

HIGH RESOLUTION MELTING FOR MUTATION SCANNING OF OLEATE DESATURASE ENCODING GENE

SALIMONTI A.*, VIZZARRI V.*, LOMBARDO L.***, MICALI S.*, PERRI E.*, ZELASCO S.*

*) CRA - Centro di Ricerca per l'Olivicoltura e l'Industria Olearia, Contrada Li Rocchi, 87036 Rende (Italy)

**) Dipartimento di Scienze dei Sistemi Culturali, Forestali e dell'Ambiente, Università degli Studi della Basilicata, Via Nazario Sauro 85, 85100 Potenza (Italy)

Olea europaea, high resolution melting, mutation, desaturases, fatty acid

Oleic acid is the major fatty acid in vegetable oils and its content greatly affects both their technological properties such as oxidative stability and nutritional characteristics. Olive (*Olea europaea* L.) oil shows genetic variability in oleic acid content ranging from 49% to 83%. The biosynthetic pathway of fatty acids has been long studied in animals and critical regulation steps have been recognized, while less is known in plants. A key enzyme is oleate desaturase (FAD 2) which catalyzes the desaturation of oleic acid into linoleic acid. In order to individuate functional markers putatively associated to oleic acid content variation, we started a candidate gene approach with a microsomal oleate desaturase (FAD 2) encoding sequence *OepFAD2-2*, isolated from olive (cv. Picual) by Hernandez *et al.* (2005). Ten pairs of gene-specific primers were designed from the full-length cDNA sequence, producing short amplification fragments (150-200 bp) and a mutation scanning approach was performed by HRM-PCR assay. A set of cultivars with a very broad oleic acid content is being analyzed. A preliminary screening on a subset of cultivars with contrasting levels of oleic acid revealed the presence of sequence variations in some samples which differentiated for their melting curves shape. Work is still in progress to assay all the phenotyped cultivars and to validate by sequencing the representatives of each variant cluster obtained in order to ultimately individuate putative functional markers.