

Title Oligoarray analysis of gene expression in ripening Japanese pear fruit
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Abstract

A custom oligoarray of Japanese pear (*Pyrus pyrifolia*) based on 9812 independent ESTs from different tissues (fruits at various growth stages, vegetative and flower tissues) was designed and used for comprehensive investigation of gene expression before and during ripening (105–147 days after full bloom). Results of one-way ANOVA test indicated that the expression of about 30% of the genes (corresponding to 3062 independent ESTs) showed a significant difference between 105 (before ripening) and 147 (ripened) days after full bloom. Classification of expression pattern of those 3062 ESTs showed 11 sets, five of them contain 545 up-regulated ESTs and the other six sets contain 1920 down-regulated ones. Among them, 16 genes showed remarkable increase of more than 100 fold from 105 to 147 days after full bloom. The largest increase (more than 9000 fold) was exhibited by the glutathione S-transferase gene. The major functional group of remarkably up-regulated genes was in a glycosyl hydrolase family such as polygalacturonase. Genes participating in ethylene metabolism and sulfate transport were also identified. On the contrary, 18 genes were down-regulated to less than 1% during the same period. Glycosyl hydrolase family genes, invertase/pectin methylesterase inhibitor genes, and genes involved in secondary metabolism were the major groups identified. In addition, putative regulatory genes such as bHLH transcription factor also showed remarkable decreasing in expression. The cDNA oligoarray analysis efficiently provided individual gene expression profiles and new insights for elucidating the biological mechanisms responsible for fruitripening in Japanese pear.