



Investigating the Dynamic Transcript Level Changes of Senescence-associated Genes in Lettuce during Postharvest Storage

YOGESH AHLAWAT¹, CATHERINE BELISLE^{1,2}, GERMAN SANDOYA^{1,2},
STEVEN SARGENT¹, AND TIE LIU^{1*}

¹Department of Horticultural Sciences, University of Florida, IFAS, Gainesville, FL

²Everglades Research & Education Center, University of Florida, IFAS, Belle Glade, FL

Abstract

Lettuce (*Lactuca sativa*) is considered highly perishable and has a relatively short shelf life due to the induced leaf senescence mechanism that is influenced by both developmental and environmental factors. It is very important to understand the molecular mechanism underlying postharvest senescence in order to breed new lettuce varieties having extended shelf-life. To this end, quality measurements and gene expression studies in lettuce cultivars were carried out to estimate the variability in the lettuce accessions for determining the shelf-life. We focused on transcriptional changes of twelve senescence-associated genes (SAGs) in four lettuce cultivars, accession 60184, 'Manatee', 'Tall Guzman', and 'Okeechobee' during postharvest storage. Among those lettuce cultivars, accession 60184 has the shortest shelf life while 'Okeechobee' has the longest shelf life. The other two cultivars were observed to have intermediate shelf life. In this study, we observed the some of the SAGs, namely ORE15, ORE1, NAC90, LUX, NAC27, and WRKY, were differentially upregulated. Others were down-regulated during postharvest storage and had enhanced expression in lettuce, namely accession 60184. We found strong positive or negative correlation between gene expression of SAGs and shelf life of lettuce cultivars. These results indicated that lettuce SAGs can be used as markers to estimate lettuce shelf life. In summary, combining results from physiological and molecular measurements will provide genetic resources to plant breeders and researchers in establishing new markers for developing lettuce cultivars with enhanced shelf life.

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*Corresponding author. Email: tieliu@ufl.edu