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FUNCTIONAL GENOMICS OF *MEDICAGO TRUNCATULA* LEAF SENESCENCE

M. TODESCO*, R. DE MICHELE*, M. ZOTTINI*, F. CARIMI****, E. BARIZZA*, M. GROTTO*, E. FORMENTIN*, F. BASTIANELLI*, D. LEISTER***, C. NOUTSOS***, F. LO SCHIAVO*, M. TERZI*

*) Department of Biology, University of Padova, Via U. Bassi 58/B, 35131 Padova, Italy – fiorella.loschiavo@unipd.it
**) Plant Genetics Institute, CNR, C.so Calatafimi 414, 90128 Palermo, Italy
***) Max Planck Institute for Plant Breeding Research, Cologne, Germany

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The study of leaf senescence in *M. truncatula*, a model plant for Legumes, has potentially relevant agricultural application. It can provide knowledges to improve biomass production and decrease post-harvest deterioration.

Two approaches have been adopted:

1) Transcriptome analysis of senescent leaves. To study the modulation of transcriptional levels during leaf senescence, we applied a cDNA-AFLP technique. This technique allows to compare the transcriptional status in different tissues or conditions (in our experiment: green and senescent leaves) and to isolate cDNA fragments from differentially expressed genes. We identified almost 850 cDNA clusters possibly involved in senescence. These fragments have been used to construct a cDNA microarray which was hybridised to validate the cDNA-AFLP results. These data have been statistically analysed to identify up- and down-regulated genes during senescence.

2) Analysis of the role of mitochondria in regulating the senescence/PCD process. Mitochondria are involved in different programmed cell death mechanisms, as well as in senescence. The proteome analysis of mitochondria led us to the identification of genes involved in PCD activation. Protocols to fractionate mitochondria and to dissolve membrane proteins have been set up. Data from protein analysis performed by MudPIT technique (Multifunctional Protein Identification Technology), in collaboration with Dr. Leister laboratory at the Max Planck Institute of Cologne, will be presented.