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Capturing natural variations in an extremophile for translational genomics of stress tolerance in crops

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Abiotic stresses adversely affect plant growth, development and productivity. Natural variations for stress tolerance exist in the primary and secondary gene pool of field crops but success with conventional breeding to develop salt and drought tolerant varieties has been slow, largely due to the complexity and low heritability of stress tolerance traits. Extremophiles possess specialized physiological and biochemical mechanisms to cope with environmental stresses through regulation of their transcriptome complexity. Genomic resources of halophytes have been exploited to improve abiotic stress tolerance in crops. Monocot halophytes are considered ideal for translational studies in important cereal food crops such as rice. *Spartina alterniflora* (smooth cord grass) is a Louisiana native halophyte grass that can withstand salinity up to double the strength of sea water. Profiling of its leaf and root transcriptome showed that transcription factors, vacuolar proton pump members and transporters were significantly up-regulated ($P<0.01$) under stress and that it possesses superior alleles that contribute to its stress adaptability. Phenotype of rice overexpresses and knock-down mutants of selected candidate genes validated their role in stress response in rice. The overexpressed rice lines manifested stress tolerance by positively regulating their relative water content, stomatal movement, photosynthetic activity, osmolytes accumulation and ion homeostasis under stress. This study demonstrated that *S. alterniflora* is a rich reservoir of stress tolerance genes that can be used to develop stress-resilient cereals including rice, a globally important food crop. Furthermore, *S. alterniflora* transcriptome resources will be valuable for novel gene discovery through comparative transcriptomics studies with other stress-tolerant/sensitive grasses.

Biography

Niranjan Baisakh has completed his PhD from the International Rice Research Institute (IRRI), Philippines. He has completed his Post-doctoral studies at IRRI and Louisiana State University Agricultural Center, Baton Rouge, LA. He is an Associate Professor at LSU Agricultural Center working on improving stress tolerance of field crops using molecular and computational biology and functional genomics tools. He has published more than 30 research papers, five book chapters and has presented his research in several national and international conferences. He currently serves as an Editorial Board Member of three journals including *PLOS ONE*.

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