



Managing genetic diversity and society needs

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ABSTRACT - Most livestock are not indigenous to Brazil. Several animal species were considered domesticated in the pre-colonial period, since the indigenous people manage them as would be typical of European livestock production. For over 500 years there have been periodic introductions resulting in the wide range of genetic diversity that for centuries supported domestic animal production in the country. Even though these naturalized breeds have acquired adaptive traits after centuries of natural selection, they have been gradually replaced by exotic breeds, to such an extent, that today they are in danger of extinction. To avoid further loss of this important genetic material, in 1983 Embrapa Genetic Resources and Biotechnology decided to include conservation of animal genetic resources among its priorities. In this paper we describe the effort to genetically characterize these populations, as a tool to ensure their genetic variability. To effectively save the threatened local breeds of livestock it is important to find a niche market for each one, reinserting them in production systems. They have to be utilized in order to be conserved. And there is no doubt that due to their adaptive traits, the Brazilian local breeds of livestock can play an important role in animal production, to meet society needs.

Keywords: Animal genetic resources, Brazilian conservation program, genetic variability, microsatellites

Introduction

Animal domestication began 12,000 years ago and many subpopulations evolved due to adaptations to varying environmental conditions to which the animals were submitted due to migration of man over the centuries. These subpopulations, usually called breeds, underwent different selection pressures due to climate, endemic parasites, illnesses, diet and criteria decided by man. Breed formation, probably, was associated with a loss of some genetic diversity in the initial stages, as well as with the concentration and eventual fixation of some specific traits (Mariante & Egito, 2002). The main evolutive source of modification between breeds was probably due to random drift (Hetzl & Drinkwater, 1992; Barker, 1994). However, animal breeding, carried out under unidirectional selection pressure, may involve both an increase in the frequency of favourable additive genes as well as break regulatory homeostatic mechanisms which were established during the process of natural selection of these populations (Notter, 1999).

The genetic diversity is fundamental for sustainable genetic improvement, facilitating the rapid adaptation to necessary and unpredicted change to the development of production systems, as it is not possible to objectively predict which traits may be necessary in the future (Mariante & Egito, 2002). In 2003, FAO estimates that genetic variability relates to approximately 6,300 breeds or populations of domestic animals.

World preservation programs have been developed based on the preoccupation with loss of genetic diversity due to breed and population extinction. It is estimated that, each week, one or two breeds are lost (FAO, 2003), which limits access to their genes and unique genetic combinations. Hanotte & Jianlin (2005) commented that the situation is especially worrying in developing countries where changes in production systems lead to the substitution or absorption, by crossbreeding, of these native breeds and, with this, they concluded that the documentation of diversity of animal genetic resources (AnGR) is urgent as well as the use of strategies for their sustainable conservation.

Conservation of Animal Genetic Resources in Brazil

In Brazil, the livestock species are not indigenous. Several animal species were considered domesticated in the pre-colonial period, since the indigenous people managed them in a manner typical of European livestock production. Over the last 500 years there have been periodic introductions of farm animals to Brazil, resulting in the wide range of genetic diversity that for centuries supported domestic animal production in the country. Through the process of random drift allied with natural selection, these naturalized breeds became adapted to the biotic and abiotic pressures typical of the different Brazilian ecosystems. From the beginning of the 20th century, some commercial breeds, selected in temperate regions, have been imported. Although more productive, most of these breeds do not have adaptive traits such as resistance to disease and parasites found in the naturalized breeds. Even so, they gradually replaced the native breeds to such an extent, that the latter are, in most cases, in danger of extinction (Mariante & Cavalcante, 2006).

To avoid further loss of this important genetic material, in 1983 the National Research Center for Genetic Resources and Biotechnology of the Brazilian Agricultural Research Corporation (Embrapa) decided to include conservation of animal genetic resources among its priorities. In Table 1 it is possible to visualize the species and breeds included in research projects of the Brazilian Animal Genetic Resources Conservation Program.

Despite some naturalized breeds having different names and inhabiting different regions, they show similar phenotypes. This fact raises doubts about their identity as a distinctive breed group or native type. These geographically separate populations may or may not be genetically similar. Even if they belong to the same breed, due to geographical isolation or their adaptation to different ecological niches, they may have accumulated different alleles due to genetic drift. Therefore, genetic characterization would permit the identification of these unique genetic groups that were isolated in their environment for a long time.

