Title Changes in gene expression during senescence and aging of a number of cut flower species

Author Michela Appiano, Michael S. Reid and Cai-Zhong Jiang

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Abstract

Senescence, or programmed cell death, is the last phase in the normal development of floral organs. This process is under tight genetic control and involves changes in the transcriptome. A large number of genes that are up-regulated during petal senescence have been isolated from various flower species including alstroemeria, iris and petunia. The goal of this study was to identify a common set of genes that are up-regulated during floral senescence in a broad range of cut flower species. We isolated several such genes including those encoding for aspartic and cysteine proteinases, metallothionein-like protein, β-galactosidase and a putative nuclease from seven different species (Alstroemeria, Antirrhinum, Gerbera, Iris, Lilium, Lisianthus, Petunia). Expression of a gene encoding for a putative nuclease increased greatly during the final stages of flower development and aging in all the species tested. These results suggest that this particular gene plays an important role in the regulation of senescence in a wide range of species. Accordingly, it may have potential use as a universal marker to predict flower freshness.