

**Title** Transcrip profiling of fruit postharvest related genes in ponkan (*Citrus reticulata* Blanco)  
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**Citation** Program and Abstracts, 11<sup>th</sup> International Citrus Congress (ISC Congress), 26-20 October 2008, Wuhan, China. 333 pages.  
**Keyword** ponkan; ripening

### Abstract

Physiological processes of fruit postharvest ripening in ponkan (*Citrus reticulata*) were proven to be sustaining events that accurately regulated by genes associated with metabolisms such as organic acids and sugar changes during storage. To delineate postharvest ripening related genes expression and investigate its regulatory mechanism, the GeneChip Citrus Genome Array with 30,396 genes was used to profile the expression patterns of Ponkan at four storage stages. The results showed that 17,849 genes were expressed in at least two stages; and these genes were further analyzed. We used k-mean clustering approach to group 7,092 genes (3 fold up-regulated or down-regulated to stage1) into 8 clusters and annotated each cluster genes. It revealed that genes related to stimulus and biopolymer metabolic process were mainly located to the up-regulation cluster. Arabidopsis KEGG maps were downloaded and used to identify regulated metabolic pathways. The results showed that citrate cycle, glycolysis, glyoxylate metabolism were up-regulated while fructose metabolism was down-regulated. A detail analysis of glycolysis, TCA cycle and glyoxylate pathway genes revealed that some key enzymes such as glyceraldehyde-3-phosphate dehydrogenase, aconitase, isocitrate lyase, malate synthase were selectively regulated. At least 58 putative mitochondrial carrier family genes present on the chip and 34 of them changed significantly which indicate that mitochondrion played an important role in postharvest citrus fruits. Additionally, 161 transcriptional factors (TF) belonging to 64 major TF families were identified which might involve in postharvest ripening regulation, and the main three components were AP2-EREBP (11.2%), HB (7.45%) and MYB (6.83%). Hierarchical cluster analysis for transcriptional factors revealed our distinct expression profiles. Typically, 12 of the 18 AP2-EREBP members were over-expressed in at last two stages, while 2 MADS family members, 2 HB family members and 1 AP2-EREBP member was characteristically over-expressed in the third stage, which inferred that these TF families participated in the gene expression regulations in postharvest citrus. Real-time RT-PCR was further used to validate our results by 11 representative genes. Our results provide fundamental information in understanding the postharvest processes of ponkan fruits at the expression level.