Evaluating Genetic Diversity of Brazilian Breeds

The strategy of using genetic characterization in animal genetic resources (AnGR) conservation programs is not recent (Fitzhugh & Strauss, 1992; Barker, 1994; Mengers et al., 1994; Egito et al., 1999; Mariante et al.,

1999; McManus et al., 2005). In 1992, Hetzel and Drinkwater affirmed that molecular techniques, based on DNA polymorphisms, for the analysis of genetic variability, were essential for rational conservation and breeding programs, as these should be based on the combination of phenotypic and genetic data. Bjornstad et al. (2000) considered characterization as a first step for the conservation of native breeds.

Table 1 - Species and breeds included in research projects of the Brazilian Animal Genetic Resources Conservation Program – 2008.

Species	Breed	Region of the country
Cattle	Caracu	South/Southeast
	Criollo Lageano	South
	Curraleiro or Pé-duro	Northeast/Central-West
	Junqueira	Southeast
	Mochó Nacional	Southeast
	Pantaneiro	Central-West
Buffaloes	Baio	North
	Carabao	North
Donkeys	Jumento Nordestino (Northeastern donkey)	Northeast
	Jumento Brasileiro (Brazilian donkey)	Southeast
Goats	Azul	Northeast
	Canindé	Northeast
	Marota	Northeast
	Moxotó	Northeast
	Repartida	Northeast
Horses	Baixadeiro	Northeast
	Campeiro	South
	Lavradeiro	North
	Marajoara	North
	Pantaneiro	Central-West
	Puruca	North
Pigs	Monteiro	Central-West
	Moura	South
	Piau	Southeast/Northeast
Sheep	Blackbelly	North
	Brazilian Bergamasca	Central-West/Southeast
	Brazilian Somali	Northeast
	Criollo Lanado	South
	Fat Tail	Northeast
	Morada Nova	Northeast
	Santa Inês	All regions

Population studies which elucidate the relationship existing between the different breeds of a given species may offer useful information for the conservation and management of AnGR such as the evolution of the breeds, the development of gene pools and the magnitude of genetic differentiation (MacHugh et al., 1997; Bruford et al., 2003). Breeds have a unique

evolutionary history, in such a way each one may possess valuable genes that might be useful in breeding programs.

National AnGR conservation programs should use the association of phenotypic data, molecular polymorphisms and adequate statistical methods which reflect the real condition of a population. This fact alone justifies the effort used in the characterization of these populations, as the cost of projects of this type is high and should be considered in making rational decisions to avoid the duplication of efforts in the maintenance of breed samples. On the other hand, it is necessary to ensure the genetic variability of a breed, to avoid that unique traits are lost, which may be culled during the conservation process (Egito et al., 1999; Hanotte & Jianlin, 2005).

Through the utilization of genomic analyses it may be possible to obtain more knowledge on wild ancestors which originated the present livestock species as well as the localization and timing of the domestication events. Processes such as mutation, genetic drift, gene flow and natural selection, which influenced the variation between the genomes and populations, may also be studied (e.g., Bruford et al., 2003; Luikart et al., 2003). Using the variation pattern at a specific locus within the populations, important demographic factors for diversity conservation may be deduced (Kantanen et al., 1999).

Techniques which help in parentage analysis and in the genetic identification of an individual may be used for successful implementation and monitoring of *in situ* conservation programs (Hanotte & Jianlin, 2005). This information can be used to direct matings in order to maintain genetic variability; to choose individuals which are genetically less similar for the formation of a conservation nucleus; and to analyze the efficiency of the work carried out on the maintenance of variability of conservation nuclei over the years (Lara et al., 1998; Egito et al., 1999; Spritze et al., 2003; Egito et al., 2005; Oliveira et al., 2005; Paiva et al., 2005a).

The mean number of alleles, as well as expected (H_e) and observed (H_o) heterozygosity are commonly calculated parameters to check within breed diversity (Hanotte & Jianlin, 2005). Genetic diversity indices, such as mean heterozygosity of a population and F statistics (Wright, 1951), may be used to check the level of endogamy of a herd (e.g. Cepica et al., 1995; Alfenas, 1998; Luikart et al., 2003) while genetic

similarity indices between individuals may be used to choose matings to maintain genetic variability in conservation nuclei (Egito et al., 1999).

