

Characterization of the cysteine protease, *PhCP10*, during the senescence of *Petunia x hybrida* flowers.

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Proteases play an important role in the degradation and remobilization of proteins during flower senescence. The majority of proteases that are upregulated during senescence and programmed cell death are from the cysteine protease class of proteases. Recently, nine putative cysteine proteases were identified from *Petunia x hybrida*. Six of the nine cysteine proteases were upregulated during petal senescence. One cysteine protease, *PhCP10*, is upregulated early in senescence, is expressed only in senescing tissues and appears to be regulated by ethylene. The *PhCP10* sequence shows high homology to *SAG12* (senescence-associated gene) from *Arabidopsis*. *SAG12* is senescence specific in *Arabidopsis* leaves, but little is known about its expression in flowers. TAIL-PCR was performed to obtain the *PhCP10* promoter. The *PhCP10* promoter sequence also shares homology with the senescence specific and basal promoter regions of *SAG12*. Promoter constructs driving GFP expression have been analyzed utilizing transient expression in lima bean cotyledons and in petunia flowers. Transient expression in lima beans and petunia flowers has detected a possible regulatory element that appears to enhance *PhCP10* expression in a similar manner to the enhancer region in the *SAG12* promoter. We are currently transforming petunias with the *PhCP10*:GFP constructs to further characterize the temporal and spatial expression of *PhCP10* during flower senescence and following ethylene treatment.

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