Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - C.54

DESCRIPTION AND COMPARISON OF SOFTWARES FOR POPULATION GENETICS ANALYSES BASED ON MOLECULAR MARKERS

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software description, population genetics, molecular markers, comparison test

Molecular markers are important tools for evaluating animal genetic resources in terms of groups of individuals or populations in order to estimate genetic diversity, statistics and similarity coefficients, genetic distances, and gene flow estimates, to test for Hardy Weinberg deviations and linkage disequilibrium levels, to infer population structure looking for clustering patterns, to find out polymorphic loci for evidence of neutral or adaptive variation and to implement assignment tests useful for breed identification. Moreover, molecular markers might assist genetic variability conservation program and could be useful to define genetic traceability methods for food safety.

Aim of this study was to describe and compare some of the software programs available to elaborate molecular marker datasets for population genetics. Recently, many software programs for the analysis of molecular polymorphisms have been developed for personal computers and their powerful statistical performances and user-friendliness make an attractive alternative to the performing of spreadsheets or simpler home-made programs. The programs described in this study are softwares widely used in population genetics as TFPGA, Arlequin, Phylip, DISPAN, Genetix, GENEPOP, PROC ALLELE of SAS, GDA, POPGENE, NTSYS and Cervus. These programs were chosen for their availability, flexibility and citations in scientific reports. Although there is a large overlap in their functionality, each of them has unique features to offer. In general, these programs grew out of an individual's or a lab's immediate research need and they were developed into user-friendly software to be shared with the larger research community. Critical aspects for these software are mainly the request of specific format input files, the availability of a clear manual and the use of many details concerning the interface with the user as warning messages, the possibility to save specific settings and to run batch files. In conclusion the major features for each program will be described and discussed.