The Nero Lucano Pig Breed

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The Nero Lucano (NL) pig is a black coat colored breed characterized by a remarkable ability to adapt to the difficult territory and climatic conditions of Basilicata region in Southern Italy.

Nero Lucano pig | Southern Italy | pedigree analysis | inbreeding coefficient

1. Introduction

The Nero Lucano (NL) pig is reared in Basilicata and is characterized by a black coat with rough coarse hair-bristles, mean size, long head with straight nose profile, brought-forward ears of medium length, long and thin legs, lean muscles, thick backfat and low number of newborns per delivery.

This breed is well adapted to the mountain habitat and climate conditions of Basilicata. Due to its rusticity, it is reared outdoors where occasional basic shelters can be found. These pigs are able to exploit feed resources available in the environment (such as thistles, carobs, alfalfa, acorns and bulbs) and occasionally receive a feed integration of common grains [1]. Cured products obtained from NL breed reared in these conditions are strongly appreciated by consumers and are sold under the brand “ANTICO SUINO NERO LUCANO”.

In Southern Italy the presence of black pigs can be traced back to 1729 [2]. The pig population consisted of native animals characterized by: black coat, remarkable rusticity and modest growth. They had different denominations in relation to the area they belonged to. The representative morphological types were: the Appulo-Lucano, the Calabro-Lucano, the Cavallino and the Italico [3].

In the second post-war period, technological innovations, evolution of agricultural and breeding methods, demand for lean meat by consumers and increasing production by farmers, have gradually determined the substitution of these native breeds with cosmopolitan ones. In 2001, few subjects (maybe six) showing the typical characteristics of the ancient black pig reared in Basilicata were identified. These subjects, thanks to institutions such as the Basilicata Region, the University of Basilicata, the Regional Breeders Association, the Comunità Montana Medio Basento and a group of breeders, were used to recover the Nero Lucano pig breed.

2. Pedigree Analysis

By using the data of the ‘Registro Anagrafico dei Tipi Genetici Autoctoni della Specie Suina’ (Italian Registrar for Autochthonous Swine Breeds) and ENDOG v.4.8 software, it was possible to construct a pedigree of 281 pigs,

distributed across 18 farms, characterized by a completeness index decreasing rapidly upstream the grandparents' generation (Table 1) due to the incomplete registration at the level of third and fourth generations back. In this pedigree, the 281 pigs were traced across three generations, the maximum number of generations traced was five, and the mean equivalent generations value was 1.39.

Table 1. Pedigree completeness index for the known generations in Nero Lucano pigs.

Generation	Completeness Index
Parents	0.851
Grandparents	0.461
Great-grandparents	0.072
gg-grandparents	0.003

The average generation interval was 2.88 years, with a maximum for sire–sire interval (3.5 years), and a minimum for dam–dam one (2.32 years) (Table 2).

Table 2. Average generation intervals in Nero Lucano pigs.

Interval	*N*	Years ± SD
sire–sire	13	3.503 ± 1.469
sire–dam	62	3.250 ± 1.320
dam–sire	13	3.187 ± 0.836
dam–dam	62	2.328 ± 0.778
Total	150	2.886 ± 1.190

Analysis of the pedigree showed that the mean inbreeding (F_{PED}) and relatedness values were 0.057 and 0.054, respectively. A total of 81 inbred animals, representing 28.82% of the whole pedigree, were characterized by a mean F_{PED} value of 0.197. These individuals were the result of mating between full siblings (13), half siblings (36), and parent–offspring (32). The high amount of parent–offspring mating is likely to be the consequence of both long generation intervals and the free rearing system. Data separated according to the three generations traced are shown in Table 3.

Table 3. Inbreeding coefficient, relatedness and effective population size of the three generations traced in Nero Lucano pigs.

Generation	*N* Pigs	Mean F	% Inbred	Mean Ffor Inbred	Mean Relat.	Eff.Pop. Size
0	42	0	—	—	0.0238	—
1	153	0.043	17.6	0.245	0.0565	11.5
2	86	0.109	62.8	0.174	0.0643	7.2

The more than doubled F_{PED} value (0.043→0.109) from generation 1 to generation 2 was determined by a strong increase (0.176→0.628) in the percentage of inbred animals. Such an increase was, however, coupled with a decreased mean F_{PED} value per inbred pig (0.245→0.174). The effective population size (Ne) was very low in both inbred generations (11.5 and 7.2, respectively). In addition, the whole current gene pool was explained by 42 ancestors, with only 8 explaining the 53.27% of the genetic variability.

3. Microarray Analysis

A total of 226 out of the 281 pigs belonging to the pedigree were genotyped by using the Illumina PorcineSNP60 BeadChip. These individuals were born between November 2006 and January 2014 and according to ENDOG pedigree analysis were distributed in the three generations traced as reported in Table 4.

