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Comparative analysis of polygalacturonase in the fruit of strawberry cultivars

H.C. Zhou, G. Li, X. Zhao and L.J. Li

Zhengzhou Fruit Research Institute, Chinese Academy of Agricultural Sciences, Zhengzhou, China

Corresponding author: H.C. Zhou
E-mail: zhouhoucheng@caas.cn

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ABSTRACT. The role of polygalacturonase (PG) in the development, ripening, and softening of fruit from two strawberry cultivars with different flesh firmness and softening characteristics was compared. Changes in PG activity and gene expression during development, ripening and softening were measured. The *PG* genes from each cultivar were cloned and analyzed, and were classified with other *PG* genes using phylogenetic analysis. In Toyonoka fruit, PG activity increased gradually, reaching a peak during the pink stage, and remained at this level during post-harvest softening. Changes in *PG* gene expression were consistent with PG activity in these softer fruits. In the firmer Sweet Charlie fruits, PG activity was detected during the initial development stage, reaching a peak at the white stage, thereafter decreasing gradually with ripening and remaining at this lower level throughout softening. Changes in *PG* gene expression and PG activity were not consistent in these fruit. For both Toyonoka and Sweet Charlie *PG* genes (*FaTPG* and *FaSCPG*, respectively), the open reading frame was 1218 bp, encoding 405 amino acids. Five different nucleotide sites were observed between the two sequences, leading to two amino acid sequence mutations. *FaTPG*, *FaSCPG*, and *PG* genes from the *Fragaria vesca* genome were classified into three clades using phylogenetic analysis. The clade containing *PG* genes involved in fruit

softening had functional similarity but there were no functional differences between *FaTPG* and *FaSCPG*. Differences in PG activity, gene sequence, and gene expression may have led to different roles of PG during ripening and softening in strawberries with different textures.

Key words: Strawberry; Polygalacturonase; Fruit texture; Fruit ripening and softening; Gene expression analysis

