

Success story for crop's salinity tolerance: unraveling the molecular mechanisms

High soil salinity results in crop decline and constitutes a major constraint for agriculture, particularly affecting arid and semi-arid areas (James et al., 2012). Irrigation, when not well practiced leaves soils with high salinity. In addition, intrusion of seawater into coastal fresh water reservoirs, and erratic weather patterns, which seem to increase and which add drought years, compound the effects of increasing soil salinity. The problem of plants cultivated in soils with high salinity is the concentration of toxic ions in the root zone, which affects water uptake and transpiration causing ionic and electric imbalances, less growth, delayed development, and may lead to senescence and plant death. The abundance of sodium ions is the most deleterious as it is toxic in the cytosol and competes with potassium ions which are essential for plant's functioning and are compatible with protein structure, even at high concentration.

Plant tolerance to salinity constraint involves complex and integrated responses, at the cell, metabolic, and even anatomic levels; the relative contribution of which is dependent on the specific species. However, for every species, it involves the ability of the plant to maintain efficient root potassium (K^+) uptake in presence of high sodium (Na^+) concentrations, and to balance the net Na^+ uptake by the roots and its



Barley experiment at ICBA greenhouse

translocation and accumulation in leaves, since young leaves and photosynthetic tissues are very sensitive to salt stress (Munns and Tester, 2008; Benderradij et al., 2011).

For screening barley core collection for salinity tolerance, 10 barley lines (5 tolerant and 5 sensitive) were selected to carry out characterization of the stress response by measuring several physiological and molecular parameters. The experiment was conducted at ICBA and designed to study the plant growth in hydroponics system (1/2 strength of Hoagland's solution) under greenhouse conditions with three replicates

for each treatment. Salt treatments (0, 7, and 15 dS/m) were applied at the 3 leaf stage and were maintained till the end of the plant cycle. Leaf, leaf sheath, and root samples were harvested after one week of exposure to salt stress from the hydroponically cultured barley plants for Na^+ and K^+ analysis and for RNA (ribonucleic acid) extraction.

Results obtained for Na^+ and K^+ analysis using the Inductive Coupled Plasma (ICP) emission spectrometry procedure reflected the retained Na^+ at the leaf sheath compartment for the tolerant lines of barley, while the sensitive ones leaked Na^+ to the



Figure 1: Effect of salt stress on plant growth on hydroponic culture under greenhouse conditions. The sensitive barely line shows biomass reduction, chlorosis and senescence due to sodium accumulation in leaf tissues.

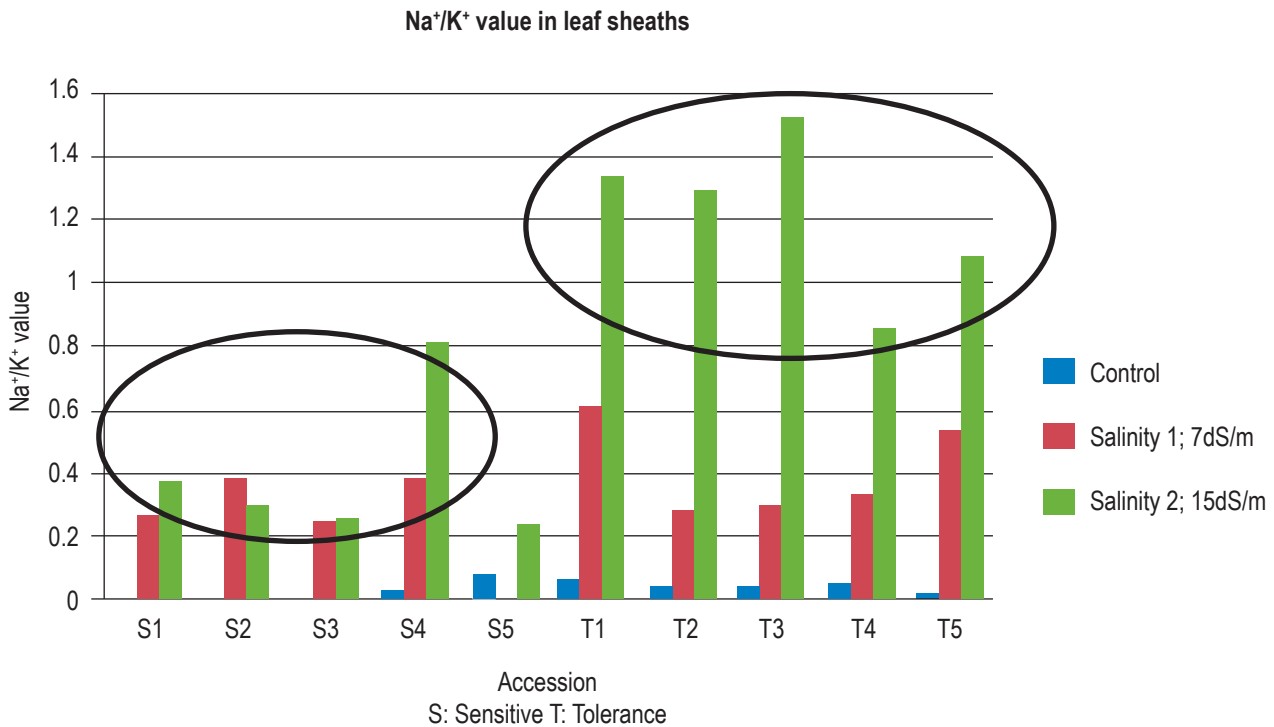


Figure 2: Sodium and potassium accumulation in leaf sheaths of the tolerant and sensitive barley lines. The tolerant lines retained and accumulated more sodium than the sensitive ones.

upper shoots showing symptoms of toxicity and senescence (Figure 1). Roots from sensitive and tolerant barley lines retained and accumulated Na⁺ to a similar concentration, indicating no difference in the uptake of Na⁺ from the nutritive solution. Accumulation of Na⁺ were noticed in the tolerant lines irrigated with 15 dS/m, while the sensitive lines exhibited severe reduction of biomass, and leaves showed chlorosis and senescence, and therefore accumulated less Na⁺ due to damage of the photosynthetic tissues. In leaf sheaths, the tolerant barley lines retained and accumulated more Na⁺ than the sensitive ones when the plants were watered with high salinity (15 dS/m). The sensitive lines didn't retain Na⁺ and leaked Na⁺ to the upper shoots (Figure 2).

It is hypothesized that Na⁺ accumulation in leaf sheaths identified in durum wheat is an efficient way to protect cells from Na⁺ injury and plays a crucial role in plant tolerance to salinity (Munns et al., 2012). To confirm the same hypothesis in barley, we studied the expression pattern of one candidate gene associated with Quantitative Trait Loci (QTL *Nax2*), controlling the unloading of Na⁺ to the xylem and in the control of root-to-shoot Na⁺ transfer. High expression level of

a salt tolerant gene *HKT1;5* was observed in leaf sheaths of the tolerant varieties, while moderate expression was observed in sensitive varieties and the control non stressed variety. These preliminary results suggest that *HKT1;5* gene might be involved in Na⁺/K⁺ transport through the plasma membrane in the leaf sheath with a more active role in the tolerant varieties.

The next step is to clone the favorable allele of *HKT1;5* gene with its native promoter from the tolerant barley variety and initiate genetic engineering to over-express this gene in salt sensitive barley variety and demonstrate its role in producing good yield in salt affected environment.

References

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