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Population structure of Brazilian Crioula Lageana cattle (*Bos taurus*) breed¤

Estructura poblacional de la raza bovina brasileña Crioula Lageana (Bos taurus)

Estrutura populacional da raça brasileira bovina Crioula Lagenana (Bos taurus)

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Abstract

Background: The lack of information on population structure is one of the main obstacles to develop breeding and conservation programs for animal genetic resources. **Objective:** To characterize the population structure of Crioula Lageana cattle breed *(Bos taurus)* in order to assess its genetic diversity. **Methods:** Database with information of 1,638 Crioula Lageana animals, collected during 38 years, was analysed using the ENDOG v.4.4 program. **Results:** Effective population size ranged from 72.53 in complete generations to 143.90 in maximum generations. Inbreeding and Average Relatedness coefficients were 0.34 and 0.91%, respectively. The effective number of founders and ancestors were 29 and 28 animals, respectively, and only ten ancestors were responsible for 50% of the genetic variability of the whole population. The average generation interval was 5.84 years in the paternal line and 7.70 in the maternal one. Wright´s F statistics indicated low

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genetic distances between subsets in relation to the total population (Fst = 0.0015), between individuals with respect to their subpopulation (Fis = -0.0027), and between individuals in relation to the total population (Fit = -0.0012). **Conclusion:** Analysis of the population indicated that, despite the small number of animals with known parentage and considerable loss of genetic variability by the constant use of a few sires, and same value of number of founders and ancestors, the population showed good genetic management, low inbreeding, low genetic differentiation among subpopulations, and probably adequate effective population size for breed preservation.

Keywords: *conservation of animal genetic resources, genetic diversity, inbreeding, locally-adapted breed, pedigree analysis.*

Resumen

Antecedentes: La falta de información sobre estructura poblacional es una de las principales barreras para el desarrollo de programas de mejoramiento genético y conservación de los recursos zoogenéticos. **Objetivo:** Caracterizar la estructura poblacional de la raza bovina Crioula Lageana (*Bos taurus*) para evaluar su diversidad genética. **Métodos:** Una base de datos con información de 1.638 animales Crioula Lageana (*Bos taurus*), recogidos durante 38 años, fue analizada utilizando el programa ENDOG v.4.4. **Resultados:** El tamaño efectivo de la población varió de 72,53 en las generaciones completas a 143,90 en las generaciones máximas. La endogamia y la relación media de los coeficientes fue 0,34 y 0,91%, respectivamente. El número efectivo de fundadores y antepasados fue de 29 y 28 animales respectivamente, y sólo diez antepasados fueron responsables del 50% de la variabilidad genética de la población. El intervalo promedio de generación fue de 5,84 años en la línea paterna y de 7,70 en la línea materna. El índice estadístico de Wright's F indica una baja distancia genética entre los subconjuntos en relación con la población total (Fst = 0,0015), entre los individuos con respecto a su subpoblación (Fis = -0,0027), y entre los individuos en relación con la población total (Fit = -0,0012). **Conclusión:** El análisis de la población indica que a pesar del pequeño número de animales con origen conocido y la considerable pérdida de variabilidad genética por el uso constante de pocos toros y el mismo valor del número de fundadores y antepasados, la población mostró un buen manejo genético, baja endogamia, baja diferenciación genética entre las subpoblaciones y probablemente un tamaño efectivo adecuado de la población.

Palabras clave: *análisis de pedigrí, conservación de los recursos genéticos animales, diversidad genética, endogamia, razas adaptadas localmente.*

