

TRANSCRIPTOME ANALYSIS OF LEAF SENESCENCE IN *MEDICAGO TRUNCATULA*

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Senescence studies are important in legumes, where key events of the process are a massive degradation of proteins and a consequent reallocation of nitrogen to grains. *M. truncatula* is a model organism for legumes (its genome is undergoing sequencing, large collections of ESTs are available) and information obtained in this species is likely to be easily transferred to agronomically important crops.

The cDNA-AFLP technique was used to identify more than 500 genes, which were cloned and sorted into functional categories according to their Gene Ontology annotation. Comparison with the *Arabidopsis* leaf senescence reveals that the process is roughly conserved. However, important differences exist in some of the transcription factors involved and in the mechanisms of amine mobilization, which might reflect the uniqueness of nitrogen biology in legumes. In addition, we have observed that a minority of the genes regulated during leaf senescence are equally involved in nodule senescence or nitric oxide treatment; nevertheless, a large part of these genes have regulative functions, suggesting a conserved mechanism in orchestrating the different processes.