

Analysis of Salt Tolerance Mechanisms in *Sporobolus Virginicus*

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Summary

We identified a line of *Sporobolus virginicus* (L.) Kunth, a halophyte turf grass, collected in Okinawa, Japan. The line showed a salinity tolerance up to 1,250–1,500 mM NaCl, a three-fold higher concentration than seawater salinity. We investigated the growth rate, water content, ion concentration and secretion, and proline concentration in comparison with the reported properties of lines collected from the other places. Shoot growth was stimulated by 100 mM NaCl and root growth was stimulated at salinities of up to 1,000 mM NaCl. Accumulation of Na⁺ and Cl⁻ in shoots and roots was rapidly elevated by salinity stress but did not exceed levels required for osmotic adjustment, due in part to ion secretion by leaf salt glands, which are common characteristics among *S. virginicus* lines. However, the Japanese lines accumulated K⁺ to a higher level than other lines even under salinity stress. An increase in proline concentration was observed that was proportional to the NaCl concentration in the culture solution and might partially account for the osmotic adjustment of shoots. We also generated and characterized cultured cells of *S. virginicus* in comparison with rice cultured cells. The cultured cells of *S. virginicus* showed an enhanced growth compared with rice cultured cells in 500 mM NaCl. The concentration of Na⁺ and Cl⁻ ions in the cultured cells in 300–500 mM NaCl was lower level than in moderate salinity. Cultured cells of *S. virginicus* accumulated proline to higher levels than rice cultured cells under salinity stress. The active regulation of Na⁺, Cl⁻, and K⁺ influx/efflux and proline accumulation might be involved in salt tolerance mechanisms at the cellular level as well as *in planta*. We also performed comprehensive salt tolerant screening of Arabidopsis plants transformed with cDNA expression library consist from *S. virginicus* shoot mRNA and identified plants with enhanced salt tolerance. Two cDNA introduced into the plants encode genes for glycine-rich RNA binding proteins (SvGRP1, SvGRP2). In the transformants, expression of stress responsive genes, *RD29A*, *DREB1A* and *RD22*, was compromised under saline condition.