

PEDIGREE ANALYSIS OF CINTA SENESE AND MORA ROMAGNOLA BREEDS

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ABSTRACT

During the last century, all the Italian pig breeds suffered a narrow bottleneck. Nowadays, only six Italian local breeds are still reared in Italy and only Cinta Senese and Mora Romagnola breeds can account on rather complete and reliable pedigree. The aim of the work was to assess both genetic variability and genetic contribution of founders and herds to the present populations for these breeds in order to explore the possibility to set up a selection of breeding animals. The results showed that both breeds still need an accurate mating management in order to contain inbreeding levels and at the moment no selection strategies could be planned.

Key words: Cinta Senese pig / Mora Romagnola pig / probability of gene origin / inbreeding / genetic diversity

1 INTRODUCTION

Nowadays, only six local breeds are still reared in Italy and keep a herdbook. These breeds are: Mora Romagnola, Apulo-Calabrese, Sarda, Nero Siciliano, Casertana and Cinta Senese. Only Cinta Senese (CS) and Mora Romagnola (MR) pigs have sufficiently complete pedigree data which allow genetic analyses producing realistic results. CS is the most important Italian autochthonous pig breed. In 1996, a genetic management program started and a reduction of the inbreeding level of the animals (from 0.21 in 1995 to 0.14 in 2003) was achieved (Franci *et al.*, 2004). The MR breed has the origin in Emilia Romagna and at the end of the last century, it was almost extinct. Only 12 animals were found in 1998 (Fortina *et al.*, 2005). Aim of the work was to analyze the pedigree information of CS and MR breeds in order to calculate the available genetic variability in terms of inbreeding levels, founders and herds contributions. Interpretation of the results would allow to assess if it is still needed to work mainly on inbreeding control or/and if it is possible to set up a genetic improvement program.

2 MATERIALS AND METHODS

Genealogical information recorded in CS and MR herdbook were obtained from ANAS (Associazione Nazionale Allevatori Suini, Roma). CS herdbook includes pedigree registrations since 1972 for a total of 53,608 animals; MR herdbook was instituted more recently and contains genealogical information since 1985 for 5,933 animals. Ancestors with both parents unknown were considered founders; if one parent was known, the unknown parent was considered a founder. To characterize CS and MR populations, pedigree completeness (MacCluer *et al.*, 1983) was assessed; depth of pedigree completeness remarkably influences the accuracy of inbreeding coefficients. Moreover, the generation interval was defined as the average age of parents at the time when selected progeny was born, and averaged. At herd level, the following parameters were calculated: effective number of herds (H_s) supplying fathers (Robertson, 1953) and genetic representation of herds at population level. This parameter was assessed summing up Boichard *et al.* (1997) contribution values of the ancestors belonging to each herd. Finally, effective number of founder

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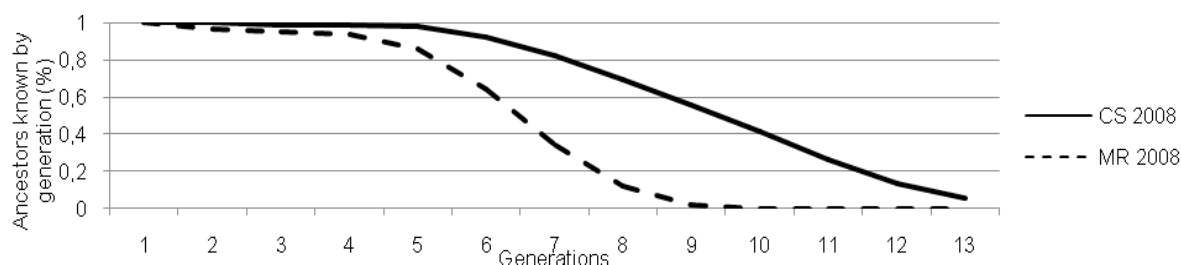


Figure 1: Pedigree completeness

herds (f_h) was estimated. Concentration of the gene origin was assessed by estimating the following criteria: effective number of founders (f_e) (Lacy, 1989) and the effective number of ancestors (f_a) (Boichard *et al.*, 1997). Moreover, inbreeding coefficient (F) and effective population size (N_e) were computed. In shallow pedigrees, N_e (calculated as $1/2\Delta F$) fits poorly with the real population giving an overestimated value of N_e . To better characterize N_e , the regression coefficient (b) of the individual inbreeding coefficient was estimated over: 1) the number of full generations of ancestors traced, 2) the maximum number of generations traced, 3) the equivalent complete generations. The regression coefficient (b) was considered as the average increase in inbreeding between two generations. Consequently, the N_e is estimated as half of regression coefficient ($1/2b$).

Table 1: Measures of pedigree completeness

Breed	CS	MR
Mean Maximum Generations	14.02	9.44
Mean Complete Generations	4.62	3.75
Mean Equivalent Generations	7.83	5.98

3 RESULTS

Pedigrees completeness is reported in Fig. 1. CS breed shows a deeper pedigree that is quite complete until the sixth generation; while MR breed has a shallow pedigree with complete information only for the first generation and a huge decline starting from the sixth generation.

Regarding the number of mean maximum generations traced (Table 1) CS herdbook has a wider depth of almost five generations; the mean of complete generations is 4.62 in CS and 3.75 in MR. The equivalent number of generations was 7.83 in CS and 5.98 in MR populations; these values are similar to those found in some French local breeds (Maignel *et al.*, 2001).

Table 2: Effective number of herds supplying boars and effective number of founder herds

Breed	CS	MR
Actual number of herds producing boars	190	43
Effective number of herds supplying boars (H_s)	23.86	18.98
Effective number of founder herds (F_h)	3.5	1.2

Average generation intervals are 2.51 and 2.01 for CS and MR, respectively. MR is still in a phase of demographic growth, so a higher number of piglets is selected as breeding animals.

