

Molecular cloning and expression analysis of hexokinase genes in peach fruit under postharvest disease stress

Wenjing Xu, Yingying Wei, Xingxing Wang, Peipei Han, Yi Chen, Feng Xu and Xingfeng Shao

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Abstract

Hexokinase (HXK) is a bifunctional enzyme and plays a critical role in plants growth and stress response. HXK is encoded by a multi-gene family in a wide range of plants. However, information of HXK family members in peach and their expression pattern under disease stress remains unclear. In the present study, 5 *PpHXK* genes in peach fruit, including *PpHXK1-3* and *PpHKL1-2*, were identified and isolated, and clustered into 4 groups by phylogenetic tree analysis. Furthermore, we investigated HXK activity, transcript levels of the 5 *PpHXK* genes and sugar content in peach fruit under *Monilinia fructicola* infection in 2018 and 2019. The results in both 2018 and 2019 showed that *M. fructicola* infection increased HXK activity and *PpHXK2* gene expression, and accelerated sucrose decomposition. HXK activity showed significantly positive correlation with *PpHXK2* expression and negative correlation with sucrose content. *PpHXK2* was localized in the cytoplasm by subcellular localization, and contained 3 W-box cis-acting elements in the promoter, indicating that *PpHXK2* may function as a sugar sensor and regulate sugar signaling and metabolism in defense response against pathogen infection. Thus, *PpHXK2* in peach fruit is capable of responding to postharvest disease stress, and the involved mechanism needs to be further studied.