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## Integrated functional genomics of soybean drought tolerance

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Profiling soybean transcriptome, proteome and metabolites will lay the foundation for a systems biology approach to understand key processes such as growth characteristics, stress responses, and yield. Understanding the concept and components of drought resistance is a key factor for improving drought tolerance of crops. Our research program focuses on an integrated genetics and genomics approach to dissect molecular processes from transcriptome to phenome. The root system plays a vital role in plant adaptation and productivity under water-limited environments. Deeper and proliferate root system help extract enough water under these environmental conditions. We have screened and identified soybean lines which exhibit genetic diversity in root system developmental plasticity in response to water stress, in order to enable physiological and genetic analyses of the regulatory mechanisms involved. We have observed maintenance of root tip growth under lower water potential and dissected these drought avoidance mechanisms utilizing integrated functional genomics tools. We have used Soybean Genechip and next generation sequencing technologies for the transcript profiling, DIGE and LC/MS for protein identifications, and GC/MS and LC/MS approaches to identify metabolites for further characterization. We have identified several root related and stress specific candidates, which help understand the biochemical networks involved in stress responses. Characterization of these candidates, engineering of selected genes through translational genomics pipeline, and field testing of the transgenics are in progress. This presentation will highlight the status of the systems approach towards the gene discovery and functional analysis of selected genes related to drought resistance mechanisms in soybean.

## Biography

Babu Valliyodan, PhD: Dr. Valliyodan has been working as the Senior Research Scientist in functional genomics at the Division of Plant Sciences and the National Center for Soybean Biotechnology, University of Missouri and has extensive experience with isolating and/or analyzing transcript, small peptides and metabolites from plants and bacterial cultures.

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