Table 4. Number of Nero Lucano pig DNA samples analyzed with Illumina PorcineSNP60 BeadChip within each generation.

Generation	*N* Pigs	
	Pedigree	DNA Samples
0	42	6
1	153	132
2	86	85

The distribution of SNPs per chromosome was updated according to the Illumina PorcineSNP60 v2.0 Manifest File by using PLINK. All the animals passed the data quality control (genotyping rate > 95%), and the available 61565 SNPs were reduced to 60600 by the minimum call rate of 95%.

In the analyzed NL pigs, 12.7% of the autosomal SNPs were monomorphic (Minimum Allele Frequency, MAF = 0), whereas 51.38% were characterized by an MAF > 0.05.

Hardy–Weinberg analysis was accomplished for generations 1 and 2 with the exclusion of generation 0 for which only six individuals were available (Table 4). The percentage of SNPs that were not in the Hardy–Weinberg equilibrium ranged from 5.03% in generation 1 to 6.76% in generation 2. The excess of homozygotes was responsible for the observed Hardy–Weinberg disequilibrium in 57.53% of cases in generation 1 and in 88.57% of

cases in generation 2. These results are in agreement with the threefold increase of inbred animals percentage from generation 1 to generation 2, as evidenced by pedigree analysis (see Table 3).

The inbreeding coefficients based on SNP frequencies (F_{MOL}) showed very high average values of 0.53 ± 0.10 and 0.53 ± 0.12 for generations 1 and 2, respectively. Since SNP frequencies estimates on only six samples are insufficiently reliable, F_{MOL} value for generation 0 was not considered. As shown in Figure 1, more than two thirds of pigs are characterized by values higher than 0.50 (about 70% of generation 1 and 73% of generation 2). The distributions of F_{MOL} were very similar in both generations and characterized by similar minimum (0.11 and 0.14) and identical mean (0.53) and maximum values (0.74).

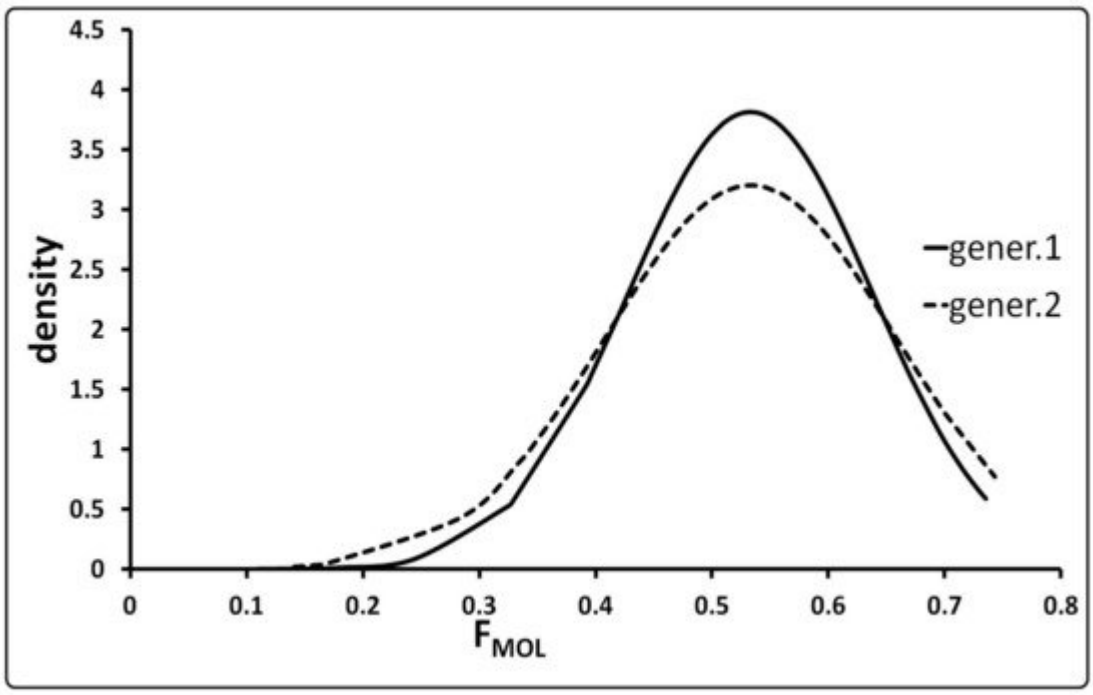

Figure 1. Distribution of the F_{MOL} (inbreeding coefficient using molecular polymorphisms) values in generations 1 and 2 of Nero Lucano pig.

References

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