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Poster Abstract – D.38

CHARACTERIZATION OF A NOVEL POTATO GENE CODING FOR A PUTATIVE RNA BINDING PROTEIN INVOLVED IN PLANT RESPONSE TO WATER STRESS

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Plants respond to abiotic stresses by complex mechanisms involving a wide gene network. In order to preserve productivity of species in adverse environmental conditions is crucial to identify and characterize molecular functions that regulate the stress response and, above all, the adaptative response.

Previously, we reported a transcriptome analysis of potato cells exposed to short (shock) and long- term (acclimation) water stress induced by PolyEthyleneGlycole. Comparison of two different responses was performed by the TIGR 10k potato array challenged with RNA isolated from untreated, PEG-shocked and PEG-acclimated cells (Ambrosone et al. 2006, Transcriptomic and gene expression analysis during water stress in potato. Proceedings of SIGA Annual Congress).

Among the genes consistently induced during long- term water deficit the EST AW906734 coding for gene sato2, acronimous of Salt Tolerance, was identified. Sato2 gene encodes for a protein conferring salt resistance by complementation of a yeast defective mutant (Ros et al. unpublished) and contains a conserved RNA-binding protein domain. We isolated the sato2 coding sequence of *S. tuberosum* by RT-PCR using primers designed on sato2 mRNA sequence of *S. lycopersicum* (BT014404). Sequence translation and BlastP search reveals that the protein is highly conserved with more than 60% identity in several species as *Beta vulgaris, Vicia faba, Spinacia olearia and Arabidopsis thaliana.*

Gene expression of sato2 was investigated in potato cells, leaves and roots by qRT- PCR confirming the gene is responsive to water deficit conditions. A characterization of the A. thaliana sato hortologous gene (Atsato, At4g16830) was carried out. Atsato codes for a RNA-binding protein of 355 aa containing a RGG box with unknown function (www.arabidopsis.org). The gene resulted up- regulated in arabidopsis cells exposed to 50 uM ABA, 150 mM NaCl and 10% PEG. Phenotypic and physiological analysis of Atsato knockout (Atsato KO) indicated that the mutant was severely affected by ABA, NaCl and PEG treatments. In particular, root elongation of Atsato KO was inhibited compared to wt Columbia genotype (Col-0) in medium containing 80 mM NaCl and in GM plates equilibrated with 35% (w/v) PEG solution .To investigate the subcellular localization of the SATO2, transgenic plants overexpressing YFP-SATO fusion protein were obtained. The SATO2::YFP-fluorescence signal revealed SATO2 localizes in the cytoplasm of arabidopsis cells. We utilized 1500 bp sato promoter- GUS fusion to understand the expression patterns of the gene in arabidopsis vegetative and reproductive tissues. GUS expression driven by sato regulatory sequences was found in leaves, stomata, petals, sepals and pollen. Gain of function

and molecular interaction studies are in progress to establish the functional role of sato2 in water stress response.