Title The potential to retard postharvest senescence using biotechnology

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Abstract

Purpose of review: Recent advances made in the study of the senescence process in plants has resulted in significant and interesting insights that have already been used to retard the process in transgenic plants by manipulating the expression of the relevant genes. This review summarises some of the studies relevant to postharvest senescence that may serve as a good base for further development of biotechnological strategies designed to control the postharvest senescence process in crop plants.

Main findings: Senescence can be retarded by manipulating various genes where products function in different aspects of senescence. These include regulatory functions such as transcriptional activation, involvement in ethylene or cytokinin biosynthesis or perception, involvement in the oxidative status of cells during senescence or participation in catabolic processes associated with senescence. The identification of appropriate target genes for manipulation of senescence should be accompanied by isolation of suitable regulatory elements for their activation. Specific activation in terms of time and localisation is crucial for effective application, as was demonstrated by the use of senescence-specific promoters or promoters that are mainly active under conditions relevant for postharvest storage.

Directions for future research: A large number of potential target genes for manipulation already exist and the number may increase further as a result of ongoing basic research. More emphasis should be given to applied studies aimed at examining the outcome of practical applications of biotechnological manipulation of these genes for retarding the postharvest senescence in crop plants. Commercialisation of such genetically-modified edible fresh produce seems uncertain at this point. However, it may materialise in the long term, thus time should now be utilised for developing efficient, senescence-retarding, biotechnological strategies that involve the identification of appropriate regulatory elements for specific activation of gene expression.