

IDT9-029 | Genome wide association mapping of four agronomic traits in wheat (*Triticum aestivum* L.) under irrigated and rain-fed environments using 18K SNP

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In bread wheat, GWAS was conducted for four traits (days to anthesis, grain filling duration, grain number/ear and grain weight/ear) relevant to drought tolerance. For this purpose, a spring wheat reference set (320 genotypes) was genotyped for ~18K SNPs using genotyping-by-sequencing (GBS), and phenotyped under irrigated (IR) and rain-fed (RF) environments. Four different models that were used for GWAS included the following: (i) single locus single trait (SLST) mixed linear model (MLM); (ii) SLST statistical machine learning (SML) approach, (iii) multi-locus mixed model (MLMM), and (iii) multi-trait mixed model (MTMM). A variable number of MTAs were identified for the four traits using two SLST approaches (543), MLMM (702) and MTMM (559); 15 MTAs were common among MTAs identified

using different approaches. Together, only 57 MTAs (12 from SLST; 24 from MLMM and 21 MTMM) were stable in RF and IR+RF environments. The MTAs identified during the present study supplemented the available information on the genetic control of traits under IR and RF conditions. Stable MTAs may be exploited for improvement of drought tolerance in wheat using MAS. Seven candidate genes associated with stable MTAs and involved each in one of the following processes were also identified: transcription, transferase activity, protein processing, positive regulation of catalytic activity, lipid metabolic process, protein serine/threonine kinase activity and cytochrome P450 oxidase activity. Further studies involving these candidate genes for drought responsive traits may prove useful.

IDT9-030 | Detection of stay-green QTL in a sorghum recombinant inbred population based on cross (N13 × E36-1)

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The progress in genetic improvement of post-rainy sorghum for drought tolerance using traditional plant breeding practices has been slow, and selection has not been much effective due to complex interaction between genotype and environment. Identification of genetic factors involved in stay-green through molecular breeding approaches would provide the basis for genetic improvement for drought tolerance. In this experiment stay-green QTLs were mapped and the effect of environment on stay-green expression was observed. For this a sorghum Recombinant Inbred Line (RIL) population was field evaluated for 2 years during the post-rainy season of 2011 and 2012, under two water regimes, (stress and control). A set of 200 entries, including 180 RILs, parents and checks were sown in a plot of 2 rows of 2m in RCBD design with 3 and 2 replications for

stress and control treatments, respectively. Data was recorded for percent green leaf area (%GLA) with a weekly interval basis (7 counts) with starting from 50% flowering till physiological maturity. This reveals significant genotypic variances along with high heritability. A genetic linkage map based on 176 RILs with 271 markers consisting of SSRs, DArT and two qualitative traits was developed. In total 45 QTLs were identified for seven %GLA scores in two seasons and two treatments. The phenotypic variation explained by each QTL ranged from 6.00 to 14.00%. In further across environment analysis, some QTLs may be environment specific and some may consistent across environment, such stable QTLs could be utilized through genomics approaches to improve drought tolerance of post rainy sorghum varieties.