

Protein polymorphisms and genetic relationships in Mouro in relation to other breeds of pigs reared in Southern Brazil

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ABSTRACT

Fourteen protein systems encoded by 15 structural loci were used to investigate genetic variability in a population of the Mouro swine breed reared in Southern Brazil. The degree of genetic variability obtained for the Mouro animals ($\overline{H_e} = 0.130$) was similar to those estimated for other breeds (Landrace, $\overline{H_e} = 0.116$; Large White, $\overline{H_e} = 0.119$; Duroc, $\overline{H_e} = 0.095$) reared in the same region. This value is also close to those computed for wild pig populations. The gene frequencies at the polymorphic loci were employed to evaluate the usefulness of these systems for paternity identification. The combined probabilities of paternity exclusion were estimated at 58% for Mouro swine. Analysis of genetic relationships revealed that Mouro and Large White samples were the most similar ($D = 0.058$) and that the Duroc animals were the most dissimilar ($D = 0.107$). These results suggest that cross-breeding has occurred between Mouro and Large White pigs in Brazil.

INTRODUCTION

The Mouro breed (Figure 1) is one of several Brazilian swine breeds. The exact origin of this breed is unknown. The first pigs that were brought to Brazil had an Iberic origin, though probably they also came from Africa and Netherlands (Barreto, 1986). The Mouro swine was one of the preferred breeds raised by many

small farmers who lived in Southern Brazil at the beginning of this century (Silva, 1987). The main morphological characteristics of Mouro pigs are: black coat intermingled with white hairs, black nails, black skin, medium-sized head and ears, and a straight face profile. On average, Mouro swine reach 85 kg at 180 days of age (Silva, 1987).

Biochemical polymorphisms have been used to characterize populations, to investigate the levels of genetic variability exhibited by breeds and to verify the relationships among them (Oishi and Tomita, 1976; Oishi *et al.*, 1980; Tanaka *et al.*, 1983; Van Zeveren *et al.*, 1990). Moreover, the gene frequencies of various polymorphic biochemical loci can be used for paternity verification (Oishi and Abe, 1970).

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Figure 1 - An 18-month old male Mouro pig.

MATERIAL AND METHODS

Blood samples were collected from 58 adult Mouro pigs (nine males and 49 females) at the Experimental Station of Canguiri, Sector of Agrarian Sciences, "Universidade Federal do Paraná".

The animals at this station preserve the main features of the Mouro breed and are the descendants of 23 pigs (two males and 21 females) from several farms in Southern Brazil. These pigs were collected to save and multiply the last remaining animals of this breed and to evaluate their productive and reproductive performance.

Genetic variations at 15 structural loci were assayed by horizontal starch/agarose gel electrophoresis. Electrophoresis and protein staining techniques were as follows: hemopexin (Hpx), amylase 1 and 2 (Amy1 and Amy2) were performed according to Kristjansson (1963); transferrin (Tf) and ceruloplasmin (Cp) were typed in accordance with Oishi and Tomita (1976); the procedures used for the study of phosphogluconate dehydrogenase (Pgd) and phosphohexose isomerase (Phi) were those employed by Gahne and Juneja (1985); the methods described by Spencer *et al.* (1964) and Harris and Hopkinson (1976) were used for esterase D (EsD), malate dehydrogenase (Mdh), isocitrate dehydrogenase (Idh), superoxide dismutase (Sod) and acid phosphatase (Acp); glyoxalase I (GloI), albumin (Al) and

hemoglobin (Hb) were typed according to the methods described by Franco *et al.* (1986), Tucker (1968) and Naoum (1987), respectively.

The allele frequencies were calculated by the gene counting method and Hardy-Weinberg equilibrium was verified by the classical χ^2 test or by using the method described by Smith (1986) for small samples. Genetic variability was estimated by the expected average heterozygosity ($\overline{H_e}$; Nei, 1975). The H_e values obtained for the different breeds were compared by the paired t-test (Beiguelman, 1988). Genetic distances (the differences between populations expressed as a function of gene frequencies) were estimated according to Rogers (1972) and the dendrogram showing the patterns of genetic relationships among samples, based on genetic distances, was constructed by Unweighted Pair Group Method Analysis, UPGMA (Sneath and Sokal, 1973), using the Biosys program of Swofford and Selander (1981). The combined probabilities of paternity exclusion were estimated by the formulas of Oishi and Abe (1970).

RESULTS AND DISCUSSION

Protein variability

Table I shows the gene frequencies of the systems investigated in Mouro pigs compared to those

Table 1 - Frequencies of various blood protein alleles in populations of Mouro, Landrace, Large White and Duroc swine.

