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ANCIENT AUTOCHTHONOUS GENETIC TYPE (AAGT) '*NERO LUCANO*' PIG : GENETIC CHARACTERIZATION BY MICROSATELLITE ANALYSIS. PRELIMINARY RESULTS

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Introduction

The recovery of autochthonous genetic types (AGTs) and ancient autochthonous genetic types (AAGTs), according to the emerging '*sustainable multifunctional rurality*' concept, represents an example of integration between environmental and productive goals.The knowledge of intrapopulation polymorphism degree is one of the major step in any biodiversity safeguard programme.

Aim

To provide, by means of microsatellite analysis, a first contribution to the knowledge of the genetic variability of '*Nero Lucano*', whose origins could go back to the ancient pig present in Lucania region (Italy).

Some traits of '*NERO LUCANO*' AAGT

Somatic:
coat : black with rare reddish hair
head : long and straight – vigorous mandible; ears medially developed pointing forward with tip pending slightly ahead; grunt normally rectilinear
body mass : not very large – adult live weight:
- sow: ~ 140 kg
- boar: ~ 180 kg

body: medium lenght; dorsal line rectilinear tending to become arched in some subjects; chest not very high; abdomen wide; rump quite inclined
legs: quite long and thin

Reproductive: farrow/year = ~ 1,5

Productive: average daily weight gain = 198g/d in 1÷ 480 d interval, at '*extensive*' farming

Material and methods

The research, carried out on 41 subjects examining 19 microsatellite *loci* (table I), involved the following phases:

- DNA isolation from blood samples (Sambrook *et al*., 1989)
- DNA amplification by polymerase chain reaction (PCR) to microsatellite *loci*
- individual genotype assignment by ABI PRISM 310 automated sequencer (*Applied Biosystem)*
- statistical analysis by GENEPOP (Raymond and Rousset, 1995) and GENETIX (Belkhir, 2000) to estimate:
  - allele number per *locus*
  - expected and observed *h*eterozigosity
  - deviation from *Hardy-Weinberg equilibrium.*

TABLE I – Investigated microsatellite *loci*.

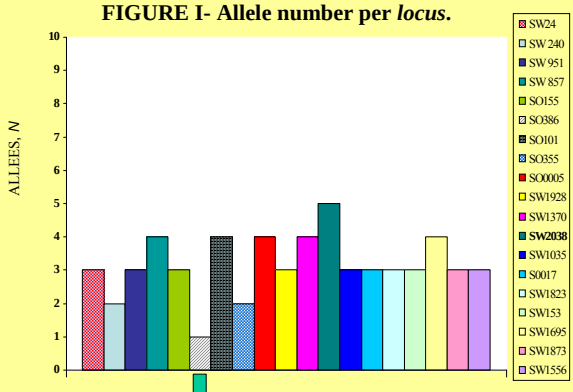
		MICROSATELLITE *LOCUS*		
N	ACRONYM	CHROMOSOMAL LOCATION	ALLELE SIZE, *bp*	*FORWARD* AND *REVERSE* PRIMER SEQUENCE (5'-3')
1	SO155	1	150÷166	TGTTCTCTGTTCTCCCTCGTTTG AAAGTGGAAAGAGTCAATGGCTAT
2	SW240	2	96÷115	AGAAATTAGTGCCTCAAATTGG AAACCATTAAGTCCCTAGCAAA
3	SW1370	2	88÷109	AGAGCAGTGGTCTGCTAAGATG GAATTGCCTAAATTACTTGTCC
4	SW1695	2	171÷205	ATAAGGGAAATCAGGCTGAGC TCCCAGGAGCTACCATATGC
5	SW153	4	219÷243	CCACGTTCTCCTTTTTGAGG ATGAGTTGTGGTGTAGGTCGC
6	SO0005	5	205÷248	TCCTTCCCTCCTGGTAACTA GCACTTCCTGATTCTGGGTA
7	SW1823	6	201÷217	CAGGTCATTGCTGTAGTGAAGG GAGCCTTGGGCTACGTAGTG
8	SW 857	6	144÷160	TGAGAGGTCAGTTACAGAAGACC GATCCTCCTCCAAATCCCAT
9	SW1873	7	105÷138	TATAATCTGGTGAACCATCCCC ATCAGATGTGCTAATACCCTGC
10	SW1928	7	83÷107	TAGGGTCAGTGCATCCTTCC ACGAGAACTCCGAACCCTG
11	SO101	7	197÷216	GAATGCAAAGAGTTCAGTGTAGG GTCTCCCTCACACTTACCGCAG
12	SO017	8	155÷179	CTAGGAGAAAATCTGAGGGTT GTTTGAATGGAGGTGCTGTA
13	SO386	10	158÷154	TCCTGGGTCTTATTTTCTA TTTTTATCTCCAACAGTAT
14	SW 951	10	125÷133	TTTCACAACTCTGGCACCAG GATCGTGCCCAAATGGAC
15	SW1556	14	220÷274	TCCCAGCACCTTGATTTTAG AGGTTGCTGGAGATAGTGAAGC
16	SW2038	14	107÷127	GCCGAGAAACCCTTCACC TAGCCTGTTCAGTGCCACC
17	SO355	15	243÷277	TCTGGCTCCTACACTCCTTCTTGATG TTGGGTGGGTGCTGAAAAATAGGA
18	SW1035	16	147÷167	TATGGGGGCCCTAAAAGAC AACGGCCTTAACCTCCTCAG
19	SW 24	17	96÷121	CTTTGGGTGGAGTGTGTGC ATCCAAATGCTGCAAGCG

Results

Within the limits of the observation field:

- average allele number per *locus*: 3.2±0,89 (*c.v.* = 28 %)
  - maximum value: 5.0 for SW2038 *locus*
  - minimum value: 1 (allele 165) for SO386 *locus*
- average observed heterozigosity : 49.13 ± 22.44 (*c.v.* = 46 %)
  - minimum value: 0, obviously, for monomorphic SO386 *locus*
  - maximum value: 92.68 % for *locus* SW 2038
- average expected heterozigosity : 47.86 ± 18.02 (*c.v.* = 38 %)
  - minimum value: 0, obviously, for monomorphic SO386 *locus*
  - maximum value: 73.17 % for SW2038 *locus*
- *loci* number deverging significantly from *Hardy-Weinberg* equilibrium under heterozygote deficit hypothesis: 3.

FIGURE I- Allele number per *locus*.



Conclusions

locus SO386 : monomorphic differently from what observed in other 12 AGTs [Ollivier *et al.* (2005); SanCristobal *et al*. (2006)]

☺ Microsatellite markers, as expected, may be considered '*valid indicators*' to estimate genetic variability '*status*'of population.

☺ If confirmed, monomorphism of *SO*386 *locus* might be used for a genetic discrimination of meat and its products derived from Nero Lucano, as support for '*tracing*' and '*tracking*' system in the management of '*pig meat chain'*.

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