## Poster Abstract - D.11

## FUNCTIONAL GENOMICS TO DISSECT DROUGHT SIGNAL TRANSDUCTION IN CEREALS BY USING A. THALIANA AS MODEL SYSTEM

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Our work present a functional genomics approach to dissect drought signal transduction in cereals by using *A.thaliana* as model system. We have analysed four clones, named *6H8*, *6g2*, *1C1* and 10d10, previously isolated in durum wheat in respone to drought using a suppression subtractive library. They showed sequence similarity with genes in *A. thaliana* never reported to be involved in stress response: a putative transmembrane protein belonging to the UPF0016 family, a RING-FINGER protein, a farnesylated protein and an E2-ligase involved in sumoylation pathway. To identify the function of these genes two approaches are currently in progress: 1) analysis of the knock-out T-DNA mutants *via* a reverse-genetics approach, and 2) protein-protein interaction analysis using yeast two-hybrid system.

The isolated <u>T-DNA mutants</u> were studied under green house and laboratory conditions to test both their phenotype and stress resistance. The knock-out mutants showed a particular phenotype in controll condition ( $20^{\circ}$ C, 8h light,  $150\mu$ E) with red leaves and trichomes. In literature is reported that the same phenotype was shown by the wild-type in high light condition, revealing that the red pigmentation, due to anthocyanins, is caused by ROS accumulation. To test the level of stress-tolerance of these mutants we measured chlorophyll fluorescence (Fv/Fm) in response to photoinibition (1h at 2000microE and  $10^{\circ}$ C). The mutants showed a lower Fv/Fm than the wild-type plant, suggesting a higher sensitivity to light stress. We have also found that the mutants flower later than the wild-type plants only in short day condition. The future aim is the caracterisation of the mutant plants in drought and cold stress conditions for understand the particular phenotype and the resistance.

The *6g2* and *10d10* genes are putatively involved in sumoylation pathway and a protein-protein interaction study *via* yeast two-hybrid system has being started.