IDT9-091 | Fine mapping of stay-green QTLs on sorghum chromosome SBI-10L – An approach from genome to phenome

Usha Kiranmayee K N S[1]*, Hash C T [3], Kavi Kishor P B[2], Ramu P[4], Sivasubramani S[1], Sakhale S A[1], Santosh P Deshpande[1]

[1] International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India
[2] Department of Genetics, Osmania University, Hyderabad, India
[3] International Crop Research Institute for the Semi-Arid Tropics, Niamey, Niger
[4] Cornell university, Ithaca, New York, United States
*E-mail: knskira@gmail.com

Sorghum is the fifth most important C_4 cereal crop grown globally in arid and semi-arid climatic conditions. Drought is the major cause for loss of productivity worldwide. Delayed senescence of plants leads to adaptation to drought stress conditions by staying-green and giving high yields. In order to identify and dissect the stay-green genomic regions we have developed a high resolution fine mapping population from introgression line cross RSG04008-6 (stay-green) × J2614-11 (shoot fly resistant). Nearly 1894 F_2 genotypes were screened with 8 SSR in order to identify double recombinants for both the parents in the sorghum chromosome-10 long arm (SBI-10L). The selected $F_{2:4}$ recombinants were GBSed to increase the marker density between flanking markers *Xgap001-Xtxp141* for stay-green QTLs on SBI-10L and a high resolution linkage map was developed using GBS SNPs. Out of 182 only 152 recombinants were replicated thrice in field for stay-green screening for two seasons (Summer 2013 and 2014). Fine mapping of the per cent Green Leaf Area (%GLA) traits identified 33 QTLs and 19QTLs were clustered into 7groups where 8 genes were identified. These were AP2/ERF transcription factor family (Sb10g025053), Ankyrin-repeat protein (Sb10g025310), WD40 repeat protein (Sb10g025320), NBS-LRR Protein (Sb10g025283), Calcium dependant protein kinase (Sb10g030150), LEA2 protein (Sb10g029570), a putative uncharacterized protein (Sb10g024920) and senescence associated protein (Sb10g030520). With this study SBI-10L stay-green genomic regions were delimited from 15Mb to 8 genes co-localized with GWAS MTAs. Further cloning and expression level studies of the identified candidate genes will improve the development of drought tolerant genotypes.

IDT9-092 | Identification and validation of genomic loci associated with Kernel-Fe and Kernel-Zn concentrations in maize

Hindu V[1,3], Palacios-Rojas N[2], Babu R[4], Usha R[3] and Nair SK[1]*

[1]CIMMYT Asia Regional Maize Program, c/o ICRISAT, Patancheru, Telangana, India-502 234.
[2]International Maize and Wheat Improvement Center (CIMMYT), El Batan, Mexico-56130.
[3]Sri Padmavati Mahila Visvavidyalayam, Tirupati, India- 517 502.
[4]Multi-Crop Research Center (MCRC), DuPont Pioneer, Hyderabad, India-500 078.
*E-mail: Sudha.Nair@cgiar.org

Iron (Fe) and zinc (Zn) deficiencies in human diets is a worldwide serious health issue. These deficiencies could overcome through fortification of these micronutrients to staple food crops. One of the global staple food crop, maize is having considerable variation for kernel Fe and Zn concentration. Genome-wide association study (GWAS) was performed to dissect the genomic loci controlling Zn and Fe concentrations in maize kernel using a panel of 923 inbred lines. Based on mixed linear model analysis, corrected for population structure and kinship, 94 significant associations (p<10-4) for Fe (50SNPs), Zn (44SNPs) were detected at the genome-wide level. The identified associations were further validated in three different DH populations by single-marker QTL analysis. The analysis revealed that 5 SNPs (Fe) accounted for 4-27% and 6 SNPs (Zn) accounted for 5-28% of the total phenotypic variation, respectively in DH populations. SNP S7_173181689 on chromosome 7 explained 28% and SNP S8_164741133 on chromosome 8 accounted for 27% phenotypic variation, for Zn and Fe in DH populations. Based on the results from this study, the validated small number of genetic loci could be readily used for germplasm enhancement by marker-assisted selection in breeding for improving Fe and Zn content.