Locus	Allele	Allele frequencies			
		Mouro (N=58)	Landrace ¹ (N=109)	Large White ¹ (N=116)	Duroc ¹ (N=57)
<i>Pgd</i>	<i>Pgd</i> *A	0.853	0.628	0.621	0.228
	<i>Pgd</i> *B	0.147	0.372	0.379	0.772
<i>EsD</i>	<i>EsD</i> *A	0.647	0.931	1.000	0.851
	<i>EsD</i> *B	0.353	0.069	0.000	0.149
<i>Amy 1</i>	<i>Amy 1</i> *A	0.000	0.133	0.090	0.000
	<i>Amy 1</i> *B	0.991	0.862	0.910	1.000
	<i>Amy 1</i> *C	0.009	0.005	0.000	0.000
<i>Phi</i>	<i>Phi</i> *A	0.371	0.156	0.444	0.184
	<i>Phi</i> *B	0.629	0.844	0.556	0.816
<i>Cp</i>	<i>Cp</i> *A	0.000	0.018	0.000	0.000
	<i>Cp</i> *B	1.000	0.982	1.000	1.000
<i>Hpx</i>	<i>Hpx</i> *0	0.000	0.064	0.004	0.000
	<i>Hpx</i> *1	0.621	0.624	0.746	0.070
	<i>Hpx</i> *2	0.009	0.046	0.000	0.140
	<i>Hpx</i> *3	0.370	0.266	0.250	0.790
<i>Tf</i>	<i>Tf</i> *A	0.172	0.037	0.168	0.096
	<i>Tf</i> *B	0.828	0.963	0.832	0.904

(1) Tagliaro *et al.*, 1993.

previously reported for Landrace, Large White and Duroc swine (Tagliaro *et al.*, 1993).

Nine of the 15 loci investigated in Mouro swine were monomorphic (*Mdh*, *Idh*, *Sod*, *Acp*, *Amy2*, *GloI*, *Al*, *Hb* and *Cp*) and the *Amy1* locus was idiomorphic, with a rare variant (*Amy1**C).

Alleles *Amy1**A and *Hpx**0, detected in Landrace and in Large White swine, were not detected in Mouro pigs, nor was the *Cp**A allele which was only found in the Landrace population.

For all systems except *Amy1*, the Mouro and Duroc breeds presented the same alleles, although at different frequencies. The rare variant *Amy1**C was verified only in the Mouro and Landrace samples, both at low frequencies.

As in the Landrace and Large White populations, the most frequent alleles of the various systems observed in the Mouro sample were *Pgd**A, *EsD**A, *Amy1**B, *Phi**B, *Hpx**1 and *Tf**B. Mouro pigs presented

the lowest *Pgd**B frequency value when compared with the other three breeds. On the other hand, the *EsD**B variant was at least twice as frequent in the Mouro sample when compared with the other breeds.

In all systems except *EsD*, the observed distributions of the phenotype frequencies were as expected by Hardy-Weinberg equilibrium. A significant deviation ($P < 0.01$) in the *EsD* system was detected in the Mouro sample, with an excess of heterozygous animals.

Considering all 15 loci, both polymorphic and monomorphic, the value obtained for expected average heterozygosity ($\overline{H_e}$) in the Mouro breed was 0.130, similar to those estimated for the other three breeds (Landrace, $\overline{H_e} = 0.116$; Large White, $\overline{H_e} = 0.119$; Duroc, $\overline{H_e} = 0.095$). For the common loci, the value of $\overline{H_e}$ was of the same order of magnitude as that computed for a wild pig population studied by Van Zeveren *et al.* (1990) and higher than some estimates obtained for other wild

pig populations (Smith *et al.*, 1980). The extent of genetic variability, at least at the loci investigated, seems not to be affected by the selection methods commonly used by breeders.

Paternity determination

Table II shows the values obtained for the theoretical probabilities of excluding the paternity of one of two possible boars for the variable systems, as well as the combined probability values. These results were estimated by the formulas described by Oishi and Abe (1970). The combined value obtained for the Mouro breed was 58% and the most efficient systems for excluding a false paternity, considering the loci investigated, were Hpx, Phi and EsD, respectively. In a previous report, Tagliaro *et al.* (1993) verified that Hpx and Phi are efficient systems for paternity exclusion in Landrace, Large White and Duroc swine, whereas the EsD system is useful for paternity tests only in Duroc animals.

In the absence of exclusion, knowing the gene frequencies of the population and the phenotypes of the pigs investigated, it is possible to calculate a paternity index (Lee, 1980).

Genetic relationships among breeds

Table III gives the genetic distances and similarity coefficients between Mouro, Landrace, Large White and Duroc swine, calculated according to Rogers (1972). The patterns of interbreed relationships revealed that the Mouro breed is most similar to Large White and most dissimilar to Duroc. These results could be explained by cross-breeding between Mouro and Large White pigs in Brazil, since these two breeds had different origins; Large White came from Great Britain and the Brazilian breeds came from the Iberic Peninsula, Africa and the Netherlands (Barreto, 1986).

