

Functional characterization of petunia petal senescence related proteins by virus-induced gene silencing.

Shuangyi Bai¹, Belinda Willard², Michael Kinter², David Francis¹ and Michelle Jones¹

¹ Department of Horticulture and Crop Science, The Ohio State University, Wooster, OH

² Department of Cell Biology, Cleveland Clinic Foundation, Cleveland, OH 44195

The senescence of vegetative and floral tissues can have a detrimental impact on the quality and subsequent value of agricultural and horticultural crops. Pollination, one of the key stimuli of senescence, can trigger and accelerate flower senescence and nutrient recycling. To profile protein expression during flower senescence, we used a proteomic approach to identify components of the senescence program in *Petunia x hybrida* cv Mitchell Diploid petals. Two-dimensional gel electrophoresis (2DE) was used to identify those proteins that were differentially expressed in nonsenescent (unpollinated) and senescing (pollinated) corollas. Proteins that increased in abundance during petal senescence are mainly involved in stress or defense responses, carbohydrate and energy metabolism, and other catabolic processes including proteolysis, nucleic acid, cell wall and lipid degradation. Since virus-induced gene silencing (VIGS) is a high throughput transient approach to analyze gene function, we are employing VIGS to further investigate the function of the senescence up regulated proteins. A fragment of the petunia chalcone synthase gene (*CHS*) and a fragment of the target gene will be ligated in tandem into the TRV2 vector. Both Agroinfiltration and Agrodrench can induce high efficiency gene silencing in petunia flowers. Currently we are studying the function of two proteins. One is a nuclease that is up regulated in senescing petals. Its molecular weight is very close to that of PhNUC1 whose biochemical characterization has been previously studied by the Jones lab. Another protein is beta-D-xylosidase, which is likely to be related to cell wall disassembly and loosening. This is a highly abundant protein, whose full-length, N-terminal and C-terminal truncated forms were all up regulated during petal senescence suggesting that this protein might be activated after post-translational modification or processing during petal senescence.