Resumo

Antecedentes: A falta de informações sobre a estrutura da população está entre os principais obstáculos ao desenvolvimento de programas de melhoramento e conservação de recursos genéticos animais. **Objetivo:** Caracterizar a estrutura populacional da raça bovina Crioula Lageana (*Bos taurus*) para acessar a diversidade genética da raça. **Métodos:** Banco de dados com informação de 1.638 animais Crioula Lageana, recolhidos durante 38 anos, foi analisado utilizando EndoG v.4.4. **Resultados:** O tamanho efetivo populacional variou de 72,53 nas gerações completas para 143,90 nas gerações máximas. Coeficientes de Endogamia e Relação foram 0,34 e 0,91%, respectivamente. O número efetivo de fundadores e ancestrais foram 29 e 28 animais, respectivamente, sendo que apenas dez ancestrais foram responsáveis por 50% da variabilidade genética de toda a população. O intervalo de gerações foi de 5,84 anos para linha paterna e 7,70 para linha materna. As estatísticas F de Wright indicaram uma pequena distância genética das subpopulacoes entre os subgrupos em relação à população total (FST = 0,0015), entre os indivíduos em relação à sua subpopulação (FIS = -0,0027) e entre indivíduos em relação à população total (Fit = -0,0012). Isto indica uma baixa diferenciação genética na população estudada. **Conclusão:** A análise populacional indicou que, apesar do número pequeno de animais com ascendência conhecida e considerável perda de variabilidade genética pelo uso constante de alguns touros e mesmo valor do número de fundadores e antepassados, a população mostrou boa gestão genética, endogamia baixa, baixa diferenciação genética entre subpopulações e provavelmente adequado tamanho efetivo da população para a preservação da raça.

Palavras-chave: *análise de pedigree, conservação de recursos genéticos animais, diversidade genética, endogamia, raças localmente adaptadas.*

Introduction

Global programs for the conservation of animal genetic resources have been developed to prevent the extinction of breeds and populations. Surveys conducted by the Food and Agriculture Organization of the United Nations (FAO) mention that, over a fourteen-year period, nearly 100 breeds became extinct and approximately 17% are threatened with extinction, while the risk status of many others (58%) is simply unknown due to a lack of data on the size and structure of their populations (FAO, 2015).

The lack of information about a certain population is among the main barriers to the development of breeding programs and conservation of animal genetic resources (Alemayehu and Getu, 2015). Genetic characterization of locally adapted breeds may offer valuable information for making appropriate decisions for the improvement and development of such programs.

Pedigree information for population studies has the advantage of low cost and simplicity when compared to using molecular markers (Carneiro *et al.*, 2009). The genetic structure of populations through pedigree information can clarify important circumstances affecting the genetic history of populations. Numerous studies to evaluate generation intervals, inbreeding, effective population size and other population parameters have been carried out to provide subsidies for breeding or conservation programs (Faria *et al.*, 2001;. Faria *et al.*, 2002; Vercesi Filho *et al.*, 2002a; 2002b; Faria *et al.*, 2004; Cleveland *et al.*, 2005; Carolino and Gama, 2008; Martinez *et al.*, 2008).

The Crioula Lageana cattle (*Bos taurus*) is the only Brazilian locally-adapted cattle breed to the coldest part of the country -the Santa Catarina plateau (Mariante *et al.*, 2009). This cattle, adapted to the local climate over centuries, has acquired unique traits, such as thick skin, long horn, and medium size, with advanced bearing, late sexual maturity and high prolificacy. It has more than 40 different types of fur, and the predominant one is African, with white loin and belly and red or black patches on the side, and red or black hair surrounding the eyes (Spritze *et al.*, 2003; Bianchini *et al.*, 2006). Since the late nineteenth century these animals have been crossed with European and zebu breeds, causing almost the total disappearance of the breed (Mariante and Cavalcante, 2006).

By the end of the 1980s, the Crioula Lageana cattle population was reduced to no more than 500 animals, of which more than 80% belonged to a single breeder (Mariante and Trovo, 1989). In 2003, the Crioula Lageana Cattle Breeders Association (ABCCL) was created and the official recognition of the breed by the Ministry of Agriculture, Livestock, and Supply happened in 2008. The current population of this breed in the Santa Catarina plateau exceeds 1,400 animals.

Knowledge of the population structure of Crioula Lageana breed is essential to understand the evolution of its genetic parameters, assist improving conservation programs, and plan for a sustainable use of this genetic resource (Biscarini *et al.*, 2015). Thus, the aim of the present study was to characterize the population structure of Crioula Lageana cattle breed to assess its genetic diversity.

Materials and methods

Location and animals

Population data was used on the Crioula Lageana cattle breed from Santa Catarina Plateau, located in the central region of the state of Santa Catarina, between parallels 26°10› and 28°40' South latitude and meridians 49°10' and 51° 0' West longitude. The altitude of this region ranges between 700 and 1,800 m.a.s.l., with altitudinal gradient declining in East-West direction. The climate, according to Köppen is Cfb type (humid temperate without drought) characterized by cold winters with high incidence of frosts and mild summers.