The precision of genetic distance measures is due to the number of independent alleles measured. Similar results are obtained when few loci with many alleles are used, or vice-versa (Kalinowski, 2002). Other factors such as true distance between populations, the heterozygosity at each locus and number of animals sampled in each population as well as the statistical model used may influence this precision (Barker, 1994; Ferreira & Grattapaglia, 1995; Nagamine & Higuchi, 2001).

For a long time the characterization of different breeds of domestic animals in Brazil was based, almost exclusively, on phenotypic data (morphology and production). This is sometimes insufficient to distinguish between pure breeds and is heavily influenced by environmental factors. However, since 1998 the genetic diversity of the main species of livestock has been estimated using different molecular markers, such as: protein polymorphisms (Lara, 2000); mitochondrial (Egito et al., 2006; Egito, 2007), Y-chromosome (Paiva et al., 2006) as well as RAPDs (Spritze et al., 2003; Serrano et al., 2004; Oliveira et al., 2005; Paiva et al., 2005b; Albuquerque et al., 2006a) and microsatellites (Paiva et al., 2005a; Albuquerque et al., 2006b; Araújo et al., 2006; Menezes et al., 2006; Egito et al., 2007).

Table 2 shows a summary of the genetic diversity observed in five livestock species in Brazil, obtained using microsatellite markers at the Animal Genetics Laboratory (AGL) of Embrapa Genetic Resources and Biotechnology. Although they show individual, breed and loci variations, four of the five species analysed showed similar inter-breed variation, except for the swine. The lowest indices of genetic diversity (H_e and MNA) were observed for buffaloes and pigs. The highest inbreeding values (F_{IS}) were observed in horses and buffaloes. These patterns may be explained by the recent introduction of buffaloes into Brazil and by the low effective population size, as well as the low number of stallions used for reproduction in the equine breeds. Of all the species analysed, the naturalised pig breeds are the most threatened by extinction in Brazil. Another pattern not shown specifically in Table 2, but which emphasises the strategic importance of naturalised

breeds, was that, within each species, these breeds present a higher diversity values than the commercial

breeds, showing that the conservation programme is moving in the right direction.

Table 2 - Genetic diversity of five livestock species using microsatellite markers.

Species	N	NB (Local Breeds)	Number of Loci	He	MNA	F _{IS}	AMOVA (%)
Buffaloes	382	05	14	0.686	10.07	0.224	11.91*
Cattle	915	10 (8)	22	0.816	13.18	0.167	11.87
Horses	328	07 (05)	11	0.875	14.36	0.204	12.37*
Sheep	383	10 (05)	19	0.775	10.84	0.015	11.76*
Pigs	182	05 (03)	24	0.702	10	0.114	15.73*

*p<0.001

N = number of individuals; NB = number of breeds; He = Expected Heterozygosity; MNA = Mean number of alleles; F_{IS} = Inbreeding Index; AMOVA = Analysis of Molecular Variance between breeds

In Brazil, as occurred previously with protein markers (Egito et al., 1999), studies on the analysis of genetic diversity in cattle using markers based on DNA polymorphisms, involve the characterization of commercial breeds such as Nellore and Gyr zebu breeds as well as Simmental and Holstein taurine breeds (Tambasco et al., 2000; Curi & Lopes, 2002; Machado et al., 2003). Recently, the genetic diversity of ten bovine Brazilian cattle breeds, including naturalized ones, was studied using a set of 22 microsatellite markers (Egito et al., 2007).

The expected introgression of zebu genes into Brazilian naturalized breeds was observed using different types of markers such as protein polymorphisms (Lara et al., 1998); RAPD markers (Serrano et al., 2004) and microsatellites (Egito et al., 2007). This introgression was also observed in other Criollo breeds in South America and the gradient observed between Argentina, Bolivia, Uruguay and Brazil, due to the presence of zebu in naturalized breeds may be explained by historic events and environmental factors (Giovambattista et al., 2000). In contrast, studying the matriarchal lineage of Zebu cattle it was possible to verify that the genetic base of these breeds (Nellore, Gyr and Guzerat) were composed by the naturalized taurine breeds that occurred in Brazil when the zebu was introduced (Egito et al., 2007).

