Poster Abstract - C.46

IDENTIFICATION OF TWO PUTATIVE CHS ISOFORMS IN OLEA EUROPEA

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Flavonoids are important secondary metabolites directly involved in the interaction between the organism and its environment (Winkel-Shirley, 2001). Plants synthesize a variety of flavonoid compounds that are the major flower pigments and also play important roles in defending plant against pathogens, in acting as signal molecules in plant-microbe interaction and in protecting plants from UV radiation (Harborne, 1994; Shirley, 1996).

The chalcone synthase gene (Chs) codes for the branch point enzyme of the flavonoid pathway, hence it may play a role in adaptative evolution. Chs is encoded by a single copy gene in some plant, such as *Arabidopsis* (Koch et al., 2001) and by multiple isoforms of the gene in others, such as members of *Asteraceae* (Yang et al., 2002).

In *Olea europea*, only a part of the Chs coding sequence has been sequenced and deposited in GenBank DNA database at the moment. The present study was conducted to isolate sequences of the Chs gene, with the aim to develop molecular markers from polymorphism for cultivars characterization.

Results obtained allowed the identification of two different sequences which are upstream to the known coding sequence and 2002 and 1466 bases pair long respectively. These sequences showed high identity to hortologous genes deposited in GenBank DNA database. In particular some portions of them showed a high identity values (80-83%) to exon I and II of the Chs isoforms gene of *Vitis vinifera*. On the contrary, low identity values to 5' UTR region and to the intron have been found. However these results seem to suggest that the isolated sequences in *Olea europea* include a portion of 5' UTR region, the exon I, an intron and a newly sequenced part of the exon II of the Chs gene. Moreover the alignments between the portions corresponding to the exons of the two isolated sequences showed high identity values (91-92%), on the other hand the regions corresponding to the introns showed low homology (10%). These results suggest that the two identified sequences could be two different isoforms of the Chs gene in *Olea europea*.

References

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