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#### Abstract

Some molecular aspects of flower senescence have been reviewed. The isolation, identification and characterization of different genes from various flowers (mainly from petals) associated with senescence have been discussed. The isolated genes were divided into different groups. A large proportion of genes have been found to be upregulated during flower senescence while some genes were also found to be downregulated indicating that there exists a complex interplay between the expression patterns of various genes. The genes involved in petal expansion are found to be upregulated during normal flower development from anthesis to open flower stage, but XTH (Xyloglucan endotransglucosylase hydrolase) is found to be involved in petal expansion as well as abscission. Cysteine proteases or the genes encoding cysteine proteases (assigned a central role in protein degradation) have been identified from various flower systems, but no cysteine protease has been identified from senescing *Mirabilis jalapa* flowers. In addition to proteases, the genes encoding ubiquitin (exhibiting proteasomal degradation by 26S proteasomes) have also been identified suggesting the two alternate pathways for protein degradation. Genes encoding specific nucleases have also been identified, but they displayed an early increase in transcript abundance before the senescence symptoms become evident and characterize the involvement of PCD during flower senescence. A range of transcription factors are described and their possible role in flower senescence has been discussed. A detailed description of genes involved in ethylene synthesis and the components involved in ethylene signaling have been presented.

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