Using molecular markers, such as RAPD (Fuck, 2002) and microsatellite (Sereno, 2002), the genetic diversity of the Pantaneiro horse was established. These studies showed that the breed descended from animals brought from the Iberian Peninsula during colonization. The Lavradeiro horse was also characterized using protein (Klautau-Guimarães &

Amaral, 1994) as well as RAPD markers (Martins et al., 1994). Both studies emphasized the need to preserve the breed due to the increasing de-characterization caused by indiscriminate crossing with animals of other breeds. The Marajoara and Puruca breeds were studied by Costa et al. (2005) using microsatellite markers. These authors observed high genetic similarity between both breeds, and with Iberian-American horse breeds, cited as founders of the Marajoara. Both breeds are genetically distinct.

A more ample study of genetic variability, on five naturalized horse breeds (Campeiro, Lavradeiro, Mangalarga-Marchador, Pantaneiro and Baixadeiro) as well as two commercial breeds (English Thoroughbred and Arab) was carried out in the AGL, together with the University of Brasilia (Silva, 2006). The study used eleven microsatellite markers and showed that the breeds are distinct genetic groups, with reasonable genetic variability, showing high levels of inbreeding. The least genetic distance was between the Pantaneiro and Arab (25%) breeds, with the highest distance between the Baixadeiro and English Thoroughbred (47%). The Baixadeiro was classified as the most distant in relation to the other breeds, emphasizing the need for conservation of this population. Management strategies need to be intensified to minimize inbreeding effects in these breeds.

Contrary to the other species of domestic animals that are found in Brazil, the buffalo was introduced more recently, around 1890, due to the importation by the breeder Vicente Chermont de Miranda, of the Dunas farm, in the township of Soure, Pará state. In the following years, a few sporadic importations were carried out, and although there was diffusion of this

species throughout the country, the Northern region still has the highest concentration. The present buffalo herd in Brazil has approximately 3,000,000 heads, and four breeds are officially recognized by the Brazilian Association of Buffalo Breeders - ABCB, as well as the genetic group known as Bay Type. The four official breeds are: Murrah, Jaffarabadi, Mediterranean and Carabao, which have well defined racial characteristics. The Bay Type is similar to the Murrah, but its coat color varies from bay to grey.

Albuquerque (2005) analyzed five buffalo groups using two types of molecular markers (RAPD and microsatellites) to estimate genetic variability within and between these groups. The combined power of discrimination and mean paternity exclusion probability of the 14 microsatellite loci resulting panel was 99.74% and 99.99%, considering respectively only one or both parents within groups. The principal component analysis from these data showed that the Bay and Carabao groups, which are part of the conservation program, are genetically distant from each other, as well as from the other groups. As they are genetically distinct groups, both need to be conserved as sources of alternative genetic variants. These two genetic groups represent important genetic material, which may serve as a source of alternative variability for breeding and conservation programs of the whole species in the future.

Sheep and goat breeds, as the other livestock species, were introduced into Brazil mainly by the Portuguese and Spanish during the colonization process. For social-cultural reasons, the rearing of these animals in Brazil was considered an inferior activity, such that, for a long time, they were only reared at a subsistence level. A profound change in the logistics of all classes involved in sheep and goat production was necessary to change this situation.

The sheep populations represent an important source of income, especially in the South and Northeastern regions, as well as hold important social, cultural and historical significance in those regions. The characterization of the existing naturalized breeds and the genetic relationship between them, as well as knowledge of their origin from other breeds, is the first step towards coherent breeding, management and conservation programs for these breeds. To date, eleven naturalized sheep breeds have been characterized using four classes of markers: RAPD, microsatellite,

mitochondrial DNA (mtDNA) and Y chromosome sequencing. The sheep breeds studied belong to two groups: naturalized (Santa Inês, Brazilian Bergamasca, Fat Tail, Morada Nova, Brazilian Somali and Crioula Lanada) and commercial or recently introduced (Île de France, Corriedale, Hampshire, Dorper and Damara).

Results from RAPD markers using five breeds of naturalized sheep (Paiva et al., 2005b) indicated that these markers could be used for diversity studies between sheep breeds. Nevertheless, these markers are not recommended for comparisons between herds belonging to the same breed. On the other hand, studies with 19 microsatellite loci with ten naturalized and commercial sheep breeds confirmed the results obtained with RAPD markers, as well as generated information on characterization and differentiation between herds within the analyzed breeds (Paiva et al., 2005a). As well as allowing for the identification of genetic variation patterns existing in sheep species in Brazil, this class of markers demonstrated its true usefulness for monitoring genetic improvement and paternity exclusion tests in controlling pedigrees (exclusion probability 99.99%) (Paiva et al., 2004).

