

Microarray analysis is a technique that can be employed to provide expression profiles of single genes and new insights to elucidate the biological mechanisms responsible for fruit development. To evaluate expression of genes mostly engaged in fruit development between *Prunus mume* and *Prunus armeniaca*, we first identified differentially expressed transcripts along the entire fruit life cycle by using microarrays spotted with 10,641 ESTs collected from *P. mume* and other *Prunus* EST sequences. A total of 1418 ESTs were selected after quality control of microarray spots and analysis for differential gene expression patterns during fruit development of *P. mume* and *P. Armeniaca*. From these, 707 up-regulated and 711 down-regulated genes showing more than two-fold differences in expression level were annotated by GO based on biological processes, molecular functions and cellular components. These differentially expressed genes were found to be involved in several important pathways of carbohydrate, galactose, and starch and sucrose metabolism as well as in biosynthesis of other secondary metabolites via KEGG. This could provide detailed information on the fruit quality differences during development and ripening of these two species. With the results obtained, we provide a practical database for comprehensive understanding of molecular events during fruit development and also lay a theoretical foundation for the cloning of genes regulating in a series of important rate-limiting enzymes involved in vital metabolic pathways during fruit development.