Diversidade genética da raça Senepol no Brasil por meio de análise de pedigree[1]

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Resumo: A manutenção da variabilidade genética em uma população é importante para garantir respostas de curto e longo prazo à seleção e para evitar problemas com endogamia. Assim, o objetivo deste estudo foi investigar a diversidade genética da raça Senepol no Brasil por meio de análise de pedigree. O arquivo nacional de pedigree da raça Senepol foi usado, o qual é mantido pela Associação Brasileira de Criadores de Bovino Senepol e Programa Geneplus-Embrapa. A diversidade genética foi investigada por meio de diferentes parâmetros propostos na literatura. O percentual de animais endogâmicos foi de 96%, contudo, a endogamia está em níveis moderados na população, visto que 93,5% dos animais apresentaram coeficiente de endogamia individual (F_i) igual ou inferior à 6,25%. O F_i médio foi igual a 1,95%. As estimativas dos números efetivos de fundadores e ancestrais e de equivalentes de genoma fundador foram baixas indicando perdas de variabilidade genética. Provavelmente, isto foi causado pelo uso de intensivo de poucos indivíduos na reprodução. A maioria da população Senepol do Brasil é endogâmica, porém, os níveis de endogamia são moderados não representando grande preocupação. Gargalos estão presentes no pedigree indicando perda de diversidade genética. Recomenda-se que os selecionadores brasileiros de Senepol utilizem ampla variedade de touros/matrizes a fim de expandir a variabilidade genética e que considerem o controle de endogamia ao realizarem os acasalamentos em seus rebanhos.

Palavras–chave: acasalamento, bovino, endogamia, taurino

Genetic diversity of Senepol breed in Brazil by pedigree analysis

Abstract: The maintenance of genetic variability in a population is important to guarantee the short and long-term responses to selection and to avoid problems with inbreeding. Thus, the objective of the present study was to investigate the genetic diversity of the Senepol breed in Brazil by pedigree analysis. The national pedigree file of the Senepol breed was used, which is kept by Brazilian Association of Senepol Cattle Breeders and Geneplus-Embrapa Program. The genetic diversity was investigated by some different parameters proposed in the literature. The percentage of inbred animals was 96%, however, the inbreeding is in moderate levels in the population since 93.5% of the animals presented individual inbreeding coefficient (F_i) equal or lower than 6.25%. The average F_i was equal to 1.95%. The estimates of effective number of founders and of ancestors and founder genome equivalents were low indicating loss of genetic variability. Likely, this has been caused by intensive use of few individuals as breeding animals. The majority of the Senepol population in Brazil is inbred, however, inbreeding levels are moderate not representing a great concern. Bottlenecks are present in the pedigree indicating loss of genetic diversity. Brazilian Senepol breeders should use broader variety of sires/dams in order to expand genetic variability and to consider inbreeding control while doing their cattle matings.

Keywords: cattle, inbreeding, mating, taurine

Introduction

Since the arrival of the first animals from Senepol breed in Brazil in 2000, the population has increased its census considerably. Considering only taurine breeds with semen marketed in Brazil in 2013, the Senepol breed was surpassed only by Angus breed (Aberdeen and Red), according to Brazilian Association of Artificial Insemination (ASBIA).

The growth of the Brazilian herd is based mainly on the use of reproductive biotechnologies, particularly embryo transfer (ET) and in vitro fertilization (IVF). Prominent sires and dams of the breed have been intensively used in ET/IVF programs leaving great number of progenies. This added to the fact of the Senepol population in Brazil to be originated from a few farms of Saint Croix (American Virgin Islands) and the United States of America, can contribute to the loss of genetic diversity, which a priori is already expected to be restricted.

Thus, the objective of the present study was to investigate the genetic diversity of the Senepol breed in Brazil by pedigree analysis.

Material e Methods

The national pedigree file of the Senepol breed was used, which is kept by Brazilian Association of Senepol Cattle Breeders (ABCB Senepol) and Geneplus-Embrapa Program (Beef Cattle Improvement Program).

Initially, purebred Senepol animals born in Brazil from 2001 to 2013 were selected, totaling 18,570 heads. Then, these animals had their pedigrees completed until founders. Finally, the final pedigree file used in the analyses had 20,228 individuals born from 1950 to 2013 (9,185 females and 11,043 males).

