ANALYSIS OF GENETIC STRUCTURE OF ‘*MAREMMANO ROMANO*’ HORSE BY MEANS OF MICROSATELLITE MARKERS

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INTRODUCTION

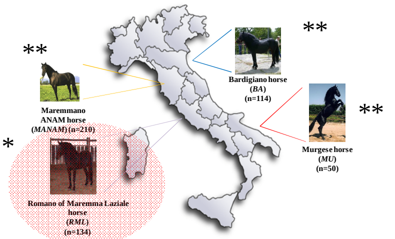
‘*Romano of Maremma Laziale* (*RML*)’ horse ancient autochthonous genetic type (AAGT) traces back to a mesomorph horse broadly represented, at least from 2nd millennium B.C., by nascent civilizations of Near East and Northern Africa. In ‘Maremma Romana’, the equide population reared was thought an optimal ecotype with improvement and refinement potential through the use of the superior local sires. The introgressions carried out in the two last centuries on equide Italic populations also concerned *RML* horse, before introducing sports competition dolicomorph thoroughbred sires *(starter)* for *“breeding improvement cross”*; this cross is influencing and modifying the aptitude and somatic aspects of *‘Maremmana’* population, making it minority and at risk of extinction. *RML* population is currently one of the little autochthonous genetic types bearing ancestral peculiar traits of the Mediterranean horse and, hence, is should be safeguarded.

AIM

To contribute to the knowledge of genetic variability degree of *‘Romano of Maremma Laziale’* horse AAGT, in the perspective to propose its registration in the Zootechnical book.

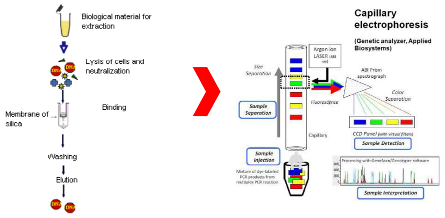
MATERIAL AND METHODS

STEP 1: SAMPLING



Legend:* genotyped at ConSDABI; ****** genotyped at Genetics and Services Laboratory (LGS)

STEP 2: GENOTYPING AT 11 MICROSATELLITE LOCI



Web refences of immages: ***www.biofabresearch.it; www.appliedbiosystems.com***

STEP 3: DATA ELABORATION

Software employed:

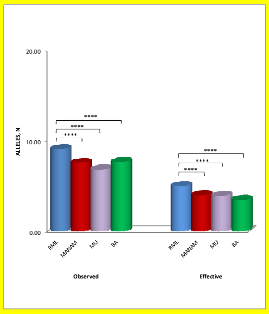
- **GENEPOP** *ver. 3.4.* (Raymond e Rousset, 1995);
- **GENETIX** (Belkhir, 2000);
- **MOLKIN** *v.2.0.* (Gutièrrez *et al.*, 2005);
- **STRUCTURE** (Pritchard *et al.*, 2000)

RESULTS

In the limits of the observation field, the results evidence in *RML*:

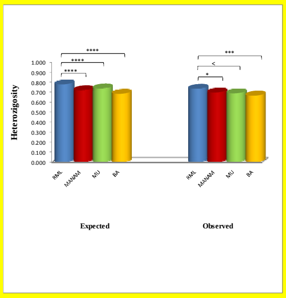
a higher genetic variability

- **‘total’ allele number** - significantly (*P*<0.001) higher value (100 *vs* 83 *vs* 84 *vs* 75 in *RML*, *MANAM*, *MU* and *BA*, respectively);
- **mean ‘observed’ allele number per *locus*** - significantly (*P*<0.001) higher value (9.09 *vs* 7.55 *vs* 7.64 *vs* 6.82 in *RML*, *MANAM*, *MU* and *BA*, respectively) *(*GRAPH 1*)*;
- **‘effective’ allele number** - significantly (*P*<0.001) higher value (4.99 *vs* 3.97 *vs* 3.91 *vs* 3.46 in *RML*, *MANAM*, *MU* and *BA*, respectively) (GRAPH 1);



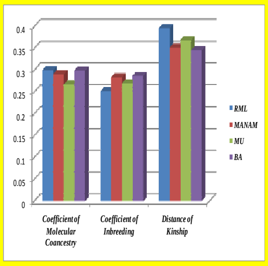
GRAPH 1. Number of observed alleles and effective number of alleles in the four GTs.

