IDT9-039 | Elucidation of differentially expressing genes in roots experiencing different levels of moisture stress using NGS in sorghum (*Sorghum bicolor* L.)

Kadam SR[1,4], Fakrudin B[2,4]*, Kavil SP[3,4]

[1]KRC College of Horticulture, Arabhavi (UHS, Bagalkot) – 591310, Karnataka, India
[2]College of Horticulture, (UHS) GKVK Post, Bengaluru - 560 065, Karnataka, India
[3]University of Greenwich, Kent – ME44TB, United Kingdom
[4]Institute of Agricultural Biotechnology, UAS, Dharwad – 580005, Karnataka, India
*E-mail: sandeepkadam15@gmail.com

Sorghum [*Sorghum bicolor* (L.) Moench], a member of C4 grass family, is an often cross pollinated diploid has more drought enduring capacity. In order to elucidate gene networks in response to moisture stress, a global overview of transcriptome was obtained by generating RNA-Seq libraries. Out of 136.9 million reads that were generated across the sorghum genome for mild, moderate and severe stressed and control treatments, 94.7 million reads aligned uniquely to the sorghum genome. A total of 34,569 gene models in each treatment could be resolved. 4,728 unique genes were classified as differentially expressed genes, which were characterized in three main gene ontology *viz;* biological class, molecular function and cellular component. Of which 1604 genes were upregulated and 3,124 genes were downregulated among all treatments as compare to control treatment. The upregulated genes that were categorized under response to abiotic stress, their fold change of expression has been compared in mild, moderate and severe, between mild and moderate stress, between moderate and severe stress and for the genes which are uniquely upregulated in moderate and severe stress. In total, we revealed the transcriptomes of the sorghum cv. M35-1 to reveal the overall transcriptional landscape in moisture stress at maximal resolution.

IDT9-040 | Mapping of quantitative trait lociin pearl millet (*Pennisetum glaucum* (L.) R. Br.) and relating to the water stress environments

Kakkera A[1], Baddam R[1], Vadez V[1]*

[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Hyderabad, 502324, Telangana, India
*E-mail: v.vadez@cgiar.org

Pearl millet, [*Pennisetum glaucum* (L.) R. Br.], is commonly grown in the dry environments of north west India, characterised by erratic rainfall that results in highly variable yields. Therefore, identification of plant types to a target environment is a big challenge. In this study, we are interested in traits that help improve yield when the crop is grown under control, mild, moderate and severe water stress based on the mean seasonal rain fall variations (460, 305, 252 and 139 mm in 1988) observed in dry environments of Rajasthan. We used F_7 progenies of the RIL cross H 77/833–2 × PRLT 2/89–33. LG 2 was associated with grain yield components i.e. grain mass, grain number of all water stress environments, tiller number (mild water stress) and PHI (severe water stress). Stover yield and flowering time were majorly associated with LG 4 and LG 6 (mild and moderate water stress). QTL interactions revealed that under well-watered conditions, a combination of two H 77/833-2 alleles enhanced yield by 21%. Under mild water stress interaction of two PRLT 2/89-33 alleles, one H 77/833–2 allele enhanced the yield by 29%. Under severe water stress, combination of three PRLT 2/89–33 alleles enhanced yield by 8%, but when this severe stress was interrupted by rain, then interaction of two PRLT 2/89–33 alleles with one H 77/833–2 allele enhanced the yield to 18%. This QTL study and their interactions elucidated the adaptability of lines to design environment-specific ideotypes.