

MOLECULAR CHARACTERIZATION OF OLIVE (*OLEA EUROPEA* L.) CULTIVARS FROM ABRUZZO REGION

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Olive (*Olea europea* L. subsp. *europaea*, $2n=2x=46$), an oil-producing tree, is considered the most important fruit crop of the Mediterranean Basin and it is characterized by a large number of varieties, most of which behave in a self-incompatible way.

So far, several methodologies have been used to evaluate olive diversity and to characterize olive germplasm such as leaf, fruit, pit, and growth habits or isozyme analysis. However, a major limitation of using these traits as genetic markers in Olive is that they are highly dependent on environmental or cultivation factors. In recent years, many papers report the successful assessment of phylogenetic relationships in the *O. europaea* complex using RAPD, microsatellite-based technique and AFLPs. Some of these techniques have proved very useful for varietal characterization and offers an almost unlimited supply of molecular traits for distinctive fingerprinting of plant materials without prior knowledge of target DNA sequences.

The development of cultivar-specific molecular markers would be highly useful for cultivar identification, varietal protection, and oil composition determination especially in a view of oil traceability.

The two main objectives of this study were to evaluate the identity of cultivars cultivated in Abruzzo region by establishing their genetic similarities/diversities and to investigate and analyze genetic intra-cultivar diversity in Dritta, Gentile di Chieti, Gentile dell'Aquila and Tortiglione cultivars.

A total of 90 olive accessions were genotyped using 12 AFLP primer combinations. A total of 1089 amplification products was scored with a percentage of polymorphism ranging from 0.3% to 0.76% depending on primer combination. Interestingly, in 14 accessions (Dritta, Gentile di Chieti, Gentile dell'Aquila, Ghiandaro, Monicella, Nebbio, San Felice, Pendolino, Nostrana, Carboncella, Tortiglione, Nostrana, Unknown), at least one accession-specific band was recorded. Moreover, for other 3 bands an accession-absence discriminated one accession from other and could be considered as informative as a cultivar-specific band (1 band for Gentile dell'Aquila and 2 bands for Leccino).

Moreover, the Pritchard method, implemented in the software STRUCTURE Ver. 2.2, was used and adapted to dominant molecular markers in order to infer the population structure and, thus, to evaluate the identity of cultivars cultivated in Abruzzo region. Based on the STRUCTURE and ΔK results the genetic structure of the whole sample was characterized by eight clusters. UPGMA, PCoA and Structure analysis of population are reported and discussed.