

Category	: International Rice Research Conference
Select Theme	: High through-put technologies: Genotyping, Phenotyping and Omics
Endorsement email	:
High through put technologies Genotyping Phenotyping and Omics Keyword 1	: Transcriptome
High through put technologies Genotyping Phenotyping and Omics Keyword 2	: SNPs
High through put technologies Genotyping Phenotyping and Omics Keyword 3	:
Title of Entry	: Connecting genes and (epi)genomic variations to abiotic stress response/adaptation in rice via integrated genomics approaches
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Select only one type of presentation : 15 minute oral presentation

Abstract : The availability of high-throughput sequencing technologies provide opportunity to unveil the genetic/epigenetic basis of abiotic stress response and adaptation. Rice is an important crop accounting for food security of over half the world population. Water-deficit and salinity are the major abiotic factors that affect rice productivity worldwide. Rice germplasm exhibit variability in their response to abiotic stresses, which may be attributed to genetic and epigenetic variations. Although several stress-responsive genes have been identified and a few regulatory networks have been proposed, tolerance/response mechanisms still remain unclear to a larger extent. We performed whole-genome, transcriptome and bisulphite sequencing of three rice cultivars with contrasting responses to drought and salinity stress. RNA-seq analysis identified several novel stress-responsive transcripts/isoforms. We discovered extensive DNA methylation at single-base resolution in rice cultivars, identified the sequence context and extent of methylation at each site. Numerous differentially methylated regions (DMRs) among different cultivars were identified and many of them were found associated with differential gene expression. The transposon-associated DMRs were found coupled to the transcript abundance of the transposon and/or proximal protein-coding gene(s). We identified thousands of high-quality SNPs and InDels among the three rice cultivars. One-fourth of the SNPs and InDels were detected in genic regions and about 3.5% of the total SNPs resulted in non-synonymous changes. DNA polymorphisms present in the differentially expressed genes within the known quantitative trait loci were also identified. Further, we could

identify dmC-SNPs among the rice cultivars and their biological relevance in abiotic stress responses. Overall, these results provide insights into the regulatory mechanisms underlying abiotic stress response/adaptation and functional markers/ target genes for stress tolerance.

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