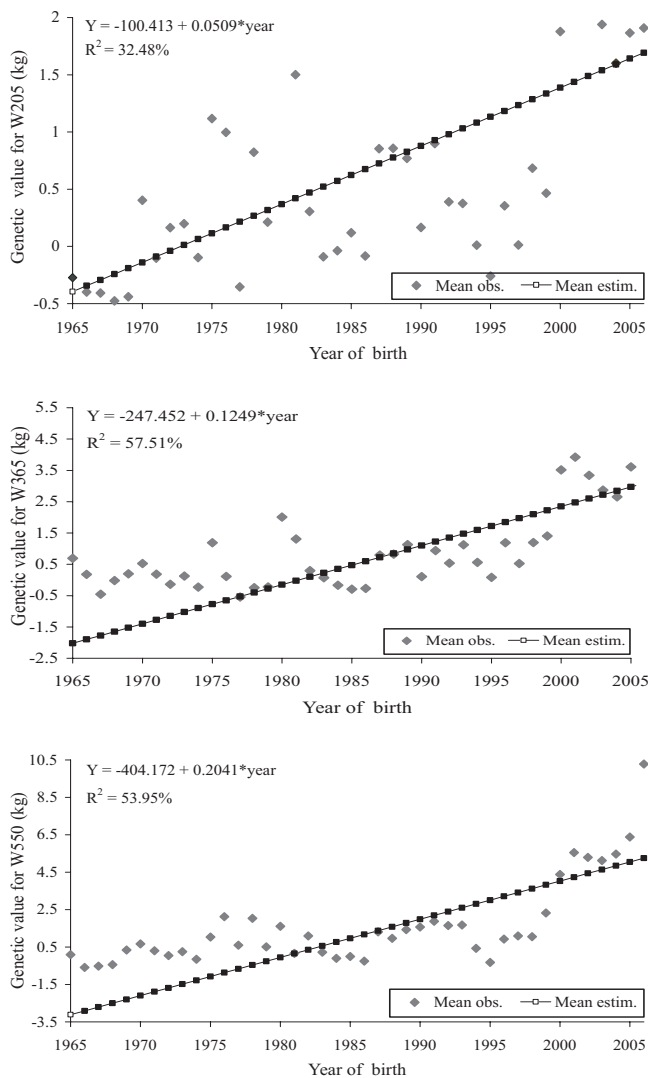


Figure 1 - Genetic trends at W205, W365 and W550 for Tabapuã animals from Northeastern Brazil, between 1965 and 2006.

Zebu breeds: Mello et al. (2002), 1.336 kg/year for Canchim, and Malhado et al. (2008b), 0.049 kg/year for the Nellore.

With relation to W365, the direct genetic trend (linear regression) was expressive ( $P < 0.001$ ) and equal to 0.125 kg/year (Figure 1), equal to a gain of 5.0 kg during the study period. In terms of annual genetic change, this result denotes an increase of 0.05% in the average population. In a study involving the same breed species, in different regions of Brazil, Ferraz Filho et al. (2002) found a higher gain (0.21 kg/year). Other authors, such as Mello et al. (2002) and Malhado et al. (2008b), in studies involving other Zebu breeds, have found positive results: 1.62 and 0.04 kg/year, respectively.

The direct genetic trend (linear regression) for W550 was also expressive ( $P < 0.001$ ), with an estimated value

of 0.204 kg/year (Figure 1), representing an increase of 8.16 kg over the 40 years of study. When it comes to annual genetic change, this corresponds to an increase of 0.07% in the average population. Ferraz Filho et al. (2002) observed an annual genetic gain of 0.275 kg/year, which is close to that found in this study. According to these authors, such gains are below that expected, possibly due to the low selection intensity applied in some herds.

Even at small magnitudes, the results found in this study show positive genetic trends for all studied traits, indicating that the growth traits of Tabapuã animals reared in Northeastern Brazil had positive genetic trends during the study period (40 years), in particular concerning weight at 550 days of life (P550).

Assuming a selection intensity of 1.24, i.e., by retaining 5% of males and 75% of females, the direct heritabilities (Table 1), phenotypic standard deviations and the average generation interval of cattle (7.3 years), it would be possible to achieve annual genetic progresses ( $\Delta G = (i \times h^2 \times \sigma_p) / ig$ ) of the order of 1.06; 1.88 and 3.64 kg/year, which corresponds to 0.61, 0.81 and 1.20% of the population mean at W205, W365 and W550, respectively.

