STUDY OF GENETIC DIVERSITY OF BÍSARO PIGS BREED BY PEDIGREE ANALYSIS

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Abstract

The objective of this work was to study the genetic diversity of the Portuguese autochthonous pig breed Bísaro by pedigree analysis. Data of Bísaro pigs breed was taken from the database of the National Breeders (Association Associação Nacional de Criadores de Suínos de Raça Bísaro - ANCSUB) concerning the period from 1997 to 2008. For both, pedigree and active population files completeness was evaluated. The number and the proportion of animals with both parents known, sire known, and dam known were computed using the SQL procedure. Population genetic diversity parameters were computed, using the PEDIG software package, for the active population which included animals born from 2003 to 2008. The effective number of founders was 78.8 for boars and 79.7 for sows, while the number of ancestors contributed with 50% of the genes in the breed pool gene was 24 for boars and 23 for sows. A high proportion (52.4%) of animals in the active population are inbred, and 43.9% of the inbreed animals presented inbreeding coefficient higher than 20%. These results suggest that genetic variability needs monitoring in order to avoid the losses of genes in the Bísaro pigs.

Key words: Demographic structure, Inbreeding, Probability of gene origin

INTRODUCTION

Genetic diversity is the basis of individual response to environmental changes, and to genetic selection and improvement. Nowadays, a high number of livestock breeds have small population size, leading to a rapid increase of the inbreeding coefficient, and to losses of genetic diversity which at long term is the primary key to the survival of populations. The reduction of fitness of the populations due to the inbreeding depression effects is well known, and a severe reduction of the population size (genetic bottleneck) increases the risk of extinction [5]. Thus, the conservation of rare livestock breeds relies on the conservation of the genetic diversity, and in the initial stage of conservation the rate of inbreeding should be minimised in order to preserve the genetic variation [1].

Pedigree data can be used to describe the genetic structure, and the genetic variability of livestock populations [4]. Boichard et al. [3] proposed an approach, based on the theory of the probabilities of gene origin, to describe the genetic diversity of livestock populations. This methodology allows estimating the genetic contributions of the founders animals (animals with unknown parents) to the active/actual population. Thus, the information extracted from the pedigree analysis can be used to identify management practises responsible for the losses of genetic diversity. The Bísaro pig breed is classified as endangered, and the definition of a plan to preserve its genetic diversity is a crucial task to its conservation.

This study aims were to describe the demographic structure, and the genetic diversity of the active population of Bísaro pigs breed by pedigree analysis.

MATERIAL AND METHOD

Data of Bísaro pigs breed was taken from the database of the National Breeders Association (Associação Nacional de Criadores de Suínos de Raça Bísaro - ANCSUB) concerning the period from 1997

to 2008. The information available at herd-book database included: animals identification, gender, sire, dam, and birth date. The herd-book records were edited and checked for logical consistency using structured query language (SQL) procedure of SAS [6]. A data subset with all actual active population was constructed; this file retained 1986 animals (212 boars and 1774 sows). The pedigree file was constructed tracing back the genealogy information of the active population on the herd book database using the SQL procedure of SAS [6]. Final pedigree file contained 3160 animals (628 boars and 2532 sows), of 7 generations, of which 358 were base animals.

For both, pedigree and active population files completeness was evaluated. The number and the proportion of animals with both parents known, sire known, and dam known were computed using the SQL procedure of SAS [6]. For all animals in the pedigree file, the equivalent complete generations (EqG) and the pedigree completeness of active population was given as the mean of EqG over all animals. Generation intervals were computed for the four pathways (sire-sire, sire-dam, dam-sire, and dam-dam) as the average age of parents at the birth of their offspring.

Population genetic diversity was described as proposed by Boichard et al. [3], and all parameters were computed using the PEDIG software package [2] using the active population (animals born from 2003 to 2008) as reference population. The effective number of founders (f_f), the effective number of ancestors (f_e), and the number of founder genomes (f_a) were computed. The f_f represents the number of equally contributing founder animals that would produce the same genetic variability found in the actual active population. The f_f is calculated as $f_f = 1 / \sqrt{\sum p_i^2}$ where p_i is the ratio of alleles in the reference population contributed by the founder i [3].

