

GRAND CHALLENGES GREAT SOLUTIONS

ASA, CSSA, & SSSA International Annual Meeting
Nov. 2-5, 2014 | Long Beach, CA

American Society of Agronomy | Crop Science Society of America | Soil Science Society of America

Start

88324 Translation of Halophyte Transcriptome Resources to Improve Salt and Drought Stress Tolerance in Rice.

Browse by
Section/Division of
Interest

See more from this Division: [C07 Genomics, Molecular Genetics & Biotechnology](#)
See more from this Session: [Genomics, Molecular Genetics and Biotechnology: I](#)

Author Index

Monday, November 3, 2014: 9:50 AM
[Share](#) |

Niranjan Baisakh¹, Venkata Mangu², Renesh Bedre³, Rohit Joshi⁴ and Luis Sanchez Timm², (1)School of Plant, Environmental, and Soil Sciences, LSU Agricultural Center - Baton Rouge, Baton Rouge, LA
(2)Louisiana State university Agricultural Center, Baton Rouge, LA
(3)Louisiana State university, Baton Rouge, LA
(4)International Center for Genetic Engineering and Biotechnology, New Delhi, India

Salt and drought stresses negatively affect rice yield. The magnitude of yield reduction depends on the genotype and developmental stage of the plant, and the severity of the stress. While natural variations for stress tolerance exist in the primary and secondary gene pool of rice, conventional breeding to develop salt and drought tolerant varieties has been slow and less successful due to the complexity and low heritability of stress tolerance traits. Extremophiles, such as halophytes, adapt to abiotic stresses through physiological and biochemical adjustments through coordinate regulation and expression of a cascade of genes. Halophytes are of interest to translate their stress adaptation machinery into crop plants. Based on the conception that monocot halophytes are ideal for translational studies for cereals, we profiled the root and leaf transcriptome of *Spartina alterniflora* (smooth cordgrass), a Louisiana native monocot halophyte that can withstand salinity up to double the strength of sea water. Digital and quantitative real-time expression profiles revealed significant enrichment ($P<0.01$) of transcription factors, vacuolar proton pump members and transporters under stress, and indicated novel transcriptional regulation networks in stress adaptation of this grass. Phenotype of rice overexpressors and knock-down mutants for a few selected candidate genes validated their role in stress tolerance in rice. The stress tolerance in overexpresser rice lines was attributed to their anticipatory preparedness by the (over)expression of halophyte genes. This was established by maintaining higher relative water content, regulation of stomatal movement, retention of photosynthetic activity, increased accumulation of osmolytes, antioxidants, and ion homeostasis. This study demonstrated that *S. alterniflora* is a rich reservoir of stress tolerance genes that can be used to develop stress-resilient rice and other cereals. Further, cross-transferability of its genic microsatellite markers indicated that *S. alterniflora* transcriptome resources will be valuable platform for comparative transcriptomics studies with other stress tolerant/sensitive grasses.

See more from this Division: [C07 Genomics, Molecular Genetics & Biotechnology](#)
See more from this Session: [Genomics, Molecular Genetics and Biotechnology: I](#)

[<< Previous Abstract](#) | [Next Abstract >>](#)

© Copyright 2014 - [Copyright Information](#), [Privacy Statement](#), and [Terms of Use](#)
[American Society of Agronomy](#) | [Crop Science Society of America](#) | [Soil Science Society of America](#)
5585 Guilford Road | Madison, WI 53711-5801 | 608-273-8080 | Fax 608-273-2021
[Certification](#) 608-273-8085 | Fax 608-273-2081