The major objective of studies on phenotypic trends is to monitor the phenotypic progress, jointly assessing the performance of selection programs and the improvement of environmental conditions on traits analyzed over the years. The phenotypic trend (linear regression) of weight at 205 days of life (W205) was expressive ( $P < 0.001$ ) and equal to 0.772 kg/year (Figure 2), denoting an increase of 23.93 kg during the analysis period. This gain is especially due to environmental improvements, as the observed genetic gain for the trait was low (0.051 kg/year). If in search for greater genetic gains in the coming years there is no selection for the trait, the phenotypic progress of this trait might reach its limit.

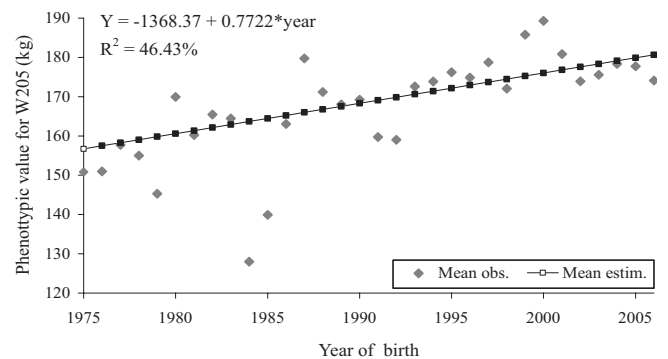


Figure 2 - Phenotypic trends regarding W205, for Tabapuã animals from Northeastern Brazil, in the period between 1965 and 2006.

There were no phenotypic trends (linear regression) for W365 or W550 ( $P>0.05$ ). Yet, the significant genetic trends observed for these traits reveal that environmental conditions were not favorable to the phenotypic progress of post-weaning traits.

In a study addressing Nellore cattle, conducted from 1970 to 2006, Malhado et al. (2008b) reported phenotypic trends of the order of 1.40, 1.65 and 2.11 kg/year for the same traits, respectively.

During the first decade, there was a small increase in the number of Tabapuã animals (Figure 3). Yet, there was a significant increase between 2001 and 2005; the latter had a peak of 2,466 animals registered in the Northeastern region. After that year, the number of births decreased, reaching 1,781 records in 2006.

As regards to the genetic structure of the population, 75.17; 26.26; 8.89 and 2.02% out of the 35831 studied animals had pedigree in the first, second, third and fourth breeding, respectively (Figure 4). It is worth stressing the great loss of information from the first to the second generation, since 24.83% of the animals had unknown

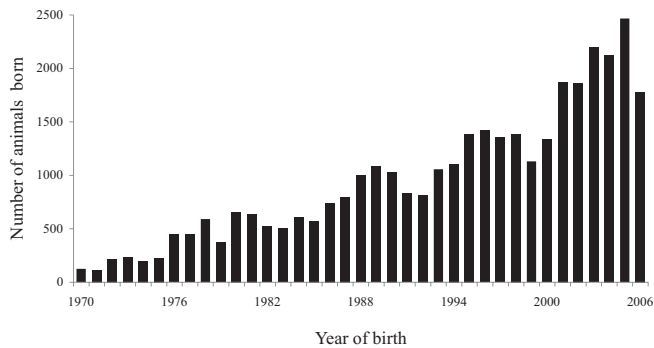


Figure 3 - Number of Tabapuã cattle born in Northeastern Brazil from 1970 to 2006.

father and mother and 73.74% did not have grandparents in the pedigree. This information is important because all the estimated parameters are a consequence of this structure. Moreover, the more complete the pedigree, the more accurate and reliable the estimates.

Generation interval estimates regarding the four gametic pathways of animals were equal to  $7.7\pm 3.4$  (sire-son),  $7.8\pm 3.7$  (sire-daughter),  $6.9\pm 3.3$  (dam-son) and  $6.8\pm 3.1$  years (dam-daughter); the average generation interval was  $7.3\pm 3.4$  years. These values are high and close to those observed for national herds. In a study on the population structure of Tabapuã bovines, Vercesi Filho et al. (2002a) observed intervals of 7.1 (sire-son), 7.2 (sire-daughter), 7.2 (dam-son) and 7.0 (dam-daughter), with an average age of 7.2 years.

