Identification of senescence-associated genes in broccoli (*Brassica oleracea*) following harvest

Yogesh Ahlawat, Song Li, Prakash R. Timilsena, Eleni D. Pliakoni, Jeffrey K. Brecht and Tie Liu

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Abstract

We used genomic tools to understand senescence and molecular signaling events in harvested broccoli florets stored at 25 or 4 °C to test the hypothesis that genetic markers can be used to identify the stage of senescence or physiological age of plant tissue. The RNA-sequencing approach provided key insights into the gradual changes in transcriptome during postharvest storage in broccoli. We found that 4279 and 4143 transcripts were differentially expressed after 3 and 5 days of storage at the two storage temperatures, respectively. We then performed genome-wide comparisons at 25 and 4 °C and illustrated the temporal and spatial-specific genes in stored broccoli. By using quantitative Real-Time PCR and transient tobacco assay, we validated our RNA-sequencing experiment. We further performed comparative analysis of *Arabidopsis* and broccoli to disclose conserved senescence genes. Concurrently, we found that 43 genes were senescence-specific genes that are common senescence-associated genes (SAGs) regardless of tissue-specific expression. Interestingly, we observed 73 transcription factors (TFs) within this group that might form a core transcriptional regulatory circuitry to control the onset and progression of senescence. Moreover, we also identified new molecular players involved in postharvest senescence including brassinosteroids (BR) perception genes, *BIK1* (*Brassinosteroid-Interacting Kinase1*), *BRL1* (*BRI1-like 1*), *BIR1* (*BAK1-Inteacting Receptor-Like Kinase 1*), stomatal patterning gene *SPCH*, and circadian clock genes CCA1. Those genes could serve as 'freshness-indicators' for the stage of senescence or relative freshness of the product. This report identified the SAGs that are essential for tissue-specific senescence and provided fundamental insights into signaling events during postharvest senescence in *Brassica* plants.