

Combined signal sequence trap and macroarray analysis identifies genes associated with differential fruit softening characteristics during ripening in European and Chinese pears

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Abstract

During ripening, European pear (*Pyrus communis* L. cv. ‘La France’) fruit undergo dramatic softening in response to increased ethylene production, whereas Chinese pear (*Pyrus bretschneideri* Rehd. cv. ‘Yali’) fruit remain firm, despite producing large amounts of ethylene. The molecular basis of this differential softening behavior is not well understood. In this study, we combined a yeast-based signal sequence trap (YSST) and macroarray gene expression analysis to identify putative genes encoding secreted proteins that control pear fruit softening. We identified 22 cDNAs annotated as encoding proteins with diverse cell wall-associated functions that were up- or down-regulated during fruit ripening in ‘La France’. Gene expression analysis in fruit that were treated with the ethylene perception inhibitor 1-methylcyclopropene (1-MCP) at 4 d after the onset of ripening revealed that 16 of the targeted genes are ethylene-regulated, while the others appear to be ethylene independent. Comparative gene expression analyses of ‘La France’ and ‘Yali’ fruit during ripening suggested that four ethylene-regulated cDNAs encoding cell wall modifying proteins, *contig 2* (*polygalacturonase 3*), *contig 15* (*expansin*), *contig 19* (*expansin*) and *contig 55* (*pectate lyase*) contribute to the different softening behaviors of ‘La France’ and ‘Yali’ fruit. Additionally, one ethylene-independent cell wall related gene, *contig 36* (*expansin*), and three genes encoding proteins of unknown function, *contigs 1, 13* and *contig 75* showed differential expression between ‘La France’ and ‘Yali’ fruit during ripening. The results presented herein represent promising candidates for future functional analysis and elucidation of softening mechanisms.