IDT7-055 | A multi-dimensional approach from seed-to-seed to understand and improve heat stress tolerance in rice

Mangrauthia SK[1]*, Vishnu Prasanth V[1], Sailaja B[1,2], Sarla N[1], Voleti SR[1], Subrahmanyam D[1], Babu VR[1]

[1]Indian Institute of Rice Research, Hyderabad-500030,Telangana, India
[2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad-502324, Telangana, India
*E-mail: skmdrr@gmail.com

In changing climatic conditions, stress caused by high temperature poses a serious threat to rice cultivation. Physiological, biochemical, and molecular analysis of rice cultivars revealed that *Nagina22* (N22) shows lesser reduction in chlorophyll content, net photosynthetic rate, spikelet fertility and grain yield, but increased membrane thermal stability, antioxidant enzymes activity and transpiration rate (*E*) at high temperature. *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 in seedling and reproductive stages. Their function is being analysed by transgene expression and CRISPR/Cas genome editing approaches. Field screening in polyhouse, late sowing and temperature gradient chamber for 20 morpho-physiological traits indicated the importance of both yield and spikelet fertility, and photosynthesis traits. N22 showed the least Heat Susceptibility Index (HSI) for yield/plant, spikelet fertility, flag leaf SPAD and stomatal conductance, while *Vandana* showed the highest HSI for spikelet fertility and flag leaf temperature. QTLs for HSI of spikelet fertility were identified on chromosome 1 and HSI of yield per plant on chromosomes 1, 2, 3, 4, 7 and 8; and PV of 6% to 57% using 174 F2-3 *Vandana* x N22 mapping population. Simultaneously, RNAseq was performed to identify the genome wide miRNAs and transcriptome of N22 and Vandana from shoot and root after short and long duration of heat stress treatments; and recovery phase for an eQTL-guided function-related co-expression analysis to identify the putative regulators and gene regulatory networks.

IDT7-056 | Selection of superior parents to derive single cross hybrids of maize for water limited and well watered conditions through development of new heterotic pools

Mani, B. R[1]*, Deshpande, S. K[2].

[1.] University of Agricultural Sciences, Dharwad-580 005, India.
[2.] University of Agricultural Sciences, Dharwad-580 005, India.
*E-mail: mbreddys8102014@gmail.com

Maize is a major cereal crop of India and the world. It is used as food, fodder, poultry feed and agro industrial raw material. Growth stages, *viz.,* flowering and grain filling, are critical periods and moisture stress during these stages reduces grain yield to the extent of 70%-90%. Therefore, development of stable Single Cross Hybrids (SCH) in maize for limited water environment is essential. We studied new heterotic pools and identified superior parents among these pools. Thirty one potential inbreds were selected, based on ASI, RWC, SPAD, yield reduction under stress and drought tolerant index. These top 31 lines were test crossed with two testers (LM13 and LM17) to derive 62 test cross hybrids. Combining ability studies were conducted during *summer*-2016 under water limited (WL) and well watered (WW) conditions, and the data was analyzed using *Windostat v8.1* software. Heterotic grouping was done according to *Heterotic Group's Specific and General Combining Ability* (HSGCA) method. HSGCA is the difference between mean grain yield of crosses and testers. The signs of HSGCA of lines and grain yield SCA of testers were compared to make heterotic groups. Out of 31 inbreds, 17 from WL and16 from WW were assigned to heterotic group-A as that of tester-1 (+sign). Similarly, 14 from WL and 15 from WW were assigned to group-B as that of tester-2 (-sign). Inbreds with the highest positive HSGCA from group-A and the least negative HSGCA from group-B were identified as superior parents to derive SCH for water limited and well watered conditions.