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Fodder Quality Comparison in two Populations under Drought in Sorghum

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Abstract

Digestibility and lignin content are very important in determining feed quality and plant fitness, with higher lignin content reducing digestibility and vice versa. A 5% variation in fodder digestibility between poor and premium fodder is reported to result in a 20% price variation. Sorghum is gaining importance as a food, feed, and fuel crop, it has similar feed quality to maize, that demands high nutrient and water availability. Additionally, drought in the semi-arid tropics is also affecting feed quality and sorghum is known to encounter drought mainly in the post rainy season. Therefore, two sorghum populations, a recombinant inbred line (RIL) population (n=320) and reference set (n=130) were evaluated under drought for fodder qualities. In this study, irrigation was withheld at the booting stage for the stress plots whereas the control plots were fully irrigated, all other crop management practices were performed equally. The dry weight (DW) was recorded at maturity, and the fodder was subjected to near infrared spectroscopy (NIRS) scanning to record: nitrogen content on dry matter basis (NDM); neutral and acid detergent fibre (NDF and ADF); acid detergent lignin (ADL); metabolisable energy (ME) and; *in vitro* organic matter digestibility (IVOMD). Significant variation was recorded across treatments and for all traits in the RIL population. Significant genotypic variation and genotype by treatment variation was recorded for the reference set in 2016 only. Pearson's correlation was pooled for across years and treatments for both populations and DW and IVOMD showed negative correlation with NDF and ADL, while positive correlations were observed between DW, ME and IVOMD in the RIL population. However, in reference set there was no strong positive or negative correlation between DW, ME and IVOMD. Genotype by sequence (GBS) analysis was used to perform quantitative traits loci (QTL) estimation for the RIL population while a genome wide association study (GWAS) was performed for the reference set. A total of 98 and 47 associated genes were extracted from Phytozome v12.1.6 for the RIL and reference populations respectively. Several genes belong to pathways that may help explain a causal functionality with the associated traits.

Keywords: Digestibility, fodder quality, GWAS, QTL, sorghum

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