The database used was provided by the ABCCL (Brazilian Association of Crioula Lageano) and contained information collected during 38 years form 1,638 animals from Coxilha Rica, Campos de Curitibanos and Campos de Caçador of Santa Catarina Plateau regions, located on the Santa Catarina Plateau. Information included the registration number, date of birth, sex, dam, and sire registration number and farm. Data analysis of the genetic structure of the

Crioula Lageana population was performed using the ENDOG program v.4.6, according to Gutiérrez and Goyache (2005).

The genetic variation in the population of Crioula Lageana animals from Coxilha Rica (n = 223), Campos de Curitibanos (n = 1,359) and Campos de Caçador of Santa Catarina Plateau (n = 56) regions was calculated using the following parameters:

- Pedigree integrity index (PI): Calculated based on animal registration and reported the percentage of known ancestors to the fifth generation of the studied population.

- Inbreeding coefficient (F): Probability that two individuals must have identical alleles because they have a common ancestor:

$$F_X = \frac{1}{2}\sum\left(\frac{1}{2}\right)^n (1+F_A)$$

Where:

F_X: Inbreeding coefficient of individual x.

n: Number of generations interspersed linking both parents to the common ancestor.

FA: Inbreeding coefficient of each common ancestor.

- Inbreeding rate (**Δf**): Average inbreeding variation from one generation to another:

$$\Delta F = \frac{F_t - F_{t-1}}{1 - F_{t-1}}$$

Where:

F_t and F_{t-1}: Average inbreeding generation tth (i = 1, ..., t).

- Effective population size (Ne): Number of males and females contributing to the genetic variability in a population (Gutiérrez *et al*., 2008):

$$Ne = \frac{1}{2\Delta F}$$

Three additional Ne values were calculated using the regression coefficient (b) of individual inbreeding coefficient on: i) the number of full generations, ii) the maximum number of generations, and iii) the equivalent number of full generations, with the regression coefficient corresponding to the increment between two generations of inbreeding (F_n - F_{n-1} = b; Gutiérrez *et al*., 2008):

$$Ne = \frac{1}{2b}$$

- Average relatedness coefficient (AR): Probability that an allele randomly chosen from the whole population in the pedigree belongs to a given animal. It is calculated using a vector c, where each element corresponds to the respective AR of an animal, defined as:

$$c' = (1/n)\ 1'A.$$

Where:

A: Is the nxn matrix of the numerators of Wright kinship coefficients (NRM).

1: Is a vector of order 1xn and the number of animals.

The NRM can be obtained from a matrix P, where p_{ij} is equal to 1 if *j* is the sire and *i* is zero otherwise, which identifies the parental animals. Thus:

$$A = (I - ½\ P') = (I - ½\ P')^{-1}\ D.$$

Where:

D: Is a diagonal matrix with non-zero diagonal elements, which are obtained by: d_{ii}= 1, neither parent is known; d_{ii}= ¾, if one parent is known; and d_{ii} = ½, if both parents are known.

- Effective founders (fe): Number of animals responsible for the genetic diversity of the current population.

$$fe = \frac{1}{\sum_{k=1}^{f} q_k^2}$$

Where:

$q_{k:}$ Is the probability that the gene is originated from the founder *k*, or alternatively, q_k is the relationship coefficient of founder *k*.

- Effective ancestors (fa): Minimum number of animals (founders or not) needed to explain the full genetic diversity of a population:

$$fa = \frac{1}{\sum_{j=1}^{a} q_j^2}$$

Where:

q_j: Is the marginal contribution from an ancestor *j* (not necessarily a founder), that is, the genetic ancestral contribution that is not explained by an earlier ancestor chosen. q_j is the CR of ancestor *j*.

- Genetic conservation index (GCI): Effective number of founders present in the pedigree of a particular animal over the generations:

$$CGI = \frac{1}{\sum p_i^2}$$

Where:

p_i: Is the proportion of genes of the founder *i* in the animal pedigree.

- Generation interval (GI): Average age of parents at the birth of their offspring, considering all animals and only those that left descendants.

