

Title Molecular and genetic aspects of flower senescence
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Citation Stewart Postharvest Review, Volume 2, Number 2, April 2006, pp. 1-7(7)
Keyword cut flower; senescence; ethylene; cytokinin; proteases; gene; sugars; cell wall; membranes; lipases

Abstract

Purpose of the review: This review gauges the effects of recent research into molecular and genetic flower senescence on the development of postharvest cut-flower technologies.

Recent findings: Ethylene, cytokinin, sugars, cysteine proteases and other hydrolytic enzymes influence senescence in cut flowers through a complex series of interactions that are being actively investigated, but have yet to be fully understood. Senescence-related genes have now been isolated and characterised in a number of model flower crops (eg, petunia, arabidopsis) and cut flower species (eg, *Alstroemeria*, carnation, *Iris*, *Sandersonia*). The expression of these genes, together with a full understanding of the function of encoded proteins, is progressing. To date, new technologies for extending the postharvest life of cut flowers have been found through manipulation of ethylene biosynthesis and sensitivity. The challenge is to find avenues for maintaining quality and extending the vase life of ethylene-insensitive cut flowers.

Directions for future research: Solving the functional significance of genes that have been linked to flower senescence will further advance our understanding of the relevance of proteolysis, sugars, membrane integrity and cell wall modifications that occur during floral organ senescence. In turn, information on genetic control points of cut flower senescence will enable development of new avenues for manipulation and extension of the postharvest life of cut flowers (either new cultivars or vase-life treatments).