

Title Proteomic analysis identifies proteases upregulated during petunia corolla senescence
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Abstract

Premature senescence of leaves and flowers can have a negative impact on postproduction quality and shelf life of ornamental plants. An understanding of the initiation and execution of senescence is therefore needed to reduce postproduction shrinkage within the floriculture industry. While most studies of senescence have focused on gene changes, there is increasing evidence that senescence is also regulated post-transcriptionally. We have therefore used a proteomic approach to profile the protein changes during flower petal senescence. A large number of the proteins found to be upregulated during petal senescence fall into the biological function category of proteolysis. Protein degradation catalyzed by proteases is a key feature of senescence, which allows the plant to systematically dismantle cellular proteins and remobilize nutrients to developing tissues. The ability to manipulate these pathways may lead to delays in the senescence program. Most of the proteases identified during the pollination-induced senescence of *Petunia x hybrida* corollas were cysteine or serine proteases. Increased protease activity correlated well with these increases and senescence related activity was due to either cysteine and/or serine proteases. Four proteins that encode components of the ubiquitin-proteasome pathway were also identified and suggest that the targeted degradation of proteins via the proteasome may regulate senescence. The role of proteolysis in flower petal senescence and postproduction quality is discussed.