Average generation interval is an essential population parameter in selection programs, as it directly affects the yearly genetic trend for the selected traits. The reduction of generation intervals is possible. Moreover, an alternative is the use of young bulls, mainly intended to reduce sire-son and sire-daughter intervals (Malhado et al., 2008b).

For nearly 20 years, there was little significant growth in population size (Figure 5). From 1988, there was a significant increase in effective size ( $N_e$ ), reaching 279 animals in 1989. After this period, there was a great deal of variation in effective size, undergoing a more stable period until 2003, when the highest  $N_e$  was observed, totaling 483 animals. As for the Tabapuã breed, Vercesi Filho et al. (2002a) found an effective size of 55 animals between 1994 and 1998. In the last study period (1998-2000), Carneiro et al. (2009) reported an effective size of 26 animals for the Indubrasil breed. This value revealed that the species is at risk of extinction in Northeastern Brazil.

The determination of effective size allows assessing genetic diversity; in turn, its quantification is important for

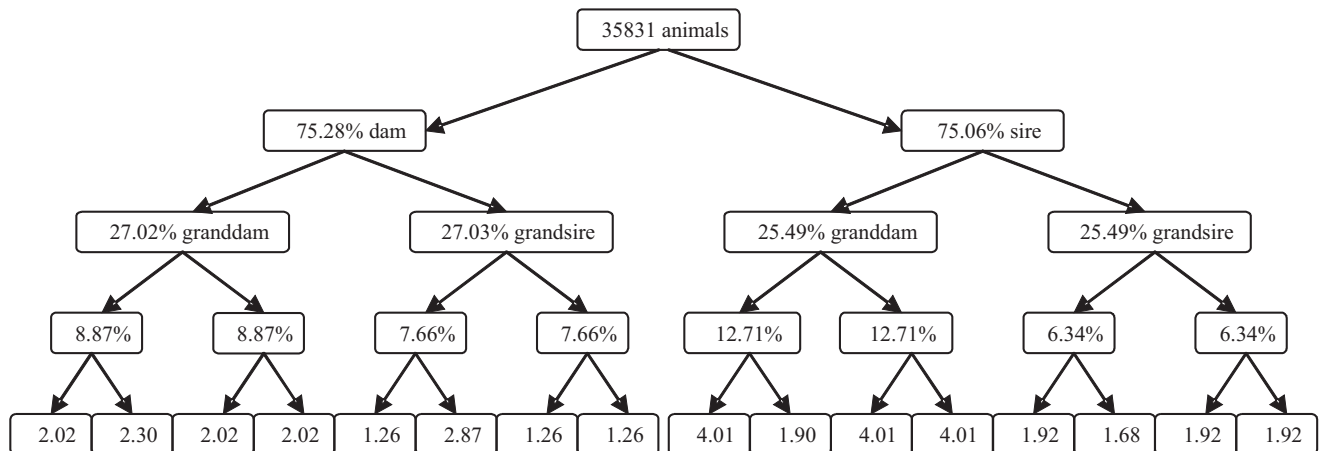


Figure 4 - Pedigree structure of Tabapuã cattle in Northeastern Brazil.

the genetic conservation of a population or species. Many researchers have attempted to define the optimum effective size in populations. Goddard & Smith (1990) suggested a minimum effective size of 40 animals per generation to maximize the economic return, whereas Meuwissen & Woollians (1994) recommended values between 31 and 250 animals so as to prevent decrease in the adaptive value of the population; Frankham (1995), in turn, suggested an effective size of 500 animals for the maintenance of evolutionary potential, highlighting that an effective size of 50 animals is sufficient to prevent inbreeding depression.

In populations with small effective sizes, the results of selection may be influenced by genetic drift and can result in large variations of genetic gains (Carneiro et al., 2006).

The highest genetic values regarding the three studied genetic traits were observed in the periods with the largest effective sizes. According to Malhado et al. (2008a), increased genetic gains depend upon a reduction in the generation interval, an increase in the effective size and use of evaluated breeding bulls, and mating control among related animals.

