

Title Identification and characterization of senescence-associated proteins in petunia corollas
Author Shuangyi Bai and Michelle L.Jones
Citation Thesis, Doctor of Philosophy (Horticulture and Crop Science),The Ohio State University.
201 pages. 2008.
Keywords Flower senescence; Proteomics; 2-DE; Senescence-associated gene

Abstract

Senescence is a degenerate process that leads to the death of plant cells, organs or whole plants. Senescence is not a passive process, but is an active developmental process regulated by plant age and other internal and external signals. The timing of natural senescence is not only controlled by developmental age, but also influenced by abiotic and biotic stimuli. The main purpose of leaf and petal senescence in plants is to remobilize and recycle nutrients from old and/or no longer necessary organs to developing parts of the plant, such as from senescing leave to young leaves, flowers, fruits and seeds. The quality and subsequent value of both agricultural and horticultural crops is impacted by the senescence of vegetative and floral organs. Therefore, it is of practical importance to understand the molecular and biochemical mechanisms of senescence initiation, regulation and execution.

The goal of my project is to identify global protein changes that occur during petal senescence. To this end, I employed two-dimensional polyacrylamide gel electrophoresis (2-DE) based on proteomic approaches to identify protein changes during petunia corolla senescence. One hundred thirty three differentially expressed spots were selected to be sequenced by tandem mass spectrometry. The majority of up regulated proteins were hydrolytic enzymes involved in macromolecular degradation and defense responses to abiotic and biotic stress. Protein sequencing data indicated that a number of proteins were post-translationally modified or processed during senescence. Our results not only support previous transcriptome studies, but also provide new insights into the post-translational regulation of senescence.

A senescence-specific nuclease (referred as to PhNUC2) from our 2-DE results was investigated. *PhNUC2* transcripts were specifically induced in senescing flower tissues. We hypothesized that suppression of PhNUC2 activity would delay nucleic acid catabolism during senescence, and this would in turn delay petal senescence. Thus, virus-induced gene silencing (VIGS) was used to knock down *PhNUC2* gene expression. *PhNUC2* gene expression and PhNUC2 nuclease activity were significantly reduced in VIGS corollas during senescence. However, the flower longevity was not prolonged in VIGS experiments. The reasons are discussed.