- Wright´s F statistics: Estimation of genetic variability of the population, using F_{st} coefficient (correlation between genes in a subpopulation in relation to the total population), F_{is} (correlation of individual genes in relation to its subpopulation) and F_{it} (correlation of genes of an individual with respect to genes of the total population):

$$Fst = \frac{\tilde{f} - \bar{f}}{1 - \bar{f}} = \frac{\bar{D}}{1 - \bar{f}}$$

$$Fis = \frac{F - \bar{f}}{1 - \bar{f}}$$

$$Fit = \frac{F - \tilde{f}}{1 - \tilde{f}}$$

Where:

$\tilde{f}$ and F: Are, respectively, the kinship coefficient and the inbreeding coefficient for the metapopulation and $\bar{f}$ the average relatedness within subpopulation. The parameter $\bar{D}$ comes from the calculation of Nei´s minimum distance (NEI, 1987).

Results

The lack of pedigree information is clear in Table 1. Even at maximum generations, the number of known generations was only 1.11. The effective population size ranged from 72.53 when full generations were considered (complete ancestor knowledge) to 143.90 in maximum generations (all generations with at least one known ancestor).

Ne values in this study varied concomitantly with the increase in inbreeding (**ΔF**) of the population (Table 1). The **ΔF** values ranged from 0.35% when all ancestral information was considered (maximum generation), to 0.69% when generations had both paternal and maternal information (full generations).

Table 1. Number of generations, increase in inbreeding (ΔF) and effective population size (Ne) per generation type in Crioula Lageana cattle (*Bos taurus*).

Type of generation	Number	ΔF (%)	Ne
Complete[1]	0.52	0.69	72.53
Maximum[2]	1.11	0.35	143.90
Equivalent[3]	0.77	0.57	87.95

[1]Generations where all ancestors are known. [2]Number of generations separating the individual from its more remote ancestor. [3]Sum of $(1/2)^n$ terms of all known ancestors, where n is the number of generations separating the individual to a known ancestor.

Of 1,638 animals included in the present study (Figure 1), less than half had both parents identified in the present generation (44.87% have known sire and 40.42% known dam).

The number of effective founders (*fe*) and number of effective ancestors (*fa)* were almost the same (Table 2), with values of 29 and 28, respectively.

Table 2. Summary of population parameters of Brazilian Crioula Lageana cattle (*Bos taurus*).

Population parameters	Value
Number of animals	1,638
Base population (one or more parents known)	986
Reference population	652
Number of ancestors that contributed to the reference population	198
Number of effective founder *fe*	29
Number of effective ancestors *fa*	28
Number of ancestors that explain 50% of the genetic variation	10

The inbreeding coefficient (F) and the average relatedness (AR) of the population were 0.34 and 0.91%, respectively. Only 10 ancestors accounted for 50% of the genetic variability of the population.

The genetic variation in the population was evaluated in Coxilha Rica (n = 223), Campos de Curitibanos (n = 1,359) and Campos de Caçador (n = 56) regions in the Santa Catarina Plateau, by calculating the Wright´s F statistics. Low genetic differentiation was observed between animals from the three regions, with values of Fst = 0.0015, Fis = -0.0027 and Fit = -0.00012.

The genetic conservation index (GCI) for Crioula Lageana ranged from 1 to 10.24, with an average GCI of 1.95, and 994 animals had a GCI lower than 2.0 (Figure 3).

The average Generation Interval (GI) was 6.41 years, with means of 5.84 years for the sire line and 7.70 years for the dam line (Table 3). The Generation interval for sire line was lower because sire replacement occurred more frequently compared to dam replacement. According to the association, females of Creole Lageana have greater reproductive longevity, therefore, females spend more time in the herd to contribute their genes.

Table 3. Generation intervals (GI) and standard deviation of Crioula Lageana cattle (*Bos taurus*).

