

FUNCTIONAL GENOMICS TO DISSECT THE ABIOTIC STRESS SIGNAL TRANSDUCTION IN CEREALS BY USING *A. THALIANA* AS MODEL SYSTEM

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This work was focused on six wheat genes previously isolated in durum wheat using a suppression subtractive library and characterized by a coordinated fast induction in response to cold and drought. After a careful databases comparison, an annotation or a putative function has been ascribed to all of them: ribokinase, a chloroplastic amino acid selective channel protein, a transmembrane protein belonging to the UPF0016 family, E3-RING-FINGER protein involved in the ubiquitination pathway, nuclear farnesylated protein and E2-ligase involved in the sumoylation pathway. Some of them were never reported as stress-related in any species. To elucidate their role in the stress response we have identified and analysed the arabidopsis homozygous T-DNA knock-out lines carrying an insertion in sequences homologous to the genes isolated in response to stress in wheat. All knock-out mutants showed the same stress-related phenotype when exposed to moderate photo-oxidative conditions, a red leaves pigmentation due to anthocyanins accumulation, an abnormal trichome development and a late flowering under short days. Based on literature data these traits can be associated to ROS accumulation. To test the level of stress-tolerance of these mutants we measured chlorophyll fluorescence (Fv/Fm) in response to photoinhibition (1h at 2000microE and 10°C). The mutants showed a lower Fv/Fm than the wild-type plants, suggesting a higher sensitivity to light stress. The analysis of the T-DNA insertional lines have demonstrated that the genes characterized in this work have a significant role in the stress response pathways most likely because they might be involved in the control of ROS accumulation. These results support the involvement of photo-oxidative stress as a component of cold and drought stress.