

IDT5-003 | Sorghum early vigor increases grain size, striga resistance and has linkages with some stay-green phenotype

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Promising agronomic crop traits could be more accessible to breeding if we understood their underlying plant processes and knew their genetics determinacy. Here, we attempt to progress understanding of the functional linkages between traits using PCA and quantitative trait loci (QTL) co-localization approach. A recombinant inbred lines (RIL; 181 progenies) population derived from a cross between senescent (N13) and stay-green(E36-1) parental lines was selected. This population was previously shown to segregate for stay-green expression and *Striga* resistance in the field. Here it was phenotyped for: (i) grain size variability under optimal field conditions; (ii) traits related to early-vigor (canopy size and growth rate) in a high-throughput phenotyping platform. Most traits had high heritability (>60%). Linkage map was constructed (271 molecular markers) and QTL

analysis (Cartographer 2.5) performed using composite interval mapping function. Two major QTLs influencing canopy size were found on SBI04 and SBI05. The SBI05 QTL harboring canopy size co-localized with the grain size QTL and with the genetic region of stg-4 (stay green) QTL (responsible for leaf size distribution). This links the vigor traits to the variability in grain size and leaf development (i.e. stay-green mechanism) the latter possibly explaining the variability in grain size. Since grain size partially regulates grain nutrients profile, such linkage calls for further exploration in breeding. The SBI-04 QTL for canopy size co-localized with QTLs for *Striga* resistance, strengthening the hypothesis that plant vigor enhances *Striga* resistance. Vigor appears to explain several traits and could be rapidly screened at the LeasyScan facility.

IDT5-004 | Exploration of rice (*Oryza sativa*. L) land races for drought tolerance

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Drought is one of the major constrains for rice production across almost all rice-growing regions. Rice lines differ greatly in their ability to tolerate drought and provide scope for combining drought tolerance in higher yield backgrounds. Genomics assistant breeding, particularly marker assisted selection and allele mining for drought tolerance genes, are two effective ways for utilization of promising lines through unlocking their genetic potentials. Keeping these as objectives, a small rice germplasm collection was developed, which included a good number of drought tolerant/ or avoiding upland rice lines. The studied lines were screened at physiological and biochemical level to decipher their ability for drought tolerance. In order to perform marker based genotyping, the genomic DNA was amplified with drought tolerance linked molecular markers.

Genomic DNA was also genotyped with miRNA linked molecular markers for deciphering the presence of drought responsive miRNAs and respective targets. For allele mining of the associated genes/elements (*DREB*, *LEA*, *CALMOD*), the genomic DNA of studied lines were amplified and sequenced to find out the different allelic forms (in form of sequence diversity among different rice lines). The main outcome of this investigation were (i) conservation and phenotyping of the selected traditional rice lines (ii) preparation of a genetic database of the studied land races with their degree of drought tolerance and (iii) identification of suitable linked markers for marker assisted selection (MAS) in relation to drought tolerance (iv) genomics and bioinformatics information of the selected genes in relation to drought tolerance.