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Poster Abstract – F.14

NUCLEOTIDE VARIATION ANALYSIS IN THE UPSTREAM REGION OF *CHS*A AND *CHS*B GENES FOR CHALCONE SYNTHASE (CHS) IN *OLEA EUROPAEA* L.

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In olive (*Olea europaea* L.) the assessment of genetic variability has been carried out with morphology-based markers (Barranco et al., 2000) and DNA-based markers. Among these RFLP (Besnard and Bervillè, 2000), RAPD (Belaj et al. 2003), AFLP (Owen et al. 2005), SSR (Bandelj et al. 2004), ISSR (Pasqualone & Caponio, 2001) have been used and different molecular markers (Belaj et al., 2003) have been compared in several studies of genetic characterization of cultivated olives and also to study the relationships among cultivars, wild forms and related species (Angiolillo et al, 1999; Baldoni et al. 2000). Recently, single nucleotide polymorphism (SNP)-derived markers, identified in coding sequences of different genes, have been developed to discriminate very similar cultivars (Reale et al., 2006; Consolandi et al., 2007) and for olive oil traceability and authenticity (Consolandi et al., 2008). In this work we present results concerning the molecular characterisation of a region upstream the ATG of *chs*A and *chs*B genes for Chalcone synthase (CHS), of different bp length, namely 956 base pairs the former and 333 base pairs the latter, previously isolated in olive in our laboratory (Scialpi et al., 2005). The analysis of nucleotide variation of these regions was then carried out in eight italian cultivars of *Olea europaea* L. (Nocellara Belice, Nocellara Etnea, Coratina, Nociara, Carolea, Bosana, Gentile di Chieti and Leccino), in one from Albania (Bardhi i Tirana), and in the wild form *O. europaea* var. *sylvestris*. Data obtained from molecular characterisation suggested a regulatory role for both the upstream regions analysed. Moreover, comparative analysis of sequences of different cultivars showed a high level of polymorphism in terms of SNPs and InDels. Genetic relationships established on the base of nucleotide diversity, using the UPGMA cluster analysis program, showed that cultivars were grouped into different clusters. In particular, Coratina clusterized with the feral form *O. europaea* var. *sylvestris*, this finding strongly suggesting for this cultivar, a possible introgression from the wild genotype. Finally, results will be discussed concerning the possibility to relate the nucleotide diversity of the upstream-*chs* sequences, with the modulation of gene activity as previously reported for other genes (Thornsberry et al., 2001).

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