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The Trehalose-6-phosphate/SnRK1 system in the response to saline conditions during germination of two rice (*O. sativa* L., ssp. *japonica*) cultivars with different salt sensitivity

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Soil salinity is extremely harmful for crops, and, among cereals, for rice (*Oryza sativa* L.), with particular regard to the ssp. *japonica*. Seed germination and seedling emergence are among the phenological stages particularly sensitive to this stress condition.

A Genome Wide Association Study (GWAS) with a total of 31.421 SNPs was conducted on a collection of 277 *japonica* rice accessions phenotyped under mid-salinity considering germination kinetic parameters and seedling emergence rate. A few Marker-Trait Associations were identified on the basis of significant genotype-phenotype association analysis. Among the genes putatively involved in the salt response, two were particularly interesting: *OsTPP7* (chromosome 9) and *OsTPP10* (chromosome 7), both belonging to the family encoding Trehalose-6-Phosphate Phosphatase (TPP) catalyzing the dephosphorylation of Trehalose-6-Phosphate (T6P) to Trehalose.

Salt stress affects carbohydrate production and the mobilization/use of C storage compounds altering the sink-source relationships, sugar allocation and energy metabolism. In this framework, the ratios T6P/Tre, regulated by TPP activity, acts as a signal in the cascade of events that regulate, through sugar metabolism, plant development with particular regard to seed germination and seedling growth. In turn, T6P regulates the activity of Snf1-Related protein Kinase-1 (SnRK1), a metabolic sensor able to regulate α -amylase and fundamental in maintaining C homeostasis under stress.

Aim of the work was to establish the role of the SnRK1/Tre6P/Tre/Sucrose system and in particular of the *OsTPP7* and *OsTPP10* genes in the tolerance of *japonica* rice to salt stress during seed germination and early seedling development. In two model rice accessions (Olcenengo, tolerant, and SR113, sensitive) with opposite behavior in salt stress, biochemical and molecular analyses were conducted. In particular, have been considered: in the growing embryos, T6P, Tre, and sucrose levels, and *OsTPP7-OsTPP10* gene expression; in the endosperm, the time-course of α -amylase activity. The results define a picture coherent with the different effects of salt stress in Olcenengo and SR113. Functional characterization of the *OsTPP10* gene and its allele mining analysis within the 277 rice accessions are in progress.

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