A greater increase in inbreeding coefficient was observed between the second and the fourth generations, from 0.38 to 1.04% (Table 2). Likewise, the percentage of inbred animals had a significant growth until the fourth generation. Yet, the F mean for inbred animals decreased from 16.60 to 7.14% from the second to the sixth generation, demonstrating that mating between close relatives was controlled.

Of the total 26,780 animals, 17,719 had at least one unknown parent. The total number of animals in the reference population - the one whose animals had both parents known - was 9,061. The effective number of founders ( $f_e$ ) was equivalent to 164 animals, while the expected increase in inbreeding due to an unbalanced contribution of founders was 0.17%. Genetic contribution of the 10, 20, 50 and 91 most influential ancestors (founders or not) explained, in the

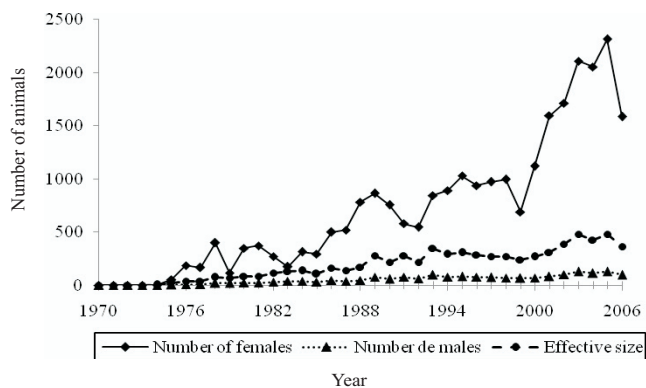


Figure 5 - Effective size of Tabapuã cattle in Northeastern Brazil from 1970 to 2006.

same order, 19.7, 28.3, 42.1 and 50% of genetic variability in the entire population.

Results indicate that few animals account for much of the genetic variability in the studied population. The values encountered by Vercesi Filho et al. (2002a) are in line with those obtained in this study. In the last study period (1994-1998), these authors observed that 50 animals accounted for 42.6% of the genetic variability. In a study involving Indubrasil animals, Carneiro et al. (2009) identified a much higher value, in which 50% of the population variability resulted from 225 ancestors (founders or not). On the other hand, Malhado et al. (2008a) reported that 414 ancestors could explain the same variability, in a study involving Nelore cattle in the state of Bahia.

Spearman's Rank Correlation of founder animals and/or ancestors was high (0.94) and statistically significant ( $P < 0.01$ ). This high degree of association indicates that most founder animals are also the ancestors and, because the effective number of founders and ancestors is low, the founder effect in the Tabapuã population of Northeastern Brazil becomes evident.

The founder effect is due to the installation of a population by a small number of individuals. Therefore, the main outcome is a reduction in the effective size and the population genetic variation, high homozygosis, and a consequent loss of alleles due to genetic drift.

The most important founder and ancestor was 1683411, a male with coefficient of relationship (AR) of 2.81%; this explained 3.72% of variability (Table 3). It should be noted that the imbalance between contributions of ancestors and founders is due to the large number of descendants left by these animals as compared with the average number of descendants per breeder in the population. It should be noted that only one animal out of the top ten founders and ancestors was female, having 15 descendants, whereas the first founder and male ancestor had 736 descendants.

The contribution of the ten original founders was high and led to reduced genetic variability, since they accounted for 19.71% of the genetic variability of the population. A more critical situation was found by Vercesi Filho et al.

Table 2 - Inbreeding coefficients and F mean values for inbred Tabapuã animals of Northeastern Brazil

Generation	Number of animals	Average inbreeding coefficient (%)	Inbred animals (%)	F mean for inbred animals (%)
1	12,421	0.00	-	-
2	5,901	0.38	2.27	16.60
3	4,304	0.45	5.41	8.29
4	2,516	1.04	14.35	7.25
5	1,754	0.99	14.25	6.94
6	182	0.82	11.54	7.14

(2002b), analyzing Indubrasil cattle, wherein the first and second ancestors accounted for, respectively, 4.7% and 3.7% of total genetic variability; the first ten ancestors, in turn, contributed with 23.5%, indicating intensive use of a few animals.

According to Marcondes et al. (2010), the lower the number of founder animals, the greater the need to monitor inbreeding in the studied herd, seeking control tools or even the introduction of animals without direct relationship with the major ancestors identified in the population.

