Genetic variability in a nucleus herd of Boer goats in Brazil assessed by pedigree analysis

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ABSTRACT

Genetic diversity and population structure were analyzed in Boer goats raised in Brazil, based on pedigree information of a population established from 92 animals imported in 1996, which received additional imported embryos in 2000 and some sires from other breeders between 2007 and 2012. Pedigree information on 1826 young kids born between 1997 and 2012 was used in the analyses. The herd census varied considerably among years, with a mean number of registered offspring of 82.1 ± 36.1 kids. The mean generation interval was 3.67 ± 1.81 years, and the mean number of offspring per parent was 19.01 ± 31.38 for sires and 3.85 ± 2.80 for dams. Parents were known for all animals in the reference population (animals born in the period 2009–2012), and 71.4% and 63.5% had grandparents and great-grandparents known, respectively. Animals in the reference population had a mean number of equivalent generations known of 3.55 ± 1.27 years, a mean inbreeding coefficient of $0.75 \pm 0.04\%$ and about 19% were inbred. The mean relatedness was $2.28 \pm 0.01\%$ for this group of animals. Over the period studied, the rate of inbreeding/year was $0.04 \pm 0.0002\%$, and the effective population size, estimated from the individual rate of inbreeding, was 173.5. The effective number of founders and ancestors represented in the reference population was 33 and 14, respectively, and 15 founders and 5 ancestors contributed with 50% of the gene pool. While in the early years the genetic contributions to the herd were mostly from American-imported animals, in recent years the influence of Brazilian- and Australian-born animals has gained importance. The results of our study indicate that inbreeding has been maintained at low levels in this population, essentially because the herd has been kept open to the introduction of new animals. This strategy should be continued, to maintain high levels of genetic diversity, which are needed for a successful selection program of Boer goats in Brazil.

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1. Introduction

In large populations, in the absence of selection, migration and mutation, gene and genotype frequencies remain unchanged through the generations, according to the Hardy–Weinberg theory, which theoretically assumes the existence of an infinite population. However, livestock populations are finite, so that in every generation those individuals that reproduce represent only a sample of the genes present in the population where they are coming from (Falconer and Mackay, 1996).

The maintenance of genetic diversity is a primary objective in the management of animal populations, both in selection and conservation programs (Fernandez et al., 2005). For a given breed, the risk of extinction and the liability of undergoing genetic erosion can be assessed by monitoring a set of parameters characterizing its structure and genetic variability (Goyache et al., 2003; Caballero and Toro, 2005).

Genetic diversity has frequently been monitored by assessing the change in inbreeding and relationships in the population of interest, and these are often converted into effective population size, which is considered a reasonable indicator of genetic erosion (FAO, 1998). However, changes in pedigrees, including recent bottlenecks, may go undetected, and alternatives have been proposed, based on the probability of genes originating from different herds

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(Robertson, 1953), founders (James, 1972) and ancestors (Boichard et al., 1997). These indicators are believed to provide better insight into short-term changes in the genetic structure and diversity of a population (Boichard et al., 1997), and have been widely adopted in analyses carried out in different livestock species, including small ruminants (e.g., Danchin-Burge et al., 2012; Gowane et al., 2014; Rashidi et al., 2015).

The Boer is the major meat-producing goat breed around the world (FAO, 2007) and was imported to Brazil in the 1990's (Sousa et al., 1998). The breed is now spread throughout the country, with the majority of the animals raised in the Northeast region, where they are used in crossbreeding programs with local goats. Boer goats were imported to Brazil from the United States and South Africa, and were brought either as live animals or as embryos. Nevertheless, the total number of imported animals did not exceed a few hundreds, and it is likely that inbreeding will increase and become a factor of concern in the near future. Therefore measures must be taken to preserve this breed in its environment, while maintaining genetic diversity.

In this study, we used information from the major seedstock herd of Boer goats in Brazil to: (1) assess the structure and genetic variability of the population, through the use of pedigree information; (2) make recommendations regarding the genetic management of the herd, for possible implementation of a breeding program aimed at conserving the genetic diversity of the breed.

