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# CHARACTERIZATION OF THE MAIN OLIVE CULTIVARS IN MOLISE REGION BY MEANS OF SSR MOLECULAR MARKERS

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*Germplasm, barcode, Olea europeae*

A very rich olive germplasm resource is present in Italy, which represents an interesting gene pool for agriculture, environment and sustenance. To this purpose, bio-molecular technology have been set up in order to clearly establish the identity of the most interesting olive cultivars in some of the Italian Regions involved in a national research project named 'OLVIVA'; characterization and exploitation studies have been carried out to the aim of eliminating cases of mislabelling and redundancies (synonymy) and to provide analytical tools for the genetic certification of the propagation plants. In particular, in the Molise region, we hav characterized eight olive cultivars from this region, cultivated at the Molise ARSIA (Regional Agency for Innovation and Development in Agriculture) catalogue field located in Larino (CB), settled for the conservation and development of local olive germplasm. Previously, the procedure of molecular characterization was optimized using 'Ring Test' method, using five DNA samples of unknown origin and 17 molecular markers (microsatellite) arranged with the specific referee. Touch down-PCR, set up for the 17 SSR loci, have been successively analyzed through capillary electrophoresis using ABI PRISM 310 automatic sequencer (Applied Biosystems). Data analysis has been carried out with Gene Mapper software (AB, version 4.0) for allele evaluation.

The same procedure has been successively transferred for the molecular characterization of the eight olive cultivar of Molise region, which were chosen in this project: Gentile di Larino, Oliva Nera di Colletorto, Aurina, Rosciola di Rotello, Cerasa di Montenero, Sperone di Gallo, Paesana Bianca e Salegna di Larino. Molecular characterization results showed that SSR locus named EMO-L was not useful for the characterization, because it produces unvaried alleles for all the analyzed samples and therefore it is not discriminating. In general, all the other loci produce different alleles (from the 3 alleles in DCA-15 locus to 11 allels for DCA18 locus) and permit thence to discriminate all the analyzed cultivars. With all the resulting sizes it was also possible to create, for each, a sort of barcode profile that quickly visualizes the different pattern of the 8 cultivars, revealing the variations. In fact, they resulted to be all different and therefore recognizable by means of the technique used in this research and therefore they do not present case of synonymy.