A NAC transcription factor BrNAC087 is involved in gibberellin-delayed leaf senescence in Chinese flowering cabbage

Zhong-qi Fan, Wei Wei, Xiao-li Tan, Wei Shan, Jian-fei Kuang, Wang-jin Lu, Xin-guo Su, Prakash Lakshmanan, He-tong Lin and Jian-ye Chen

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Abstract

Phytohormone gibberellins (GAs) regulate leaf senescence. A global view of the regulatory pathways associated with GA-mediated inhibition of leaf senescence, especially in economically important leafy vegetables such as Chinese flowering cabbage, remains unclear. In this study, exogenous supply of gibberellin (GA_3) delayed postharvest Chinese flowering cabbage leaf senescence. By comparative transcriptome analysis of leaf tissue, a total of 4682, 5059, and 2362 differentially expressed genes (DEGs) were identified between the comparison of 0d (cabbages at the harvest day) and CK3d (control cabbages at day 3 post-harvest), 0d and GA3d (GA_3-treated cabbages at day 3 post-harvest), and CK3d and GA3d, respectively. Further analysis of identified DEGs involved in chlorophyll and GA degradation during leaf senescence, and the activity of chlorophyll catabolic genes (*CCGs*) *BrPPH* and *BrRCCR*, and bioactive GA degradation gene *BrGA2ox1*, was greatly reversed with GA_3 application during leaf senescence. More importantly, a NAC transcription factor (TF), BrNAC087, was found to be associated with leaf senescence. BrNAC087 is a nuclear localized gene with transcriptional activity, highly expressed during senescence but downregulated by GA_3. Significantly, BrNAC087 positively regulated *BrPPH*, *BrRCCR* and *BrGA2ox1* expression by binding to NAC-binding sequences in their promoters in *vitro* and in *vivo*. These findings collectively provide evidence for a new molecular regulatory pathway explaining, at least in part, a mechanistic basis for gibberellin-mediated leaf senescence inhibition in postharvest Chinese flowering cabbage.