There is a large discrepancy between the actual and the effective number of herds producing boars (Table 2). The difference is more pronounced in CS breed (190 to 23.86) than in MR breed (43 to 18.98). The number of effective number of founder herds (3.5 in CS and 1.2 in MR) is very small in both breeds. All these results the evidence that both breeds suffer a high concentration of the origin of the breeding animals. This makes these breeds rather weak in genetic terms. The risk is even more evident when considering the large unbalanced contribution of herds to the gene pool (Table 3): In both breeds, only five herds represent more than 90% of the total genetic variability (99.7% in MR). In MR breed, almost all the variability is provided by one herd (92.4%) but also in CS more than 69% of variability is provided by two herds only.

The total number of founders is noticeably higher than the effective number of founders in both breeds. At the beginning, both herdbooks were opened so all animals with the right morphological characteristics were enrolled even with unknown parents. This practice led to an overestimation of the total number of founders.

Table 3: Contribution of the most important herds (%) to genetic variability

Breed	Herd 1	Herd 2	Herd 3	Herd 4	Herd 5	Cumulated Contribution
CS	46.4	23.1	6.7	9.1	5.1	90.5
MR	92.4	3.1	2.5	1.0	0.6	99.8

Table 4: Contribution of major ancestors to the genetic variability

Breed	CS	MR
Number of ancestors contributing to 50% of the genetic variability	4	1
Highest contribution of single ancestor	0.22	0.57

Contrary, the effective number of founders (f_c) and effective number of ancestors (f_a) describe more realistically the contribution of founders/ancestors to the actual gene pool. In CS, f_c (11) and f_a (10) values were similar to some French local breeds (Maignel *et al.*, 2001), while f_c (3) and f_a (2) values were very low in MR. Small differ-

of inbreeding in MR was even higher at the beginning and did not reduce much (0.34) in the period observed, due to the reduced genetic base and the high relatedness among breeding animals.

Anyway, the inbreeding in MR breed is decreasing.

Table 5 reports the percentage of matings between close relatives.

Effective population size (Table 6) estimated by the regression coefficient (b) over the equivalent complete generations were 40.32 in CS and 10.87 in MR. The

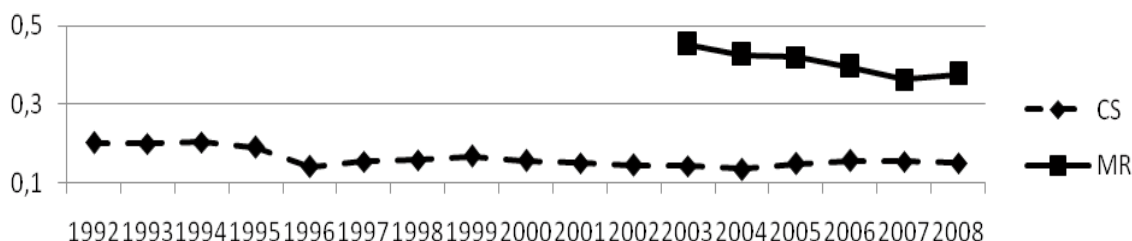


Figure 2: Changes of the average inbreeding coefficient

ence between f_c and f_a can be appreciated in both breeds: it is probably due to the fact that bottlenecks have been occurred before herdbooks reopening. Four ancestors (Table 4) contribute to 50% of the genetic variability in the present population in CS, while only one ancestor explains 57% of the genetic variability in MR (Table 4).

Table 5: Percentage of mating between close related animals (%)

Breed	Between full sibs	Between half sibs	Parent-offspring
CS	1.47	5.87	6.54
MR	5.06	14.68	8.51

Realized trends of the average inbreeding coefficients in CS and MR are reported in Fig. 2. Initially, CS had an average inbreeding coefficient very high (about 0.2); conservation strategies, based on a minimization of matings between close relatives, reduced the average level of consanguinity to 0.15. A value is similar to some French local breeds (Maignel and Labroue, 2001). Level

Table 6: Effective population size (N_e) estimated as $1/2b$

Breed	number of full generation traced	maximum number of generation traced	equivalent complete generations
CS	501.16	15.84	40.32
MR	35.88	6.51	10.87

Food and Agriculture Organization of the United Nations (FAO, 2000) suggested that N_e for a breed should be maintained above 50, even though Meuwissen and Wooliams (1994) indicated a minimum range for N_e of 31 to 250 to maintain population fitness. Effective population size in both breeds is clearly under the threshold defined by FAO. Thus, results indicate that both breeds are still suffering because of huge demographic collapse occurred in the last century.

4 CONCLUSIONS

CS pedigree is rather complete and deep, on the contrary MR pedigree is shallower and more incomplete. Both breeds have a scarce number of founder herds in-somuch more than 90% of the genetic variability is explained by only 5 herds (1 in MR breed). Regarding the concentration of gene origin, CS shows f_c and f_a similar to French local breeds, while MR has very low values for both parameters. Anyway, both breeds have an excessive concentration of gene origin; in CS 4 ancestors represent more than 50% of total variability, in MR only 1. Inbreeding level is adequate and stable in CS whereas it is still too high although decreasing constantly in MR breed. Even though, the analysis evidenced that mating between close

relatives is still carried out due to a scarce exchange of breeding animals. Finally, N_e is very low in both breeds and it is clearly under the threshold suggested by FAO. Results suggest that it is still too early to set up any selection program to improve both breeds. It is still necessary to manage mating for inbreeding control and to promote the exchange of breeding animals to enlarge the genetic base of these breeds.

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