Track	Mean (years)	Standard deviation
Father - Son	5.88	0.43
Father - Daughter	5.80	0.21
Mother - Son	8.70	0.72
Mother - Daughter	6.71	0.25
Total	6.41	0.16

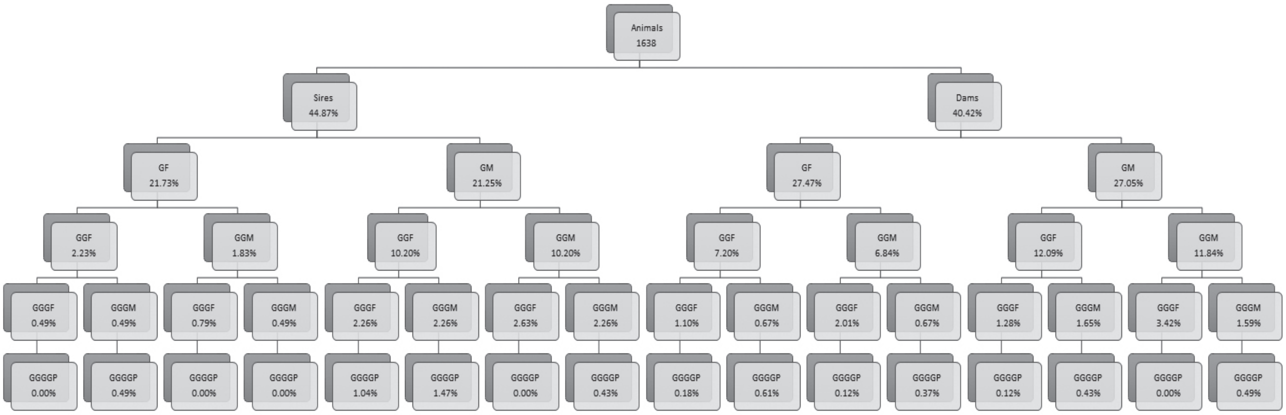

Figure 1. Pedigree structure of Crioula Lageana breed (*Bos taurus*) and level of identification of the ancestors to the fifth generation. GF – grandfather; GM – grandmother; GGM and GGF – great grandmother and father, respectively; GGGM and GGGF – great great grandmother and father, respectively; GGGGp – great great great grandparents.

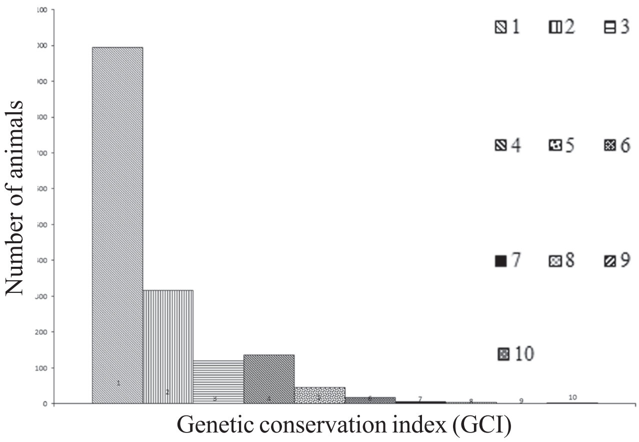

Figure 3. Genetic conservation index (GCI) for Crioula Lageana cattle (*Bos taurus*).

Discussion

An in-depth analysis of the pedigree completeness level of the breed is important since all results in terms of inbreeding and relationship are dependent upon it (Gutierrez *et al.*, 2003). The low percentage of ancestor knowledge in the present generation can be explained by the fact that the herd founders, which represent almost 20% of the animals included in the database, do not have a known sire or dam, as they were captured in the Santa Catarina Plateau forests in the 1970s. Only in 2003, with the creation of the breeders' association, it was possible to improve the management of the genealogical data record. There was also an increase in the number of herds registered and diversification in the use of sires.

The amount of ancestor knowledge in the present study is similar compared to other conservation programs. Gutierrez *et al.* (2003) studied the pedigree integrity of eight indigenous Spanish cattle breeds and identified 49 and 63% of known sires and dams for Bruna dels Pyrenees breed, respectively; 59 and 58% of known sires and dams for Asturiana de los Valles breed, respectively; 60 and 57% of known sires and dams for the Morucha breed, respectively. Cañas-Álvarez *et al.* (2014) found density of pedigrees average completeness indexes of more than 96% in the first generation and 80% when 6 generations were considered. Barros *et al.* (2011) studying Marota goats, found ancestors identified only up to the third generation, with a low percentage of ancestor knowledge in the population studied.