The average AR between individuals was 0.40%, while the highest individual coefficient was 2.81%. The AR remained stable over the period from 1965 to 1974, with annual values of 0.01% (Figure 6). From 1975 to 1994, the average coefficient of relationship showed gradual increases as it ranged from 0.09 to 0.52%. In the period from 1995 to 2006, the highest values were observed when AR had an average of 0.47% and a maximum value of 0.60%, in 2001.

The mean inbreeding coefficient (F) was equal to zero from 1965 to 1977, followed by abrupt changes until 2006, reaching a maximum value of 0.65% in 2003. The low values of inbreeding coefficients and average relationship in the eighties are probably not due to the fact that there are no inbreeding animals in the population, but primarily due to the inability to estimate these parameters, since the

Table 3 - Description of ten founders and ten ancestors of major importance in the population structure of Tabapuã animals in Northeastern Brazil<sup>1</sup>

Founder	Father	Mother	Sex	Year of birth	AR	Number of sons/breeder
1683411			M	1975	2.81	736
461197			M	1982	1.94	319
2139175			M	1995	1.79	965
1541405			M	1980	1.73	859
1742050			M	1990	1.49	470
298056			M	1987	1.31	419
1279160			M	1991	1.15	401
842033			F	1981	0.92	15
1859783			M	1993	0.89	411
328640			M	1980	0.72	240
				Ancestral Contribution		
1683411			M	1975	3.72	736
461197			M	1982	2.58	319
2139175			M	1995	2.39	965
1541405			M	1980	2.31	859
1742050			M	1990	1.99	470
298056			M	1987	1.75	419
1279160			M	1991	1.52	401
842033			F	1981	1.22	15
1859783			M	1993	1.18	411
1767496	1213694	1645237	M	1993	1.04	367

<sup>1</sup> Data on the identification of animals, fathers and mothers, sex, year of birth, average relatedness coefficient (AR) of founders and contribution in the genetic variability, all expressed as percentage.

pedigree did not allow for this calculation during the first seven years.

The increase in inbreeding and correlation coefficient was directly associated with the increase in the equivalent number of generations. According to Queiroz et al. (2000), better knowledge of and genealogical control over the generations allows a more accurate calculation of F and AR, with a consequent increase in their values. The knowledge of more generations of an individual increases the possibility of an important ancestor to appear several times in the pedigree.

The estimates of F statistics of Wright (1978) observed in this study were:  $F_{it} = 0.0004$ ;  $F_{st} = 0.0128$  and  $F_{is} = -0.0129$ . The low and negative value of  $F_{is}$ , which determines fixation index in mating, indicates a slight predominance of mating between subpopulations, which contributes to reduce inbreeding. The negative value of  $F_{is}$  may be associated with the use of artificial insemination and exchange of breeders. These practices are important for the genetic improvement of a breed and the connectivity between herds. Carneiro et al. (2009) found a similar value (0.0185) for  $F_{st}$  and found that this low value indicates the absence of population structure.

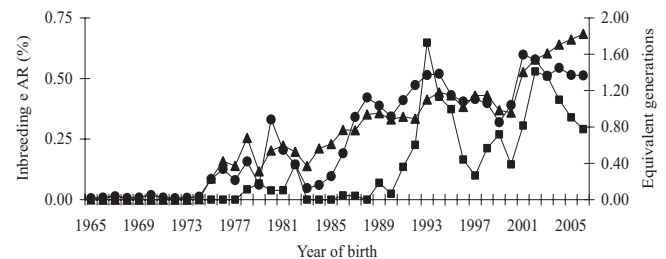


Figure 6 - Inbreeding variation (squares) and average relatedness coefficient (AR; circles), both in percentage, and mean values of equivalent generations (triangles) for Tabapuã cattle in Northeastern Brazil.

## Conclusions

There is the possibility of genetic gain by selection; however, genetic progress is modest. The phenotypic gains observed must be mostly ascribed to environmental improvements. Due to the short pedigree, inbreeding can be underestimated. In order to improve genetic gains, a decrease in the generation interval and the use of evaluated breeders are needed; in addition, the maintenance of mating control between related animals is an important measure to avoid further losses of genetic variability and therefore enable the genetic progress of Tabapuã cattle in Northeastern Brazil.

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