SNPs IDENTIFICATION FOR DISCRIMINATION OF OLEA EUROPAEA CULTIVARS

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Olive trees cultivation plays a major part in the Mediterranean agricultural tradition. Large is the number of cultivars grown in this area and the identity of most of them is closely linked to specific regions. Molecular tools able to discriminate different cultivars and to assign individuals to varietal populations have become an important issue for the safeguard of local genetic resources.

A wide range of molecular markers have been used for cultivars discrimination in olive, but not many SNPs markers have been identified until now. These markers are very useful since they are genetically stable and can be associated with phenotypic traits.

The objective of this work is to explore the possibility to identify SNPs, able to discriminate among olive cultivars, within genes that encode the enzyme chalcone synthase (CHS), that catalyzes the first step of the biosynthetic pathway of anthocyanin as well as of other flavonoid compounds.

With this aim exon I, intron and a part of exon II of two different chs genes were amplified in ten olive cultivars, typical of different regions of the Mediterranean basin, and in the feral form O. europaea var. sylvestris. SNPs were identified within the coding sequences and these changes were mostly silent or resulting in like-for-like amino acid changes. SNPs and INDELs were found within the introns. The number of transitions was larger than for transversions among the single base changes identified. Overall analysis of the obtained results suggested that the polymorphic patterns in the amplified regions can be able to characterize different cultivars and that the polymorphisms set allows clustering the varieties into different groups.