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Transmembrane transporters and salt tolerance in temperate *japonica* rice

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Several investigations aimed at identifying molecular tools useful for the selection and/or the constitution of high-yield salt tolerant rice have been successfully carried out, concerning in particular *indica* and/or tropical rice genotypes. The global warming process is nowadays determining the intrusion of saline wedge into coastal fresh-water streams, and the soil salt concentration of many European rice areas, where temperate rice cultivars are mainly grown, is more and more increasing.

In order to identify molecular markers and/or new *loci* related to salt tolerance, a Genome Wide Association Study (GWAS) has been carried out using a panel of 277 *japonica* rice accessions. The panel has been subjected to Genotyping By Sequencing and phenotyping concerning tolerance to a mild-salt stress soil condition (5 dS m⁻¹) expressed at the 4th-5th leaf developmental stage using the Standard Evaluation Score (SES) proposed by IRRI. On the basis of GWAS, a QTL including a few genes that in the *indica* rice genome are localized within the major salinity tolerance-related QTL 'SalTol' have been identified. Among them, the *Os01g0337500* gene encoding the vacuolar H⁺-pyrophosphatase 6 (*OsOVP6*) is present. Since the role of the *OsOVP6* activity is considered central in regulating the cellular Na⁺ homeostasis in both roots and leaves, investigations comparing some elements of the complex mechanisms involved in this process have been carried out. A physiological approach evaluating this possibility has been conducted in two *japonica* rice varieties (Galileo and Virgo) that resulted salt-tolerant, in one *japonica* rice variety (PL12) known to be quite salt-susceptible, and in the salt-tolerant *indica* inbred genotype FL478 (containing the 'SalTol' QTL) as reference genotype.

The root and shoot Na⁺/K⁺ ratio, Na⁺ influx and K⁺ efflux, H⁺ extrusion activity, cytosolic and vacuolar pH by *in vivo* ³¹P-NMR techniques were evaluated in roots of the four rice genotypes. The results obtained, together with the electrophysiological evaluation of the whole root Na⁺ conductance, allow to define a picture that may explain the different salt tolerance observed among the rice genotypes analyzed.

As a whole, these results confirm the interest towards a deep allele mining analysis, concerning *OsOVP6*, within the most significant members of the *japonica* rice accession panel under investigation.

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