

IDT6-057 | Genetic variability for fodder quality traits in sorghum under different water regimes

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Sorghum is grown as a dual purpose crop yielding food (grain) and fodder (stover) in marginal environments of Asia and Sub-Saharan Africa. Application of genomics and trait discovery tools in breeding program can expedite genetic improvement of fodder quality. Earlier reports suggested that a difference of one percentage unit in stover digestibility increases livestock output of 6 to 8%. To characterize fodder quality traits in sorghum and to identify genomic regions related to those traits, a set of mapping population parents (24) were evaluated under two water regimes (control and stress) over 3 years at ICRISAT-Patancheeru. *In vitro* organic matter digestibility (IVOMD%) – a key stover quality trait, test weight (TW-g), stalk yield (SY-Kg/ha) and grain yield (GY-Kg/ha) recorded significant variation across

genotype, treatment, year and interaction effects. Across season analyses revealed a range of 45.8% to 50.4% for IVOMD, variation from 1.9g to 4.1g for TW. The SY and GY recorded a mean value of 4552 Kg/ha and 3152 Kg/ha, across years. While heritability estimates across seasons were on higher side for TW (0.85), SY (0.77) and IVOMD (0.70), it was lower for GY (0.39). A positive correlation of 0.63 and 0.79 was observed for SY – IVOMD and plant height (PH) – SY, respectively. This further implied that an opportunity exists for simultaneous improvement in both yield and fodder quality. We identified a parental set of ICSV1 and ICSV700 having consistently contrasting values across all seasons for IVOMD for further genetic mapping of the fodder quality traits in sorghum.

IDT6-058 | Identification of QTL and eQTL for drought stress tolerance and leaf senescence in juvenile barley

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Premature leaf senescence induced by drought stress is a main factor for yield losses in barley (*Hordeum vulgare* L.). Research in drought stress tolerance has become more important, as climate change will increase the number of drought periods. Hence, tolerance to drought stress has become an important goal in barley breeding. The aim of this study was to identify genomic regions involved in drought tolerance and leaf senescence in early developmental stages of barley. For this purpose phenotyping, genotyping and expression analyses were conducted on 156 genotypes, and based on these data genome wide association studies (GWAS) were performed. After a four weeks stress period (BBCH 33), six physiological parameters for drought stress and leaf senescence were determined in the control and stress variant in greenhouse pot experiments. Leaf colour and biomass yield, the main traits for leaf senescence and drought stress,

were significantly correlated ($r=0.36$) under drought stress conditions and significant phenotypic variation was observed. Analysis of variance revealed significant genotype and treatment effects. Based on these phenotypic data and 3,212 polymorphic SNPs with a minor allele frequency >5% derived from the Illumina 9k iSelect SNP Chip, 47 quantitative trait loci (QTL) were detected under stress conditions. Major QTL for drought stress and leaf senescence were located on chromosome 2H and 5H. Expression analyses of a set of 14 genes involved in drought stress and early leaf senescence on these 156 genotypes resulted in the identification of 13 eQTL, of which one is located in the same region of chromosome 5H as the QTL for biomass yield and leaf colour under drought stress. Respective markers may be used in future barley breeding programmes for improving tolerance to drought stress and leaf senescence.