The f_e determines the minimum number of ancestors (founders or not) required to explain the complete genetic diversity in the reference population. This parameter is obtained by computing the marginal contribution of each ancestor [3] as $f_e = 1 / \sqrt{\sum p_k^2}$ where p_k^2 is the marginal contribution of ancestor k in the population. An ancestor may not be a founder animal, although it may share genes with other ancestors, and the expected contribution in the population p_k may be redundant and add up to more than one. As a result, only the marginal contribution of the ancestor under investigation can be used to assess the contribution of an ancestor's allele in the reference population.

The f_a represents the number of founders with the same contribution that would lead to the same genetic diversity found in the population and would not cause loss of alleles due to genetic drift. The f_a was computed as $f_a = 1 / \sqrt{\sum (p_i^2 / r_i)}$ where r_i is the expected ratio of alleles from founder i that would remain in the reference population, and p_i is the expected ratio of alleles from founder i that contributed to the reference population. A total of 500 segregations were simulated for the calculation of f_a for boars and for sows.

The inbreeding coefficient (*F*) was computed using the method by Van Raden [7] implemented in the PEDIG software [2]. The number of inbreed animals in the pedigree and in the active population was grouped into inbreeding classes.

RESULTS AND DISCUSSIONS

The information concerning the pedigree completeness for the pedigree file and for active population is presented in Table 1. The pedigree included 3160 animals (2532 sows and 628 boars), and there were 358 animals with both parents unknown, which represents the base population. The active population was composed of 1986 animals (212 boars and 1774 sows). For both, pedigree and active population files, around 75% of animals have both parents known (Table 1).

Table 1: Pedigree and active population information

	Pedigree		Active population	
	Number	Proportion, %	Number	Proportion, %
Animals	3160	100	1986	100
Both parents known	2420	76.6	1492	75.1
Sire known	230	7.3	156	7.9
Dam known	152	4.8	95	4.8

The equivalent number of known generations (EqG) per generation is shown in Figure 1. Pedigree completeness gives information about the average number of generations with known ancestors. The EqG was 100% for animals in the first generation, however a quick decrease was observed in the pedigree quality. Thus, the EqG decrease to lower than 50% at 5th generation and becomes close to 20% at 7th generation (Figure 1). This noticeable reduction on the pedigree information shows that efforts must be made to increase the quality of pedigree recording of Bísaro breed in order to keep the genetic links trough generations.
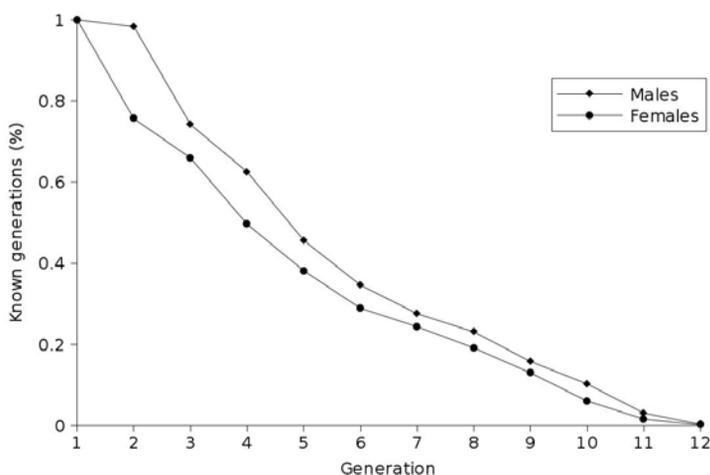

Figure 1: Equivalent number of known generations per generation

The distribution of inbred animals is shown in Table 2. A high proportion (52.4%) of animals in the active populations are inbred, and 43.9% of the inbreed animals presented a *F* higher than 20%. The increase of the relationship average reduces the probability of mating unrelated animals [8], thus at short term the mating systems must give advantages to less related animals (with lower levels of homozigoty) representing a higher number of founders animals. The average inbreeding was 22.9%, which shows the need to the definition of a mating strategy in order to avoid the mating of related animals. Thus, the pedigree information should be used to define the mating in order to minimize the inbreeding rate in the Bísara population. In populations with pedigrees of reduced length, the true autozygosity is highly underestimated. That is the case of the Bísaro breed, thus special actions must be undertaken in order to improve the pedigree information in order to control the rate inbreeding in the Bísaro breed. Baumung and Sölkner [1] showed that taking more than five generations of a correct pedigree into account leads only to a marginal increase of the correlation of pedigree inbreeding coefficients and autozygosity. However, if the false parentage is higher 20% is a more severe problem for the identification of the most autozygous animals than does incompleteness and shortness of pedigrees.