The genetic diversity was investigated computing some different parameters proposed in the literature. The number of equivalent complete generations (ECG) was computed as the sum over all known ancestors of the terms ($1/2^d$), where d is the ancestor's generation number, which is equal to one for the parents two for the grandparents, etc. Effective population size was estimated on the basis of individual rate of inbreeding (N_{eFi}). The effective numbers of founders (f_e) and ancestors (f_a) were obtained to evaluate the concentration of the origin of both animals and genes. Parameter f_e is defined as the number of equally contributing founders that would be expected to produce the same genetic diversity as observed in the population under study. When founders contribute to the reference population more equally, the effective number of founders is higher. Parameter f_a is the minimum number of ancestors, not necessarily founders, explaining the complete genetic diversity of a population. This parameter complements the information provided by f_e by accounting for the losses of genetic variability caused by the unbalanced use of breeding individuals producing bottlenecks. The founder genome equivalents (f_g) can be defined as the number of founders that would be expected to produce the same genetic diversity as observed in the population under study if the founders were equally represented and no loss of alleles occurred. The generation interval was defined as the average age of the parents at the birth of their progeny that were subsequently kept for reproduction.

The analyses were performed using EVA (Berg et al., 2007), PEDIG (Boichard, 2002) and RelaX2 (Strandén and Vuori, 2006) softwares. All parameters were computed for the reference population of animals born from 2006 to 2013. This definition is equivalent to animals born in the last generation interval.

Results and Discussion

The number of individuals in the reference population was 16,214, which represented 80.15% of the entire population used in this study. This result shows how fast the Senepol population has been increasing in Brazil since its arrival in 2000.

Despite of Senepol breed has arrived in Brazil recently, the ECG for Senepol (6.79) was greater than the values found by Santana et al. (2012) for Marchigiana (4.52) and Bonsmara (2.19) breeds in Brazil, which arrived in this country before Senepol.

The percentage of inbred animals for Senepol (Table 1) was quite greater than the ones reported by Santana et al. (2012) for Marchigiana and Bonsmara, 60.43% and 8.97%, respectively. However, the inbreeding is in moderate levels in the population since 93.5% of the animals presented individual inbreeding coefficient (F_i) equal or lower than 6.25% (Table 1). Additionally, average F_i (Table 1) was lower than the ones reported by Faria et al. (2009) for zebu breeds and by Santana et al. (2012) for Marchigiana.

The estimates of f_e, f_a and f_g (Table 1) were low indicating loss of genetic variability. Likely, this has been caused by intensive use of few individuals as breeding animals, which is common in Brazilian Senepol herds. The disproportion between f_a and f_e and specially between f_g and f_e indicates the presence of bottlenecks in the pedigree of the Senepol population raised in Brazil. In this context, it is advisable to stimulate the Senepol breeders to use a broader variety of sires and dams in order to minimize inbred matings and to expand genetic variability. Futhermore, it is recommended that breeders consider inbreeding control while doing their cattle matings.

The estimate of N_{eFi} for Senepol (Table 1) is within the range of 31 to 250 suggested by Meuwissen and Woolliams (1994). According to these authors, to keep the effective population size in this range would help to prevent decline in fitness as a consequence of inbreeding depression.

Table 1. Summary statistics of the pedigree analysis of the Senepol breed in Brazil for individuals in the reference population (born between 2006 and 2013)

Variable[1]	
Inbred animals, %	96.00
Average F_i , %	1.95
$F_i = 0$, %	4.00
$0 < F_i \leq 6.25$, %	89.50
$6.25 < F_i \leq 12.5$,%	4.00
$12.5 < F_i \leq 25$, %	1.99
$F_i > 25$, %	0.51
Maximum F_i, %	32.02
Effective number of ancestors (f_a)	34.81
Effective number of founders (f_e)	82.40
Founder genome equivalents (f_g)	18.21
f_a/f_e ratio	0.42
f_g/f_e ratio	0.22
N_{eFi}	120.60

[1] F_i = Individual inbreeding coefficient; N_{eFi} = Effective population size based on individual rate of inbreeding.

Conclusions

The majority of the Senepol population in Brazil is inbred, however, inbreeding levels are moderate not representing a great concern.

Bottlenecks are present in the pedigree indicating loss of genetic diversity.

Brazilian Senepol breeders should use broader variety of sires/dams in order to expand genetic variability and to consider inbreeding control while doing their cattle matings.

Acknowledgements

To Capes and Fundect for providing scholarship for the second author of this study, Vinicius Okamura.

To ABCB Senepol for providing Senepol pedigree file used in this study.

To Geneplus-Embrapa Program, especially to Dr. Paulo Roberto Costa Nobre and Renato Lemos Peixoto, for providing Senepol pedigree file used in this study and support on data analysis.

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