- **‘observed’ heterozigosity** - significantly (P<0.001) higher value respect to *BA* (0.735 *vs* 0.668, *P*<0.001) and to *MANAM* (0.735 *vs* 0.698, *P*< 0.05) and tendentially higher value (0.735 *vs* 0.690; *P*<0.10) respect to *MU* (GRAPH 2*)*;
- **‘expected’ heterozygosity** - significantly (*P*<0.001) higher value (0.779 *vs* 0.739 *vs* 0.722 *vs* 0.686 in *RML*, *MANAM*, *MU* and *BA*, respectively) (GRAPH 2);



GRAPH 2. Expected and observed Heterozygosity in the four GT.

- **coefficient of molecular coancestry** - lower value (0.229 *vs* 0.266 *vs* 0.290 *vs* 0.298 in *MU*, *MANAM*, *BA*, respectively) (GRAPH 3);
- **Coefficient of Inbreeding** - higher value (0.251 *vs* 0.269 *vs* 0.283 *vs* 0.286 in *RML*, *MU*, *MANAM* and *BA*, respectively) (GRAPH 3);
- ***distance of Kinship*** - higher value (0.396 *vs* 0.368 *vs* 0.351 *vs* 0.345 in *MU*, *MANAM*, *BA*, respectively) (GRAPH 3);



GRAPH 3. Parameters of molecular coancestry in the four GTs.

a divergence respect to *MANAM* subjects; in particular, the Figure 1 evidences a transvariation area between the two populations, confirming a common ancestral origin;

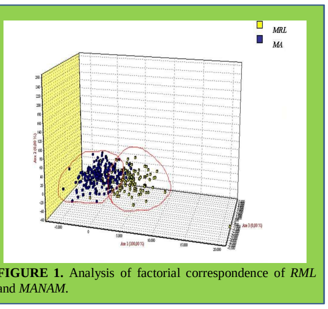
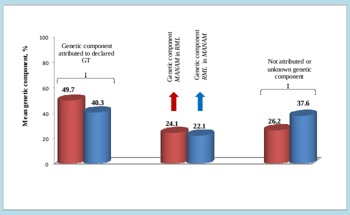


FIGURE 1. Analysis of factorial correspondence of *RML* and *MANAM*.

a major genetic component attributed to the genetic type declared (GRAPH 4);



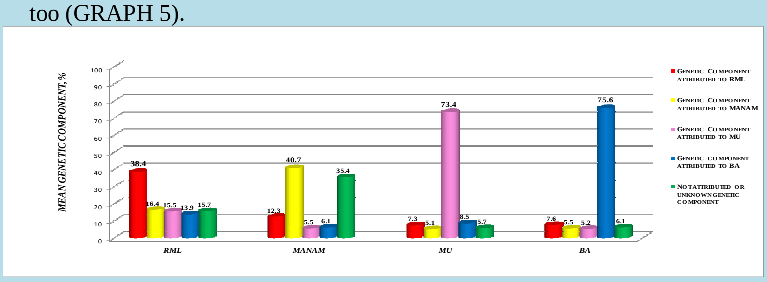
GRAPH 4. Distribution of mean genetic component ‘*attributed*’, ‘*not attributed’* to the GT declared and ‘*unknown*’.

TABLE 1. Value of Fst for the possible comparisons among the 4 GTs considered (*P*<0,05).

	RML	***MANAM***	***MU***	***BA***
RML	*	*	*	*
MANAM	0.0260	*	*	*
MU	0.0491	0.8083	*	*
BA	0.0638	0.8009	0.1100	*

a different degree of differentiation in comparison to the other genetic types (TABLE 1);

a higher genetic heterogeneity in comparison with the other genetic types, too (GRAPH 5).



GRAPH 5. Distribution of mean genetic component ‘*attributed*’ and ‘*not attributed*’ to the GT/AGT/AAGT ‘*declared’* as well as the ‘*unknown*’ genetic component.

CONCLUSIONS

This study may confirm the hypothesis that continous genetic exchanges happened during the centuries among mesomorphic Mediterranean populations and numerous ecotypes of ‘bioterritory’of Maremma. In particular, the ‘*Romano of Maremma Laziale*’ horse evidences a different genetic structure respect to the other genetic types considered. We think that molecular typification should be a major instrument in order to perform an effective safeguard of ‘*Romano of Maremma Laziale*’ horse.

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