

Category	: 8th Rice Genetics Symposium
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High through put technologies Genotyping Phenotyping and Omics Keyword 1	: Transcriptome
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High through put technologies Genotyping Phenotyping and Omics Keyword 3	: Phenotype
Title of Entry	: Multifactorial transcriptomic analysis and gene network approach revealed contrasted molecular patterns of two rice varieties submitted to controlled water deficit during the reproductive phase
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Select only one type of presentation	: 15 minute oral presentation
Abstract	: Transient water deficit in rainfed rice can occur at any time of crop cycle due to rainfall variability. In contrast to the vegetative phase, quantifying plant response to water deficit during the reproductive phase implies to account for any differences in phenology between genotypes. Two contrasted tropical japonica varieties, Cirad 409 and IAC 25, were grown in pots in a phytotron under irrigated and stressed conditions. Under stress, irrigation was stopped ten days after panicle initiation, and fraction of transpirable soil water was maintained at 0.2 until heading. Fine morpho-physiological traits were measured, and internode (organ under elongation) samples collected for mRNA sequencing (Illumina). Read assembling and alignment were performed on <i>Oryza sativa</i> spp. japonica reference genome (Hisat2) and counts quantified (Stringtie). A multifactorial transcriptomic analysis was performed based on appropriate statistical approaches. First, genes were selected for the full model “genotype + treatment + genotype*treatment” by testing the significance of all factors at once using the DESeq2 likelihood ratio test. Quality and structure of gene selection was assessed using a multivariate statistical analysis (PLS-DA), highlighting genotype and water supply as the first and second factors driving transcriptomic internode response. Water deficit response of each genotype was then evaluated by performing classical pairwise comparison using the selected gene set. Second, Gene Co-expression Network Analysis (WGCNA)

was applied on the same selected gene set to identify, without a-priori, groups of correlated genes. Several networks, with expression level specifically related to water deficit response, were revealed per genotype, while others were more representative of the genotypic response regardless of the treatment. Moreover, significant correlations between networks and phenotypic variables were highlighted. In conclusion, this study highlighted contrasted molecular response to water deficit of two rice genotypes during the reproductive phase, thanks to the rigorous control of the start and intensity of the water deficit and the use of an appropriate multifactorial statistical analysis. Overall this work ended up to (i) identify specific phenotypic and genotypic water deficit response of each genotype, (ii) extract correlated genes representative of either the genotypic or stress response, and (iii) relate key gene to fine phenotypic traits.

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