The results obtained for this species in AGL are useful for basic and fundamental knowledge on genetic diversity of sheep in Brazil and will help in the implementation of conservation and breeding programs of naturalized breeds in Brazil. The Santa Inês breed has the largest herd of hair sheep at present in the country, with a high potential for meat production. Molecular results will also be useful in breeding programs for this breed. The other naturalized breeds have low effective population size, which suggests that efforts should be concentrated in consolidating their conservation programs together with private breeders and research institutions within the country.

The goat population in Brazil, contrary to sheep, is heavily concentrated in the Northeastern region and to date few studies have been carried out on their genetic diversity. Oliveira et al. (2005) in a study also carried out in the AGL, analyzed genetic diversity between seven herds of Moxotó goats in the states of Pernambuco, Paraíba and Rio Grande do Norte. The dendrogram generated shows that the naturalized Canindé breed, used as an outgroup, grouped together with the Moxotó populations, indicating a possible common origin of naturalized breeds, as well as recent crossbreeding events between the same breeds. The similarity matrix of pairs analysis it was possible to

choose animals for culling (due to high genetic similarity) and the probable founders for a representative nucleus of this breed formed from different herds. Other works using microsatellites were done with Brazilian naturalized goat breeds (e.g., Araújo et al., 2006; Menezes et al., 2006).

Taking the diversity of environmental regions which make up Brazil into account, with their climatic, cultural and social peculiarities, there are different types of farms situated in opposing ends of the technological spectrum of pig production. While at one end there are farms using high technology, showing production levels comparable with highly developed countries, on the other hand a large number can be found with extensive or semi-extensive production systems. The latter are characterized as family subsistence which is very important for a social-economic standpoint, especially for rural populations. Depending on the Brazilian region in question, this subsistence may represent almost 70% of the herd. The pig populations are composed of, in their totality, genetic groups which show specific characteristics ("local breeds", composed of lard type pigs) and differ from the "specialized" breeds reared in pig farms in intensive and highly technical systems (meat type) (Egito et al., 2004a).

Therefore, Brazilian pig production can be divided into three groups: Group I – made up of exotic or specialized breeds, including crossbred products or hybrids; Group II – composed of naturalized breeds and their crosses; Group III – made up of products of crossing between exotic and naturalized breeds (Egito et al., 2004a).

DNA studies to gather knowledge on the pig genome began in the 1990s. The pig, specifically, has contributed to the comparative mapping with humans (Guimarães, 2004). Studies with genetic characterization of populations/breeds are still incipient with this species. Fang et al. (2005) used microsatellite markers to differentiate Chinese and European breeds, while analysis of studies diversity and genetic variability were carried out in Mexico (Canul et al., 2005), Cuba (Martinez et al., 2005) and Portugal (Ramos et al., 2003). The structure, genetic variability and relationship between three naturalized Brazilian pig breeds (Piau, Monteiro and Moura) as well as two commercial groups (MS60 and Landrace) were studied in the AGL with microsatellite markers (Sollero, 2006). Results have shown that there is a sub-structure within

the naturalized Monteiro and Piau breeds and that the Monteiro and Moura have higher genetic diversity when compared with the other breeds being studied. The results of this study will contribute towards the planning of conservation programs for this species.

Valuing and Promoting Strategic Resources for the Future

It is important to emphasize that the Brazilian Program for the Conservation of Animal Genetic Resources is meeting its objectives, conserving *in-situ* and *ex-situ* valuable genetic material, characterizing it genetically and revealing its importance to the various segments of society (Mariante, 1993).

The preservation of the Brazilian naturalized breeds has its historical side, which is the "genetic memory" of animals that helped to colonize the country. In a more or less intensive form, there are still remains of all of these breeds, through their crossbreds. If these breeds were able to overcome, after dozens of generations of natural selection, the environmental challenges to which they were subjected, it is because they unite genotypes compatible with the most diverse conditions. Also, man's intervention in their reproductive and selection processes were, at most, modest and did not cause any appreciable modification in their potential, other than those received from nature.

