

Proteomic Profiling of Pollination-induced Senescence in *Petunia* Corollas

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The senescence of vegetative and floral tissues can have a detrimental impact on the quality and subsequent value of agricultural and horticultural crops. Treating petunia flowers with cycloheximide, an inhibitor of protein synthesis, delays flower senescence, confirming the importance of newly synthesized proteins during senescence. We are therefore using a proteomic approach to identify components of the senescence program in *Petunia x hybrida* cv Mitchell Diploid flowers. Total soluble proteins were extracted from petunia corollas at 24, 48, and 72 hours after flower opening (i.e. unpollinated, nonsenescing flowers) and at 24, 48, and 72 h after pollination (i.e. senescing flowers). Two-dimensional gel electrophoresis was used to identify those proteins that were differentially expressed in nonsenescing (unpollinated) and senescing (pollinated) corollas. PDQuest 7.4.0 image analysis (BioRad) software was used to identify those proteins up or down regulated by two fold in pollinated corollas. One hundred forty differentially expression proteins were identified. Most of these were identified by comparing 72 h unpollinated to 72 h pollinated corollas. Electrospray ionization-tandem mass spectrometry (ESI-MS/MS) was used to determine the identity of these proteins. Searching the NCBI nonredundant protein database we have been able to assign a putative identification to greater than 80% of these proteins. Identified proteins are involved in many metabolic pathways including proteolysis; nuclei acid, cell wall and lipid catabolism; and signal transduction. To further characterize the role of these proteins in flower senescence, we will knockdown the expression of the corresponding genes using virus-induce gene silencing.