

SPRESS

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1. Accession	Agency Identification No.	5. Work Unit/Project No.	6. Status
0216539	2. CSREES 3. LA.B	LAB93942	Annual Report
7. Title			
Molecular Genetics and Genomics of Abiotic Stress Tolerance of Smooth Cordgrass and Sea Oats for Improvement of Wetland Native Plants and Rice of			
12. Investigator Name(s) (Last Name and Initials)			
Baisakh, N.			
20. Termination Date 06/30/2013		40. Period Covered (mo/da/year): 01/01/2011 TO 12/31/2011	
Outputs:			
<p>The project resulted in four outputs in the form of two refereed journal articles and two presentations at the Annual meeting of the Crop Science Society of America and the Plant and Animal Genome meeting. The significance of the research was shared with a wide range of scientists and researchers engaged in plant sciences, especially plant molecular biology and biotechnology.</p>			
Outcomes/Impacts:			
<p>Sixty-one simple sequence repeat and 49 randomly amplified polymorphic DNA (RAPD) markers were used to fingerprint 13 smooth cordgrass accessions. A total of 276 polymorphic markers were generated where RAPD and SSR markers generated average polymorphism percentages of 57.3% and 56.7%, respectively. Both marker systems showed a comparable value of expected genetic diversity per locus (SSR - 0.33; RAPD - 0.35). At 0.20 of similarity, five major coefficient clusters were observed: Cluster I (CP1, CP2, CP3, CP4 and CP6), Cluster II (CP7), Cluster III (CP5, CP8, and CP10), Cluster IV (CP11, CP13 and CP12), and Cluster V (CP9). Principal coordinate analysis (PCoA) explained 30% of the variation. Analysis of molecular variance showed 62% genetic variation within a group as compared to 38% among groups (<math>F_{st} = 0.38</math>), which suggested the presence of sufficient genetic diversity among the accessions for exploitation in breeding programs. Unique genetic profiles were identified for six smooth cordgrass elite clones that can be used as probes for genetic identity of breeding lines. With a long term goal of phytoremediation for petroleum hydrocarbon-contaminated wetlands, the gene expression profile of <i>Spartina alterniflora</i> subjected to 40% PHC was studied under greenhouse conditions. The plants exposed to PHC showed 21% reduction of total leaf chlorophyll after two weeks of stress. Twenty-eight differentially expressing genes (DEGs) were identified in leaf and root tissues in response to PHC stress. Eleven DEGs had roles in either molecular function (chlorophyll a-b binding protein, HSP70, NADH, RAN1-binding protein, and RNA-binding protein), biological processes (cell wall protein, nucleosome/chromatin assembly factor) or cellular function (30 S ribosomal protein). All DEGs reduced transcript accumulation in root under oil stress, whereas they showed up- or down-regulation in their transcript abundance leaves depending on PHC concentration. The genes identified through this study could be used in the genetic screen of <i>S. alterniflora</i> for resistance to PHC. The expression of a vacuolar ATPase gene from <i>Spartina alterniflora</i> (SaVHAc) in rice enhanced tolerance to salt stress compared to the wild-type plants. SaVHAc1 expression led to up-regulation of other native in genes, including those involved in cation transport and ABA signaling. The SaVHAc1-expressing plants maintained higher relative water content through closure of the leaf stoma and reduced stomata density. The increased <math>K^+/Na^+</math> ratio and other cations established an ion homeostasis in SaVHAc1-expressing plants to protect the cytosol from toxic <math>Na^+</math> and thereby maintained higher chlorophyll retention than the WT plants under salt stress. The role of SaVHAc1 in cell wall expansion and maintenance of net photosynthesis was implicated in higher root and leaf growth, and yield of rice plants expressing SaVHAc1 compared with WT under salt stress. Genes contributing to natural variation in grass halophytes could be effectively manipulated for improving salt tolerance of field crops within related taxa.</p>			
Publications:			
<p>RamanaRao Mangu V, Weindorf D, Breitenbeck G, Baisakh N. 2011. Differential expression of the transcripts of <i>Spartina alterniflora</i> Loisel (smooth cordgrass) induced in response to petroleum hydrocarbon. <i>Molecular Biotechnol.</i> DOI: 10.1007/s12033-011-9436-0.</p> <p>Subudhi P.K., and N. Baisakh. 2011. <i>Spartina alterniflora</i> Loisel., a halophyte grass model to dissect salt stress tolerance. <i>In Vitro Cell.Dev.Biol.-Plant</i>, DOI 10.1007/s11627-011-9361-8.</p>			

Bernaola L, Venkata M, Knott, C, Harrison S, Materne M, Subudhi P, Baisakh N. Genetic diversity of smooth cordgrass (*Spartina alterniflora* Loisel) collections in Louisiana. Poster presented at the ASA.CSSA.SSSA. International Annual Meeting, October 16-19, 2011, San Antonio, TX.

Baisakh N, Ramanarao MV, Rajasekaran K, Subudhi P, Janda J, Galbraith D, Vanier C, Pereira A. 2011. A vacuolar proton pump (SaVHAc1) from halophyte *Spartina alterniflora* confers salt tolerance phenotype in transgenic plants through various physiological adjustments. Abstract, Annual Plant and Animal Genome Meeting XIX, January 15-19, 2011, pp. 251.

Participants:

N. Baisakh (PI), V. Mangu, L. Bernaola, S. Harrison, G. Breitenbeck, D. Weindorf, P. Subudhi, C. Knott, and M. Martin, LSU AgCenter; A. Pereira, University of Arkansas; C. Vanier, University of Nevada; D. Galbraith, and J. Janda, University of Arizona; K. Rajasekaran, SRRRC, USDA, New Orleans.

Target Audiences:

Scientists and researchers with interest in plant biology, biotechnology

Project Modifications:

Nothing significant to report during this reporting period.

Approved (Signature)	Title	Date
		