

**W898****Looking at the Bright Side of an Invasive Species: *Spartina alterniflora* from an Abiotic Stress****Tolerance Perspective***Date: Tuesday, January 13, 2015**Time: 3:10 PM**Room: Esquire - Meeting House**Venkata R. Mangu , Louisiana State University, Baton Rouge, LA**Renesh Bedre , Louisiana State University Agricultural Center, Baton Rouge, LA**Hana Zandkarimi , Louisiana State university Agricultural Center, Baton Rouge, LA****Niranjan Baisakh** , Louisiana State University, Baton Rouge, LA*

Spartina alterniflora (smooth cordgrass) is considered an invasive weed species by itself or by hybridizing with other *Spartina* species along San Francisco Bay. It is a dominant grass along the Gulf and Atlantic coasts of the U.S. In Louisiana, it is extensively used as an environmental engineer for marshland restoration. *S. alterniflora* is an extremophile that can withstand salinity up to double the strength of sea water. Genome-wide profiling of its transcriptome (~6x sequence coverage) revealed the role of genes in ion homeostasis and transcriptional regulation in its ability to adapt to highly saline environment. Superiority of the halophyte alleles was validated through overexpression and knockdown strategies in heterologous systems, including *Arabidopsis*, tobacco and rice. Overexpressers of *S. alterniflora* genes (for inositol phosphate synthase, vacuolar H⁺-ATPase, ADP-ribosylation factor, Sal-miR397a etc) showed salt and/or drought tolerance phenotypes, mainly through molecular adjustments in early stage and preparatory physiological responses, such as tissue tolerance by maintaining higher relative water content and ion homeostasis, and protecting damage to PSII, thereby maintaining higher net photosynthesis. Expression of the transgenes modulated endogenous genes expression associated with the physio-biochemical pathways for abiotic stress-tolerance. Also, the marker resources generated from *S. alterniflora* transcriptome were useful in establishing genetic diversity among different accessions of *S. alterniflora*. The transcriptome of *S. alterniflora* provides a platform for comparative genomics studies in grasses. Our study suggested that the transcriptome resources of *S. alterniflora* can be translated to improve stress tolerance of economically important crops including rice, a food crop of global importance.

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