This study reflects the difficulty in obtaining genealogical data of most conservation breeds. Pedigree integrity is important for assessing the genetic structure of the population because all estimated parameters are a result of this structure, and the more complete the pedigree, the more accurate the other estimates will be. Thus, as with most locally adapted breeds, more enforcement is needed to increase ancestor knowledge of Crioula Lageana breed.

The effective population size was above the minimum recommended by the FAO (2007) of 50 animals, to guarantee the maintenance of maximum genetic variability over generations. So, even with a small population of 1,638 animals, a high Ne was observed when compared to other cattle breeds with larger populations. Research using data from more than 46,000 Indubrasil cattle reported a Ne of 45.75 (Vercesi Filho *et al.*, 2002b); a Ne of 39.50 was reported for a population of nearly 30,000 Polled Gyr (Faria *et al.*, 2001); and a study using 122,000 Tabapuã cattle reported a Ne of 55 (Vercesi Filho *et al.*, 2002a).

Although Ne was within a safe range considering the risk of extinction, the breeders should be vigilant regarding the use of only a few sires in their herds. A big difference was seen between the number of males and females, with 1,455 females and only 183 males. If this trend continues, Ne could shrink in the near future, as this parameter considers an ideal population where the same number of males and females are randomly mating. A previous study on Sindhi cattle reported Ne values decreasing from 161 (1979-1983) to 9 (1994-1998; Faria *et al.*, 2004). The authors attributed this fall to the difference in the number of males and females in reproduction. Thus, ABCCL should allocate a higher percentage of males for breeding.

The smaller the number of known ancestors, the less likely it is to detect an increase of inbreeding, due to the lack of ancestor knowledge. This justifies the lower **Δ**F found in full generations.

The low inbreeding rate observed in the Crioula Lageana may be associated with the absence of complete relationship information, as only 44.87 and 40.42% of the animals of the present generation had known sire and dam, respectively.

The number of known maximum generations of 1.11 means that the most remote ancestor of the population mean was its own parent. This is due to lack of careful record keeping and the recent expansion of the herd.

Similar to that observed with Ne, in which even with a small population of 1,638 animals, a low F value was observed when compared to breeds with larger populations where the inbreeding rate varied between 1 and 4% (Peixoto *et al.*, 2006). However, the F value for the Crioula Lageana population may be underestimated because of the lack of knowledge of complete genealogy. Thus, although this study shows low inbreeding, the breeders should be alert, as this result may be a consequence of the lack of full pedigree information. So, an increase of the inbreeding coefficient and a reduction in Ne is expected with increasing registry of animals. We believe that, in this case, F is underestimated and Ne overestimated, as it is expected with conservation herds. Egito *et al.* (2007) using microsatellite markers found inbreeding levels around 5%, one of the lowest levels for the locally adapted breeds studied.

Another parameter that tends to increase with ancestor knowledge is the average relatedness (AR) of the population. This index can be used as an alternative to the inbreeding coefficient, as it takes into account in its calculation the percentage of full pedigree originated from a founder. The AR observed in the present study is in agreement with other studies on locally adapted breeds (Cortés *et al.*, 2014; Kadlečík *et al.,* 2013). Gutierrez *et al.* (2003) also found low AR coefficients for some indigenous Spanish breeds, ranging from 0.10 to 0.73% for Avileña-Negra Iberica, Asturiana de los Valles, Morucha, Bruna dels Pyrenees, Asturiana Montana, and Alistana Sanabresa breeds.

The *fe* and *fa* were almost the same, which means that almost all animals that contributed to the generation of the breed continue to act effectively in the current herd, with no evidence of recent bottlenecks. Although these parameters are less sensitive to the pedigree completeness level than inbreeding coefficients, this could be overestimated since, for the calculation of this index, relationship information is necessary.

According to Gutierrez *et al.* (2003), in a population where genealogy knowledge is sparse, animals with unknown ancestors automatically become founders. For this reason, the results of the present study are in agreement with those reported by Barros *et al.* (2011), who, when studying small ruminants in conservation programs, also found similar values of *fe* and *fa*. An increase in the difference between the actual number of founders and the effective number of ancestors can cause "bottleneck" effect in the population, not seen here. This effect cause loss of genetic variation in the population over generations because of unbalanced use of individuals for reproduction, and is more common in populations with known historical pedigree.

