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

Poster Abstract - E.09

INTERGENIC SPACER POLIMORPHYSMS FOR *OLEA EUROPAEA* L. CULTIVARS IDENTIFICATION

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Olea europaea L., cultivar fingerprint, molecular traceability, trnT-trnD spacer

The identification of cultivars and accessions by molecular markers is a crucial cue of modern horticulture, with application in breeding programmes, in germplasm collections management and in products traceability. In fact, food molecular traceability is becoming a primary interest for high quality human nutrition.

The case of the olive oil is particularly complex due to the great number of cultivars, the synonymy and the ambiguous cultivar assignments. Moreover chemical analysis of different compounds, or the analysis of morphological traits haven't led to cultivar identification due to environmental effects on the chemical composition and phenotype.

Genetic fingerprinting seems to be the best way for genotyping the specific cultivar and the oil deriving from it. However, the molecular identification should be based on the development of unambiguous markers to guarantee the oil high quality, DOP or IGP, and their producing areas.

The aim of this work is to identify simple and reliable PCR markers useful in cultivar identification and olive oil traceability. We used the trnT/trnD, intergenic spacer of the chloroplastic DNA to examine 10 cultivars of *O. europaea.*

We use samples provided by "Istituto Sperimentale per l'Olivicoltura". A single individual for each accession have been used, the use of a so small sample size is consistent with a low intracultivar expected variation.

The trnT/trnD, intergenic spacer, was amplified by PCR with specific primers and the obtained amplicons of each cv have been directly sequenced, using the same forward and reverse primers. The sequences have been performed twice, to avoid possible errors in single product sequencing such those induced by Taq-polymerase. All sequence reactions were made by using the AutoRead Sequencing kit, and run in an automated laser fluorescent sequencer (ABI Prism, Perkin Elmer).

The already found low variation in restriction pattern of the whole cpDNA molecules, is reflected also by the sequences of intergenic trnT/trnD spacers even if this marker is able to identify some of the cultivar analysed. Only point mutations and a indel in a poly – $(T)_{12}$ stretch are present among the cultivars analysed.

However, the chloroplastic markers analysed in this work show a sufficient pattern of variation able to discriminate cultivars and to analyse phylogenetic relations. This kind of marker, if validate in intracultivar analysis, will be a convenient assay in traceability protocols.