2. Material and methods

2.1. Animals

The Boer herd studied here was established in 1996 in a research-oriented farm located the State of Paraiba (Northeast Brazil), from a group of 92 registered Boer goats imported as live animals from the United States. Another importation took place from South Africa in 2000, consisting of 150 Boer embryos. In addition, 11 animals (males) from private Boer herds in Brazil were also used for breeding in the experimental herd (2007–2012). These animals were either born in Brazil or imported from Australia by those breeders. Over the period of 1997 to 2012 reported here, 1826 young kids were born in this herd, from 70 sires and 345 dams which were used for breeding.

2.2. Database and pedigree file

The approval of animal welfare and ethics committee on animal use was not necessary for this study because the data were obtained from the existing data files of Company for Agricultural Research of State of Paraiba—EMEPA/PB, Brazil. This herd is traditionally raised under semi-intensive conditions on native and cultivated pastures (*Andropogon gayanus* Kunth and *Cenchrus ciliaris* L.), with supplementation of minerals and concentrate throughout the year, and supplementation with forage (hay and silage) during periods of low supply of pastures. Reproduction takes place through controlled natural mating, so that sires are known for all offspring.

This study includes animals born between 1997 and 2012. For each animal included in the analyses, information was available regarding sire, dam, sex and birth date. The records were edited and validated with respect to the consistency of information on pedigree, sex, date of birth, and duplicate records. Other sources of information were also available for this group of animals, including type of birth, weights at birth and various stages, etc. but these were not considered in the current analyses. For imported animals, the information of sire and dam, plus any known ancestor were included in the database, making the pedigree of animals born in Brazil progressively fuller.

2.3. Pedigree analysis

Basic demographic information, including number of animals born by year, age distribution of parents and number of offspring produced per sire and dam, were computed with SAS 9.2 (SAS Inst. Inc., Cary, NC).

The degree of pedigree completeness was evaluated by calculating the equivalent number of complete generations known per animal (n_i) as in Carolino and Gama (2008):

$$n_i = \frac{n_s + n_d}{2} + 1$$

where n_s and n_d are the number of generations known for the sire and dam, respectively, when s and d are known; if s or d are unknown, then n_s or n_d, respectively, assume a value of -1. Base animals, i.e., those with unknown parents, were assigned a number of generations known equal to 0. The degree of pedigree completeness was also studied by counting the proportion of known ancestors several generations back (Gutiérrez et al., 2003).

Individual coefficients of inbreeding (F_i) and additive genetic relationships among pairs of animals were computed based on the algorithm proposed by Meuwissen and Luo (1992). An inbreeding level of 0 was assigned to individuals with 1 or both parents unknown. The rate of inbreeding per year ($\Delta F/y$) was estimated by the regression coefficient of F_i on year of birth, through the GLM procedure of SAS software version 9.2 (SAS Inst. Inc., Cary, NC).

The generation interval was defined as the average age of the parents at the birth time of their progeny, and it was computed across the four paths of selection (sire to son, sire to daughter, dam to son and dam to daughter). The mean of the four selection paths was considered to correspond to the mean generation interval (L), which was used to compute the rate of inbreeding per generation ($\Delta F/g$) as $\Delta F/g = L (\Delta F/y)$. The effective population size (N_e) was then calculated as (Falconer and Mackay, 1996):

$$N_e = \frac{1}{2\left(\Delta F/g\right)}$$

in which $\Delta F/g$ refers to the relative increase in inbreeding per generation. In addition, N_e was also calculated based on the individual change in inbreeding following Gutiérrez et al. (2009), as:

$$\Delta F_i = 1 - {}^{n_i-1}\sqrt{1 - F_i}$$

where F_i is the coefficient of inbreeding of an individual and n_i is its equivalent number of complete generations known.

A reference population was defined, in order to represent the current set of genes represented in the breed. This reference population is often used to investigate the genetic contributions of various ancestors in the pedigree, and usually covers a short period of time, to avoid the possibility of including both parents and their offspring, as this could bias the results (Boichard et al., 1997). In this study, the reference population corresponded to the group of goats born in the years 2009 and 2012.

The genetic contributions of founder and ancestor animals to the reference population were computed, as described by James (1972), Lacy (1989) and Boichard et al. (1997). Briefly, these methodologies are based on the assumption that an allele taken at random from any locus of an individual has a probability of 0.5 of having been received from a given parent, 0.25 from a grandparent, etc. (Carolino and Gama, 2008). The effective number of founders (f_e)