Another aspect, which deserves consideration, is in relation to the proper dynamics of natural selection, which turns these native germplasm into authentic genetic reserves, especially when selection provokes the exhaustion of additive genetic variation and there is no more response in the animal breeding programs (Pereira, 1996).

Preliminary studies are being made in naturalized breeds in order to characterize the frequency of alleles of some candidate genes related with traits of economic interest. These studies are being conducted in an attempt to integrate naturalized breeds in the market. These markers can be used in early life for selection purposes or to demonstrate the existing potential in these populations so helping to encourage their development and sustainable conservation.

The calpain and thyroglobulin - TG5 genes (related to meat tenderness) and DGAT1 (diacylglycerol O-acyltransferase) and K-casein (both related to the production, as well as percentage of fat

and protein in milk) were analysed in different cattle breeds reared in Brazil (Lara et al., 2002, Egito et al., 2004b and 2005a). These molecular markers, related to organoleptic traits in meat may be used in breeding schemes for Brazilian breeds, especially on a wide scale such as in the Nellore, to improve meat quality (Egito et al., 2004b), as breeds of zebu origin have a lower degree of marbling, reflecting a meat that is less tender (Marschall, 1999).

The presence of allele 3 of the TG5 gene, related to a higher degree of marbling in meat (found at a 43% higher level in the naturalized breeds when compared with the Nellore, the main beef cattle breed in Brazil) shows the potential that naturalized breeds have for the meat industry in relation to products of higher quality and added commercial value (Egito et al., 2004b). The CPAN2A allele of calpain, related to meat tenderness, was found at a 43% level in naturalized breeds compared to 10% in beef cattle zebu breeds (Lara et al., 2005).

Genomic information between humans and pigs has been well established and there are molecular markers associated with production traits in the pig such as the estrogen receptor associated with high prolificacy; the riandin receptor associated with high muscular development capacity; the IMF gene associated with the control of intramuscular fat and KIT, the gene for predominant skin color (Faria, 2004).

The application of molecular techniques for naturalized Brazilian pig breeds began with the detection of a mutation in the gene for growth hormone, interfering in meat quality, in an F2 generation, product of a divergent cross from naturalized males of the Piau breed crossed with commercial females (Faria, 2004). From this population, the relation between PSS (Porcine Stress Syndrome) – one of the main reasons for losses in the pig industry - and meat quality (Band et al., 2005) was studied. This study indicated a negative effect of pig meat traits due to the production of muscular acidity which led to the loss of water during storage and cooking. PSS is known to be associated with variations of the gene of this syndrome (Plastow, 2000 cited by Band et al., 2005). According to the authors, results of this study may be used in selection programs as well as in the increase the quality of pig products.

Conclusions

Conservation and promotion of the sustainable use of livestock genetic resources has to be understood as part of a complex process. Complementarities, mix of technologies and capabilities, together with effective approaches to networking must be viewed as key ingredients in developing this process. One of the key problems limiting the effective implementation of a complex process is the difficulty to build effective teams and networks (Lopes, 2000). But it seems that in this specific case, the network is well established and the number of partners increasing.

For many reasons, developing countries do not put conservation of livestock genetic resources as a priority, mainly because their main goals are increased production and competitiveness in the global market in the short term. Brazil is one of the countries in this situation. Future configuration of domestic animal genetic resources and breeding programs is dependent on knowledge to guide strategic decisions about structures, methods, and capacities in order to take advantage of new opportunities and technological niches that can benefit from strong programs in the use and conservation of genetic resources. Unfortunately, there are very few prospective efforts directed to thinking about the future of genetic resources and breeding programs.

Research organizations need information that is not currently available, about the changes and influences and their impact in the future of key activities (Lima et al., 2005). To obtain and organize this information, new studies on the present and future performance of genetic resources and breeding programs and their related activities will have to be systematically developed in the country. These prospective studies and priority setting mechanisms, together with cost benefit analysis will be valuable to guide informed decisions on how to organize and manage future livestock genetic resources and breeding programs in Brazil.

To effectively save the threatened local breeds of livestock it is important to find a niche market for each one, reinserting them in production systems. They have to be utilized in order to be conserved. And there is no doubt that due to their adaptive traits, acquired after such a long period of natural selection, the Brazilian local breeds of livestock can play an important role in animal production, to meet society needs.

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