Table II - Estimate of the average probability of excluding one of two possible boars as a parent with the aid of different variable loci.

Locus	Breeds			
	Mouro (N=58)	Landrace ¹ (N=109)	Large White ¹ (N=116)	Duroc ¹ (N=57)
<i>Pgd</i>	0.110	0.179	0.180	0.145
<i>EsD</i>	0.176	0.060	0.000	0.111
<i>Amy1</i>	0.009	0.108	0.075	0.000
<i>Phi</i>	0.179	0.114	0.186	0.128
<i>Cp</i>	0.000	0.018	0.000	0.000
<i>Hpx</i>	0.191	0.287	0.158	0.180
<i>Tf</i>	0.122	0.034	0.120	0.080
All loci	0.576	0.587	0.542	0.500

(1) Tagliaro *et al.*, 1993.

Table III - Genetic distances and similarities of the Mouro breed in relation to three other swine breeds reared in Southern Brazil (x1000).

Breed	Mouro	Landrace	Large White	Duroc
Mouro	****	927	942	893
Landrace	73	****	956	916
Large White	58	44	****	894
Duroc	107	84	106	****

Below the diagonal: Genetic Distance. Above the diagonal: Genetic Similarity (Rogers, 1972).

Figure 2 shows the genetic relationships among Mouro and the other breeds. This phenogram was constructed from the genetic distances estimated according to Rogers (1972) and using the UPGMA method. The phenogram clustered Mouro, Landrace and Large White, with Duroc in relative isolation.

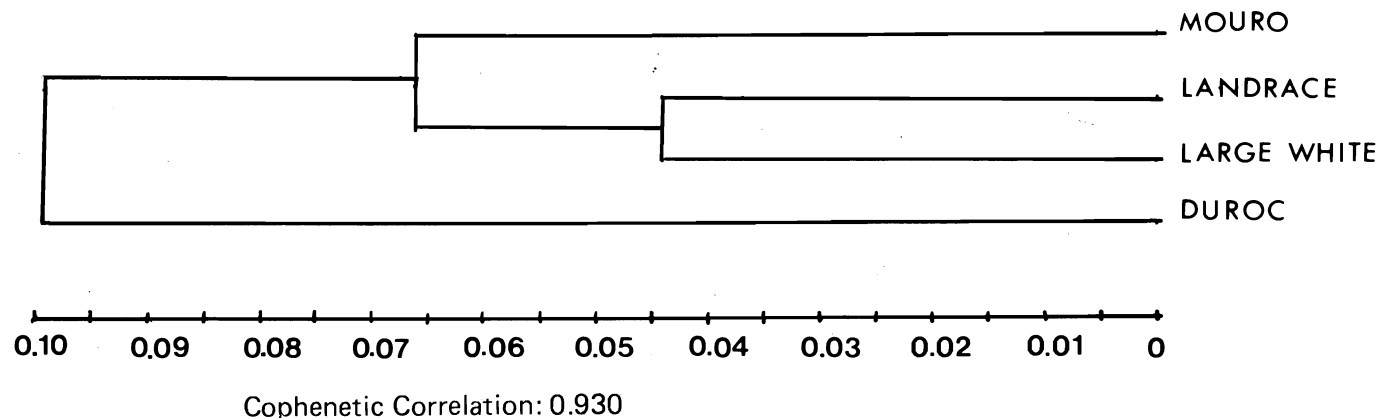


Figure 2 - Cluster analysis by the UPGMA using the Rogers Distance Matrix (1972) calculated for four swine breeds.

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RESUMO

Foram usados quatorze sistemas protéicos, codificados por 15 locos estruturais, para investigar a variabilidade genética em uma população de suínos da raça Mouro, criada no sul do Brasil. O grau de variabilidade obtido para os animais Mouro ($\overline{H_e} = 0,130$) foi similar aos estimados para outras raças criadas na mesma região (Landrace, $\overline{H_e} = 0,116$; Large White, $\overline{H_e} = 0,119$; Duroc, $\overline{H_e} = 0,095$). Este valor também está próximo aos encontrados para populações de porcos selvagens. As frequências gênicas dos locos polimórficos foram empregadas para avaliar a utilidade destes sistemas para a identificação de paternidade. As probabilidades combinadas de exclusão de paternidade foram estimadas em 58% para suínos Mouro. A análise do relacionamento genético revelou que, em relação aos suínos Mouro, os porcos Large White foram os mais similares ($D = 0,058$) e que os animais Duroc foram os mais distintos ($D = 0,107$), sugerindo que possa ter havido no Brasil cruzamentos entre animais Large White e Mouro.

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