

Title Profiling ethylene-responsive genes in mature mandarin fruit using a citrus 22K oligoarray
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Abstract

A comprehensive transcriptome analysis using a citrus 22K oligoarray was performed to identify ethylene-responsive genes and gain an understanding of the transcriptional regulation by ethylene in mandarin fruit (*Citrus unshiu* Marc.). In the 72 h after ethylene treatment, 1493 genes were identified as ethylene-responsive with more than 3-fold expression change, and an interesting aspect of gene regulation by ethylene was observed, namely, that more than half of the ethylene-responsive genes were repressed. This aspect might suggest that ethylene demotes numerous biological processes and plays an important role in fruit ripening and senescence. Ethylene repressed the transcription of most genes involved in photosynthesis, chloroplast biogenesis, and sugar metabolism, while it induced the transcription of several genes related to resistance, defense, stress, amino acid synthesis, protein degradation, and secondary metabolism. In carotenoid metabolism, the sensitivity and responsive patterns to exogenous ethylene were significantly different among carotenoid biosynthesis genes. Ethylene might cause a change of their transcriptional balance and influence carotenoid composition of fruits. Besides, most of ethylene biosynthesis genes and its signal transduction components did not show any significant expression change (<2-fold) against exogenous ethylene treatment. A type II ethylene receptor (ETR2) showed higher sensitivity to exogenous ethylene than two other type I ethylene receptors (*CsETR1* and *CsERS1*) in mature fruit, providing a new assumption that ETR2 might be associated with low ethylene sensitivity in mature fruit.