

MOLECULAR FINGERPRINTING OF OLIVE CULTIVARS OF SOUTHERN ITALY

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Olive is one of the oldest cultivated plants and it is one of the most important oil-producing crop in Italy. Such plant is characterised by a high degree of genetic diversity because of its ancient domestication, the simplicity of the vegetative propagation, the long life span and the high self-incompatibility. A very large number of varieties are described in the Mediterranean countries, although it is likely that the variability of the morphological traits in different areas of cultivation, has contributed to the description of several synonymous. This large olive collection is valuable for germplasm resources as well as for research, and the evaluation and characterisation of these genetic resources is necessary to maximise the efficiency of germplasm management, preservation and pre-breeding programs. The development of various molecular marker techniques and their application in genetic diversity studies have resulted in improved discrimination among or within several olive cultivars. Here we are reporting on the molecular characterisation of 22 cultivars (for a total of 39 samples) locally cultivated in Southern Italy, and many of these cultivars are listed in the regulations for the production of DOP olive oil. The identification was carried out on fluorescent-based capillary electrophoresis and automated size estimation of six polymorphic DNA microsatellites (SSR), four of them belonging to the microsatellites set selected to carry out a ring-test on olive cultivar identification coordinated at national level by the IGV, Perugia. The total number of detected alleles was 48, with a minimum of 7 in three loci. The allele size range of all amplified fragments was from 100 to 250 bp. The average observed heterozygosity was 0,793. The results indicated that there is sufficient genetic diversity to distinguish all but two cultivars, as only Sant’Agostino and Uova di Pavone have an identical allelic pattern in all the loci analysed. However, principal co-ordinate analysis on the SSR data could not clearly cluster the cultivars according to the regions of diffusions or the destination of use. In conclusion, our data indicated the presence of genetic variability among the cultivars analysed and, furthermore, this work can provide data to enforce legislation for the control of olive oil genetic origin.