

Identification of Genes Involved in Polyphenol Synthesis in Olive Fruits

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Polyphenolic compounds accumulating in olive fruits play a primary role in plant defense mechanisms and are responsible of the extra virgin olive oil taste and its benefits on human health.

They are mainly represented by oleuropein, demethyleuropein and ligustroside aglycon derivative and lignans.

In order to identify genes involved in the synthesis and degradation of olive phenols, mainly secoiridoids such as oleuropein, demethyleuropein and ligustroside, we have first measured phenolic composition in a pool of varieties. Fruits were collected at different stages of ripening and phenolic profiles were evaluated along the maturation process.

To identify differentially expressed genes potentially involved in the metabolism of oleuropein different approaches have been applied. A full length cDNA library has been constructed from the mesocarp of a high-phenolics variety, and it is currently under sequencing. Sequences of this library will be screened using microarray technology to generate quantitative gene expression profiles.

A cDNA-AFLP approach has also been applied to monitor the presence of transcripts across fruit ripening in low and abundant phenolics varieties. More than 100 cDNA fragments have been recovered, sequenced and identified by in silico analysis.