

Cloning and functional analysis of type I and type II metacaspases during flower senescence in *Petunia x hybrida* cv. Mitchell Diploid

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Senescence is a highly regulated process and the final stage of plant development, which ultimately results in the programmed death of cells, organs, tissues or whole plants. Caspases are key regulators of the cell death program in animals, but to date no homologs of caspases have been found in plant genome databases. While caspase-like activity has recently been demonstrated in various plant cell death models, the corresponding genes for these activities have never been identified. While a caspase related family of proteases (metacaspases) has been identified in plant and fungal genomes using iterative PSI-BLAST, the function of metacaspases in plants is still largely unknown. As a first step to understanding the role of metacaspases, a type I (*PhMCA1*) and a type II (*PhMCA2*) metacaspase have been cloned from *Petunia x hybrida* cv Mitchell Diploid. The expression of *PhMCA1* and *PhMCA2* has been investigated in various petunia tissues using real-time RT-PCR. *PhMCA1* transcript abundance increased during flower senescence, while abundance of *PhMCA2* increased following *Botrytis cinerea* infection. *PhMCA1* expression was not increased in ethylene insensitive petunias during flower senescence. In order to further investigate the functional role of *PhMCA1*, RNAi lines have been generated and phenotypic analyses of T₁ plants is underway.