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A POSSIBLE ROLE OF THE TREHALOSE/TREHALOSE-6-PHOSPHATE/SNRK1 SYSTEM IN RICE RESPONSE TO SALT STRESS

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Among the abiotic stresses exacerbated by climate change, soil salinity is one of the most harmful for crops. Rice (*Oryza sativa* L.) is a very salt-sensitive cereal, with particular regard to the cultivars belonging to the subspecies *japonica*.

In order to identify genomic traits conferring salt tolerance, a collection of 277 rice accessions (ssp. *japonica*) has been phenotypized under mild-salinity considering germination kinetic parameters and seedling emergence rate. Genotyping By Sequencing (GBS) followed by a Genome Wide Association Study (GWASs) were carried out. A total of 31.421 SNPs were used for the analysis.

Significant genotypic-phenotypic associations were observed and a few Marker-Trait Associations (MTAs) were identified. By alignment with the rice reference genome (Os-Nipponbare-Reference-IRGSP-1.0), some of the genes putatively involved in salt stress were highlighted. Among them, our interest has been focused on *OsTPP7* (chromosome 9) and *OsTPP10* (chromosome 7), genes that belong to the *OsTPP* gene family encoding for Trehalose-6-Phosphate Phosphatase (TPP) enzymes catalyzing the dephosphorylation of Trehalose-6-Phosphate (T6P) to Trehalose (Tre). The level of T6P plays a central role in abiotic stress tolerance, acting as a signal in the cascade of events regulating sugar metabolism (sucrose) during seed germination and seedling growth. This activity is mediated by Snf1-Related protein Kinase-1 (SnRK1), a metabolic sensor fundamental in maintaining carbon homeostasis under stress condition.

Biochemical and molecular analyses were performed on two rice accessions showing opposite behavior under salt stress (Olcenengo, tolerant, and SR113, sensitive). Results concerning T6P, Tre and sucrose levels in growing embryos, the evaluation of the time course of α-amylase enzyme (target of the SnRK1 system) activity and of *OsTPP10-OsTPP7* gene expression appear to allow us to define a picture coherent with the different effects of salt stress in Olcenengo and SR113. Functional characterization of *OsTPP10* gene and its allele mining analysis within the 277 rice accessions are in progress.

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