

International Conference on

Plant Physiology & Pathology

June 09-10, 2016 Dallas, USA

Regulation of the lignocellulose pathway in rice as a model for grasses

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In the quest for alternative energy sources, biomass feedstocks play an important role. Crop wastes are often overlooked because of the complexities involved in adapting crops for industrial scale utilization in biofuels. Nevertheless, cellulose from plant biomass is the largest renewable energy resource of carbon fixed from the atmosphere, which can be converted into fermentable sugars for production into ethanol. Rice straw especially is a major crop waste that is often burnt or removed from fields. However, the cellulose present as lignocellulosic biomass is embedded in a hemicellulose and lignin matrix from which it needs to be extracted for efficient processing. In our research we found that overexpression of the Arabidopsis transcription factor SHINE (AtSHN) in rice altered lignocellulose composition, increasing cellulose by 34% and reducing lignin by as much as 45% with no compromise in plant strength and agronomic performance, supporting its use as a regulatory switch for altering lignocellulose composition in grasses. The AtSHN regulatory pathway was characterized by ChIP-Seq and ChIP-qPCR with AtSHN affinity tagged lines, and AtSHN targets confirmed by transactivation assays of promoter targets in rice protoplasts. Knockdown lines of the rice OsSHN gene were characterized phenotypically and the downstream pathway analyzed by RNA-Seq analysis. Integration of the information from AtSHN and OsSHN functional studies in rice, provide a framework model of the role of the SHN gene family in regulating biochemical and physiological pathways in rice and underpin its potential utility in understanding regulation of the lignocellulosic pathway in grasses.

Biography

Andy Pereira completed his PhD from Iowa State University, with postdoctoral studies from Max-Planck Institute (Germany), and worked as a scientist in Plant Research International (Netherlands) and Virginia Tech before joining the University of Arkansas as Anheuser-Busch Endowed Professor in Rice Plant Molecular Genetics. He has published more than 100 publications in the fields of insertional mutagenesis, Arabidopsis and rice functional genomics, systems biology studies of drought stress in interaction with basic biological processes.

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