

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Genotype x Environment Interactions
Keyword 2	: Genome editing
Keyword 3	: Abiotic stress tolerance
Title of Entry	: A comprehensive approach to understand the complexity of high temperature tolerance and development of climate resilient genotypes in rice
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Abstract : In changing climatic conditions, stress caused by high temperature poses a serious threat to rice cultivation. In this study under ICAR-NICRA project (Indian Council of Agricultural Research- National Innovations on Climate Resilient Agriculture), a large number of rice germplasm lines including introgression lines derived from *Oryza nivara* and *O. rufipogon* were screened for tolerance to high temperature. Two KMR3 x *O. rufipogon* ILs (377-24 and 458), one Swarna x *O. nivara* IL 175-2 and Nagina22 (N22) mutant NH219 were identified as higher yielding under high temperature stress in seven heat affected rice-growing locations in India during wet season 2016. In field screening by three methods i.e. 1-late sowing 2-using polycover, and 3-temperature gradient chamber, and evaluation of 20 morpho-physiological traits showed both yield and spikelet fertility as important traits for large scale screening of genotypes for heat stress tolerance. Physiological, biochemical, and molecular analysis of rice cultivars revealed that an aus variety N22 shows least reduction in chlorophyll content and net photosynthetic rate, but increased membrane thermal stability, antioxidant enzymes activity and transpiration rate at high temperature. It showed least Heat susceptibility Index (HSI) for yield/plant (Y), spikelet fertility (SF), flag leaf SPAD and stomatal conductance. Seven major QTLs for HSI for Y and SF were mapped on chromosomes 1, 4 and 8 with PV 7-28% in Vandana/ N22 F2-3 mapping population. Simultaneously, RNAseq helped to identify genome wide microRNAs and genes of N22 and Vandana from shoot and root after short and long duration of heat stress and also recovery phase. DREB, RAB, LEA, and genes associated with hormones signalling were induced during germination while OsFd (an iron sulphur cluster binding protein) and CWIP (cell wall integrity protein) emerged as high priority candidate genes at seedling and reproductive stages. These genes and microRNAs are being functionally characterized using transgene expression and CRISPR/Cas genome editing approaches. We thus aim to identify putative regulators and gene regulatory networks for an eQTL-guided function-related co-expression analysis.

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