

A transcriptional repressor BrDof2.4 regulates protease genes involved in postharvest leaf senescence in Chinese flowering cabbage

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Abstract

Protein degradation is an integral process of leaf senescence, and this catabolism is strongly associated with proteases in diverse plant species. However, the characterization of proteases as well as their upstream regulators during postharvest senescence, especially in economically important leafy vegetables such as Chinese flowering cabbage, remains to be determined. In this study, temporal and spatial gene expression patterns of eight proteases showed that three of them, namely, *BrAPM1*, *BrASPG2* and *BrSAG12*, were most up-regulated during postharvest leaf senescence. Their expressions were also significantly induced by senescence-accelerating phytohormones abscisic acid (ABA) and methyl jasmonate (MeJA), but were inhibited by senescence-delaying hormones gibberellin (GA₃) and cytokinin (6-BA). Importantly, using yeast one-hybrid screening, we identified a Dof (DNA-binding with one finger) transcription factor, BrDof2.4, as the putative binding protein of *BrAPM1*, *BrASPG2* and *BrSAG12* promoters. Nucleus-localized *BrDof2.4* was senescence-, ABA- and MeJA-repressible, but was GA₃- and 6-BA-inducible. Furthermore, gel mobility shift and transient dual luciferase reporter assays revealed that BrDof2.4 suppressed the transcription of *BrAPM1*, *BrASPG2* and *BrSAG12*, through binding to their promoters. Taken together, our findings demonstrate that BrDof2.4 acts as a potential repressor of postharvest leaf senescence in Chinese flowering cabbage by the direct suppression of protease expression. Our work contributes towards improving the technology for increasing the shelf-life and commercial value of this important leafy vegetable.