

## **FUNCTIONAL GENOMICS APPROACHES FOR THE STUDY OF AROMA DETERMINATION IN PEACH (*PRUNUS PERSICA*)**

A. VECCHIETTI\*, C. ORTUGNO\*\*, F. BARALE\*\*, B. LAZZARI\*, O. AMBROSINO\*,  
M. OSNATO\*\*, C. POZZI\*

\*) Parco Tecnologico Padano - CERSA, Via Einstein, Località Cascina Codazza, 26900 Lodi, Italy

\*\*\*) Dipartimento di Produzione Vegetale, Università di Milano, Via Celoria 2, 20133 Milano, Italy

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Peach flavour consists of a huge variety of volatile compounds. Esters, alcohols, aldehydes, terpenes, lactones, C6 compounds are the main components of the peach aroma and their relative abundance is a fingerprint of a particular variety.

From GC/MS chromatogram of ripe peach fruit shikimic acid derivatives (eugenol, isoeugenol, chavicol, methyl benzoate) are present in a high concentration. An enzyme involved in eugenol biosynthesis belongs to the family of O-methyl transferase. O-methyl transferase (OMT) enzymes catalyse the transfer of a methyl group to an hydroxyl group of an acceptor molecule with the formation of its methyl ether derivatives.

Among other volatiles compounds produced during ripening, lactones are a quantitatively important part of the peach aroma. Lactones are supposed to derive from fatty acid degradation and an epoxide hydrolase (EPOX) is suggested to be involved in their production. Here we report the cloning, the expression and the mapping of genes coding for OMTs and EPOXs. Moreover we report the primary data analysis of ESTs derived from peel cDNA library.