Table 2: Number of inbreed animals in the pedigree and in the active population of Bísaro breed

Inbreeding class	Pedigree		Active population	
	Number	Proportion, %	Number	Proportion, %
0-5	232	13.6	198	19.0
5-10	207	12.2	143	13.7
10-15	218	12.8	149	14.3
15-20	158	9.3	94	9.0
20-25	92	5.4	73	7.0
25-30	170	10.0	38	3.7
30-35	158	9.3	77	7.4
35-40	98	5.8	30	2.9
40-45	96	5.6	65	6.2
45-50	68	4.0	46	4.4
50-55	69	4.1	37	3.6
55-60	39	2.3	10	0.96
60-65	65	3.8	50	4.8
65-70	22	1.3	21	2.0
70-75	10	0.59	10	0.96
Average inbreeding	24.7 (max 73.5)		22.9 (max 73.5)	
Inbreed animals	1702	53.8	1041	52.4
Total number of Animals	3160		1986	

The generation intervals for the four pathways parent-offspring are presented in Table 3. A slightly lower generation interval was observed in sire-son pathway, in fact boars starts its reproductive activity earlier than sows, and this can be more pronounced with the use of artificial insemination. For all four pathways, an increase on the generation interval was observed from 1997 to 2008, this trend can be explained by the reduction of artificial insemination during the last years.

Table 3: Generation intervals (years) for the four pathways parent-offspring

Period	L_{ss}	L_{sd}	L_{ds}	L_{dd}	Average
1997-1999	1.26	1.49	1.24	1.38	1.35
2000-2002	1.21	1.45	1.25	1.39	1.33
2003-2005	1.33	1.47	1.39	1.46	1.41
2006-2008	1.70	1.93	1.87	1.81	1.83

L_{ss} - sire to son, L_{sd} - sire to daughter, L_{ds} - dam to son, L_{dd} - dam to daughter.

The effective number of founders and ancestors for Bísaro breed are shown in Table 4. For active population, the effective number of founders was 216 boars and 287 sows, thus around 500 ancestors (founders or not) contributed with 100% of the alleles present in the active/actual population. However, the f_e is much smaller (78.8 boars and 79.7 sows), and around 80 founders would represent the genetic variability in active/actual population (animals born between 2003 and 2008). A total of 23 sows and 24 boars contributed to 50% of the gene pool of sows and boars in the active population, respectively.

Table 4: Number of founders (f_f), effective number of founders (f_e), effective number ancestors (f_a), number of ancestors contributed with 50% genes to Bísaro gene pool (N_{50}), and gene contribution of the most important ancestors (C_{max}) by gender

	Males	Females
f_f	216	287
f_e	78.8	79.7
f_a	22.1	25.6
N_{50}	24	23
C_{max}	5.4	5.2

In spite of the high number of inbred animals, the maximum unique animal contribution for the active population was 5.4% for boars and 5.2% for sows. The marginal contribution of ten sows explained 34.3% of the genetic variability observed in the females and 10 males explained 31.9% of the variability in boars. The ratio f_e/f_a gives the magnitude of loss as a result of a bottleneck [8], this ratio was 3.6 for boars and 3.1 for sows and shows that Bísaro population suffered considerable losses of genetic variability. Generally, males contribute with more genes in the population, since they produce more offspring; however the Bísaro breed doesn't show that typical pattern.

CONCLUSIONS

This study shows that efforts must be made to increase the quality of pedigree recording of Bísaro breed, since is of crucial importance for the breed genetic management. Bísaro breed suffered high losses of genetic variability, thus a mating system program should be implemented in order to minimize the rate of inbreeding in the population. The monitoring of genetic variability can avoid the losses of genes affecting economically important traits and Bísaro breed fitness.

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