The number of founders of the current population was of 291 animals. These animals had no known pedigree and were the first recorded animals. Of this total, 198 animals were ancestors and half of the genetic variability in the population came from only 5% of the ancestors. Thus, the current population developed from a narrow genetic base, which may have contributed to loss of genetic material throughout the generations.

An investigation of the structure and genetic diversity of Brazilian Zebu cattle breeds by pedigree analysis also reported that few ancestors were responsible for a high percentage of the genepool, e.g., 11-32 ancestors explained 50% of the gene pool of the reference population of all breeds (Peixoto *et al.*, 2010). These results confirm that the continuous use of specific breeding individuals can contribute to a considerable reduction in the genetic diversity of a population.

In the present study, 994 animals had GCI bellow two, which means that over 60% of the population had genes from only two founders. However, some animals had up to ten founders in their genetic composition. According to Alderson and Bodó (1992), as the goal of a conservation program is to retain the maximum number of alleles from the base population, the ideal would be that the individual received contributions from all the founders.

The average generation interval observed in this study was shorter in sires due to the replacement of breeding males, which occurs more frequently than replacement of females since, according to ABCCL, the Crioula Lageana females have high reproductive longevity, remaining longer in the herd. Another factor that may justify a lower sire line GI is the possible use of artificial insemination in this population. In a previous study using Morota goats, a generation interval of 5.28 was reported (Barros *et al.*, 2011).

The present findings are similar to other estimates for maternal line (Vercesi Filho *et al.*, 2002a), but higher than those for paternal line where AI was used (Razook *et al.*, 1993; Faria *et al.*, 2001). Peixoto *et al.* (2010) reported that sire-progeny GI (7.14-11.36 years) was always longer than the dam-progeny GI (5.20-7.96 years) for all breeds. In genetic conservation programs, when the number of animals available for reproduction is low, the use of breeding animals for longer periods tends to increase and longer generation intervals are expected.

Although the Crioula Lageana breed is linked to an animal genetic resource conservation program, the only source of income for most breeders is from selling these animals for breeding and slaughter, so it is natural that some of these breeders have an interest in promoting some kind of selection for characteristics to increase profitability. Therefore, male calves tend to be sold reducing the number of males available for breeding.

In this study, the F_{st} value was close to zero, demonstrating a minimal differentiation between subpopulations. F_{is} was below zero, indicating a higher frequency of matings between unrelated animals, which may have contributed to an increase in the number of heterozygous individuals. The negative F_{it} indicates a large number of heterozygotes in the population.

Research of the genetic structure of the Brazilian Red Sindhi breed using pedigree records from 1979 to 1998 reported increase in Fst from 0.07 to 5.65% and Fis from 0.30 to 4.74% (Faria *et al.*, 2004). Faria *et al.* (2002), studying the genetic structure of Polled Nelore in Brazil found values of Fst = 0.0056 and Fis = 0.0045. However, the low genetic differentiation observed in the Crioula Lageana population may be underestimated since the inbreeding coefficient, which was based on information from a little-known genealogy, was used to calculate this parameter. Thus, with the increasing genealogical records of the animals, another study should be conducted in a few years to confirm these findings.

The analysis of the genetic structure of Crioula Lageana cattle population indicates a reduced number of known ancestors and considerable loss of genetic variability due to the development of a population with a narrow genetic base. The population had low levels of inbreeding, low genetic differentiation among subpopulations and an effective population size above the recommended by FAO to maintain maximum genetic variability over the generations.

The results of the analyses shown here reflect a common problem with farm generated data, especially with small extensively reared breeds in less well developed countries. It is important to note that these farms, different from commercial breeds, frequently have farm staff who are illiterate and do not understand the importance of record keeping. Records can be lost or are not carefully maintained, although this has improved in recent years. This needs to be addressed in future conservation policies. While generation intervals are 6 to 7 years (Table 3) and there are almost 40 years of data, failure to register all animals led to the situation where data is available for only a few complete generations (Figure 1).

While the data obviously has limitations, the results can help policy makers to better design conservation and breeding schemes with locally adapted cattle breed in Brazil.

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