

COMPARISON OF GENETIC DIVERSITY BETWEEN 'AMIATA DONKEY' GENETIC TYPE AND A DONKEY AUTOCHTHONOUS POPULATION FROM LAZIO

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INTRODUCTION

In a context where the belief is more deeply rooted that small animal populations are a 'patrimony' to be defended as well as a 'key feature' for the development of farming 'bioterritory', it is urgent to implement operative and suitable strategies for their 'protection' and 'valorisation'. Undoubtedly, 'microsatellite' genotyping is also an essential action to contribute to the knowledge of 'ratial evolution' in a route of autochthonicity 'safeguard'. Since 13rd century, Italian domestic autochthonous donkey population has been characterized by Mediterranean grey mousy ancestral phenotype, currently typical of 'Amiata donkey' population. This phenotype persisted up to 16th century when a marked introduction of Hispanic and French big sized and dark bay or darkish coloured sires occurred.





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To contribute to the knowledge of the genetic variability degree of 'Amiata donkey' (AD) and autochthonous donkey population from Latio (ADPL) for implementing safeguard activity.

'AMIATA DONKEY (AD)

AUTOCHTHONOUS DONKEY POPULATION FROM LAZIO (ADPL)

In the limits of the observation field:

THE DIFFERENCES BETWEEEN ADPL AND AD WERE NOT:

*significant for genetic variability degree (Table 1)

TABLE 1. SOME PARAMETERS OF GENETIC VARIABILITY GENETIC TYPE 2.98<u>+</u>1.20

MATERIAL AND METHODS

>DNA extraction from blood samples of: •ADPL, N=85 AD, N=50



DNA typification at 16 microsatellite loci (4 multiplex PCR)

- *notable for 'molecular coancestry' level (Table 2) TABLE 2. SOME PARAMETERS OF 'MOLECULAR COANCESTRY
 - PARAMETER 0.428

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

Genetic similarity was calculated according to Ciampolini et al. (1995).

CONCLUSIONS

Although the two populations have the same heterozygosity level, they evidence a remarkable quali-quantitative allelic difference and would seem to be genetically different (Graph 1). It would be desirable to enlarge the number of observations within ADPL for a better knowledge of the origin of its subdivision in sub populations: farming bioterritory?

THE QUALI-QUANTITATIVE ALLELIC DIVERSITY BETWEEN ADPL AND AD WITHIN EACH *LOCUS,* AS WELL AS THE HIGHER PRIVATE ALLELIC RICHNESS IN ADPL (28 *VS* 23) (TABLE 3) WERE





SOLIDIFYNG IN

ABSENCE OF TRANSVARIATION AREA BETWEEN THE TWO GENETIC TYPES (FIGURE 1)

is (AFC) between the two GTs

EVIDENT SUBDIVISION OF THE SUBJECTS IN TWO POPULATIONS WITH A FURTHER DISTRIBUTION OF ADPL IN TWO SUBPOPULATIONS (GRAPH 1); THIS BEHAVIOUR WAS JUST EVIDENT FOR K = 3 (GRAPH 1)

GRAPH 1. Population assignment test on two GTs considering thoretical population number (k) equal to 3.

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