PLANT & ANIMAL GENOME XXII
The Largest Ag-Genomics Meeting in the World.
January 11-15, 2014
San Diego, CA
www.intlpag.org

P795

Genome-Wide Transcriptome Analysis of the Halophyte Grass *Spartina alterniflora* Reveals Molecular Basis of its Salt Adaptation Responses

Date: Monday, January 13, 2014
Room: Grand Exhibit Hall

Renesh Bedre , Louisiana State University Agricultural Center, Baton Rouge, LA
Venkata R. Mangu , Louisiana State University Agricultural Center, Baton Rouge, LA
Subodh Srivastav , University of Arkansas, Fayetteville, AR
Luis Eduardo Sanchez , Louisiana State University Agricultural Center, Baton Rouge, LA
Julio Solis , Louisiana State University Agricultural Center, Baton Rouge, LA
Andy Pereira , University of Arkansas, Fayetteville, AR
***Niranjan Baisakh** , Louisiana State University Agricultural Center, Baton Rouge, LA*

Soil salinity negatively affects growth and yield of most crop plants. Plants respond to salinity through physiological and biochemical adjustments that involve a coordinate regulation and expression of a cascade of genes. Naturally highly salt tolerant plants, such as halophytes, have been of particular interest to understand the biology of their salt adaptation mechanisms. *Spartina alterniflora* (smooth cordgrass) is a Louisiana native monocot halophyte that can withstand salinity up to double the strength of sea water. To dissect the genetic mechanisms underlying its salinity adaptation, the leaf and root transcriptome of *S. alterniflora*, subject to 500 mM NaCl, was sequenced using 454/GS-FLX. Altogether 770,690 high quality reads with an average length 324-bp were assembled de novo into 73,131 contigs (average 577-bp) with a sequence coverage 5.9X. Digital expression profiles revealed significant enrichment ($P<0.01$) of transporters, vacuolar proton pump members and transcription factors under salt stress, which suggested the role of ion homeostasis and transcriptional regulation in the salinity adaptation of this grass. Strong correlation of digital expression with qRT-PCR and enhanced salt tolerance of transgenic overexpressors of select candidate genes validated their role in salt tolerance. Also 10,805 SSRs markers from 9,457 unigenes were generated and validated through genetic diversity analysis among 13 accessions of *S. alterniflora*. The sequenced transcriptome of *Spartina* provides platform for further gene finding studies in grasses. This study suggested that *S. alterniflora* is a rich reservoir of salt tolerance genes, which can be used for improving salt tolerance in other economically important crops, especially cereals.

Back to: Genes & Pathways (Gene Expression, Proteomics, Metabolomics): Cellular Processes and Regulatory Networks

<< Previous Poster | Next Poster >>

Home/Search

Browse by Day

Browse by Type

Author Index

Poster Categories

Meeting Information

When:
January 10 - 15, 2014
Where:
San Diego, CA