

OLIVE CHLOROPLAST GENOME SEQUENCING AND IDENTIFICATION OF INTERVARIETAL POLYMORPHISMS

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The cultivar Frantoio has been used for the sequencing of the first complete *Olea europaea* L. chloroplast genome. Conserved primers designed by Grivet et al. (2001) have been used to sequence the large single copy (LSC) region. For the small single copy (SSC) and the inverted repeat (IR) regions, primers were constructed on conserved sequences homologous to *Jasminum*, the closest genus to *Olea*, and other fully sequenced plant chloroplast genomes.

Availability of the cpDNA sequence has allowed to detect areas of major polymorphism among cultivars useful for cultivar characterization, DNA barcoding and ancient DNA studies. In particular, cultivar-specific SNPs or indels were found on the *psbk* gene (A/G), on the intergenic *trnK-rps16* area (poly-T 11 or 12) and on the *trnT-trnD* intergenic spacer (A/G). These polymorphisms allow to distinguish cultivars of different geographical origin as well as cultivated from wild plants.

Valuable information on the organization, gene arrangement and nucleotide substitution within the Oleaceae family will derive from the cpDNA molecule sequence, while phylogenetic relationships among lineages within the *Olea europaea* species are currently under assessment.