

**Title** Differential expression of ethylene biosynthetic genes in climacteric and non-climacteric Chinese pear fruit

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### Abstract

We investigated the differences in capability to produce ripening-associated ethylene between climacteric ('Yali', 'Xinqingli', and 'Zhuzuili') and non-climacteric ('Hongli', 'Yuanbali', and 'Hongxiaoli') Chinese pear (*Pyrus bretschneideri* Rehder) fruit varieties. Three *ACS* (*PbACS1*, *PbACS2*, and *PbACS3*), two *ACO* (*PbACO1* and *PbACO2*), and three MADS-box (*PbMADS1*, *PbMADS2*, and *PbMADS3*) genes were cloned from ripening fruit. Fruit were harvested at the mature stage and treated with  $5000 \mu\text{L L}^{-1}$  propylene for 4 days. Ethylene production was induced by propylene in the climacteric but not in non-climacteric type fruit. In the ripening climacteric fruit, *PbACS1* and *PbACO1* transcript accumulation accompanied ethylene production but the accumulation of other *ACS* and *ACO* mRNAs was not detected. In 'Yali' fruit, 1-MCP exposure prior to propylene treatment completely inhibited the expression of these genes, while exposure after the commencement of ethylene production weakened their expression. Transcripts of *PbACO1* accumulated in response to propylene treatment even in non-climacteric fruit but this accumulation was eliminated after the termination of propylene treatment. In response to wounding, transcripts of *PbACS2*, *PbACS3*, and *PbACO2* genes accumulated in both climacteric and non-climacteric fruit, but accumulation of *PbACS1* and *PbACO1* mRNAs was not detected. In the Southern analysis of *PbACS1*, *Hind*III digests of genomic DNA showed 8.3, 3.5 and 2.9 kb bands. The 2.9 kb band was detected only in climacteric varieties while the 3.5 kb band was detected in both climacteric and non-climacteric varieties except in 'Yali'. These results suggest that Chinese pears may have two copies of the *ACS1* gene, in which *PbACS1A* could be linked to the varietal differences in the capability to produce ripening-associated ethylene. There was no correlation between the expression patterns of the three MADS-box genes cloned and the differences in ripening-associated ethylene production among the Chinese pear varieties.