

Category	: 8th Rice Genetics Symposium
Select Theme	: Genetics of Abiotic interactions: Stress tolerance and Mitigation
Endorsement email	:
Genetics of Abiotic interactions Stress tolerance and Mitigation Keyword 1	: Drought
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Title of Entry	: Expression profiling of Two Rice Genotypes under Drought Stress during Reproductive Stage
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Rice is one of the most sensitive crops to water deficit, especially during reproductive stage. It is imperative to develop varieties that thrive and have good yield under drought conditions. The aims of this study are to evaluate agronomic traits and to perform transcriptomics study of two rice cultivars, Rondo and the advanced breeding line 4610, under drought stress during reproductive stage. Rondo is an elite cultivar with high yield but sensitive to drought stress; while the advance breeding line 4610 was previously reported as less affected by drought. A field experiment was conducted in Beaumont Research center in 2016. The drought treatment was conducted prior to flowering stage. Transcriptome data were gathered from leaf samples taken from 14 days after drought treatment. TruSeq Stranded RNA-Seq libraries were prepped at the Texas A&M AgriLife Genomics and Bioinformatics Service (TxGen). Libraries were run on an Illumina HiSeq 4000 to provide at least 25 million reads per sample. The raw sequencing reads were trimmed using the program Trimmomatic; then mapped to the reference genome using HISAT2. The number of reads mapped to each gene are counted using StringTie. For detecting the differential expressed genes (DEGs), DESeq2 package in R was used. This data will then be subjected for gene ontology annotation and further analysis. The field experiment data showed that 4610 is more tolerant than Rondo, with higher hundred-seed weight, less decrease in spikelet fertility, less decrease in filled

grain number and less decrease in yield. RNA-seq data analysis identified 855 DEGs in Rondo and 1051 DEGs in 4610. Based on biological process, a high proportion of DEGs, mapped to response to abiotic stimuli, lipid metabolic process, and response to endogenous stimulus. Metabolic and cellular processes, including photosynthesis was very significantly downregulated. Further analysis is underway to gain more insight about the function of these genes under drought stress.

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