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Tagging and Mapping of Major QTLs for Complex Traits in Sorghum

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SUMMARY

Many agriculturally important traits such as productivity, quality, tolerance to environmental stresses, and some forms of disease resistance are quantitative (polygenic, continuous, multifactorial, or complex traits) in nature. The genetic variation of a quantitative trait is controlled by the collective effects of numerous genes, known as quantitative trait loci (QTLs). Identification of QTLs for agronomic importance and its utilization in sorghum crop improvement requires tagging and mapping of the genome of crop species using molecular markers. The major QTL have been validated in different genetic backgrounds and are therefore ready for application through MAS in sorghum.

INTRODUCTION

Production and productivity levels of sorghum have reached a plateau with conventional breeding efforts. Progress through conventional breeding to improve these complex traits is not satisfactory mainly because of complex genetic control of these traits coupled with significant influence by environment. However, quick genetic gains can be achieved if selection is based on DNA markers. Therefore, application of DNA markers (MAS) is gaining importance in the genetic improvement of sorghum crop. Several marker systems have been developed and used for tagging and mapping of major effect genes and quantitative traits (QTL) of economic importance such as grain yield and its component traits, resistance to insect pests, diseases, striga, drought, salinity and cold. QTL is a gene or chromosomal region that affects a quantitative trait. The process of constructing linkage maps and conducting QTL analysis *i.e.* to identify genomic regions associated with traits is known as QTL mapping.

Grain Yield and Component Traits

Eight QTL involving different genetic backgrounds were identified on LG 2, 3, 6, 9, and 10. Three QTL identified on LG 10 are meta-QTL indicating their consistent expression in different genetic backgrounds (Mace and Jordan, 2011). Six of the eight QTL are major effect QTL controlling >10 % of phenotypic expression for grain yield. For grain weight, 28 QTL were detected across genetic backgrounds, of which 9 are meta-QTL accounting trait variance ranging from 4.8 % to 35 % (Mace and Jordan, 2011). Four major loci affecting sorghum plant height (Dw1, Dw2, Dw3, and Dw4) have been reported (Hilley *et al.*, 2016). Six major effect genes (Ma1, Ma2, Ma3, Ma4, Ma5, and Ma6) influencing flowering time/maturity in sorghum have been reported (Rooney and Aydin, 1999). Major QTL, QPle-sbi06-2 between markers GlumeT-Xtxp145 on LG 6 contributing >50 % of the panicle length variation was reported (Srinivas *et al.*, 2009). Three seed dormancy QTL for mature grains were identified (qGI-3, qGI-7, and qGI-9) consistently with no epistasis, and candidate genes SbABI3/VP1 and SbGA20ox3 were located within qGI-3 (Cantoro *et al.*, 2016). Two major QTL on LG 1 are associated with protein digestibility one QTL (linked with Xtxp11) unfavorably affects digestibility and one QTL (linked with Xtxp88) 20 cm away favourably affects digestibility (Winn *et al.*, 2009).

Pest Resistance

Satish *et al.*, (2009) reported 29 QTL for shootfly, *viz.*, four each for leaf glossiness and seedling vigour, seven for oviposition, six for dead hearts, two for adaxial trichome density, and six for abaxial trichome density. IS18551 contributed resistant alleles for most of the QTL, and the related QTL were co-localized, indicating they may be tightly linked genes. Two QTLs for midge resistance was located on SBI-03 and SBI-09 were associated with antixenosis explaining 12 % and 15 % of variation in egg number per spikelet. One region on SBI-07 was significantly associated with antibiosis and explained 34.5 % of the variation of the difference of egg and pupal counts. Multiple QTL for green bug resistance in different genetic resistance sources have been conducted against

green bug biotypes C, E, I, and K. Three loci present on SBI-05, SBI-06, and SBI-07 conferring resistance to green bug biotype I were identified (Katsar *et al.*, 2002).

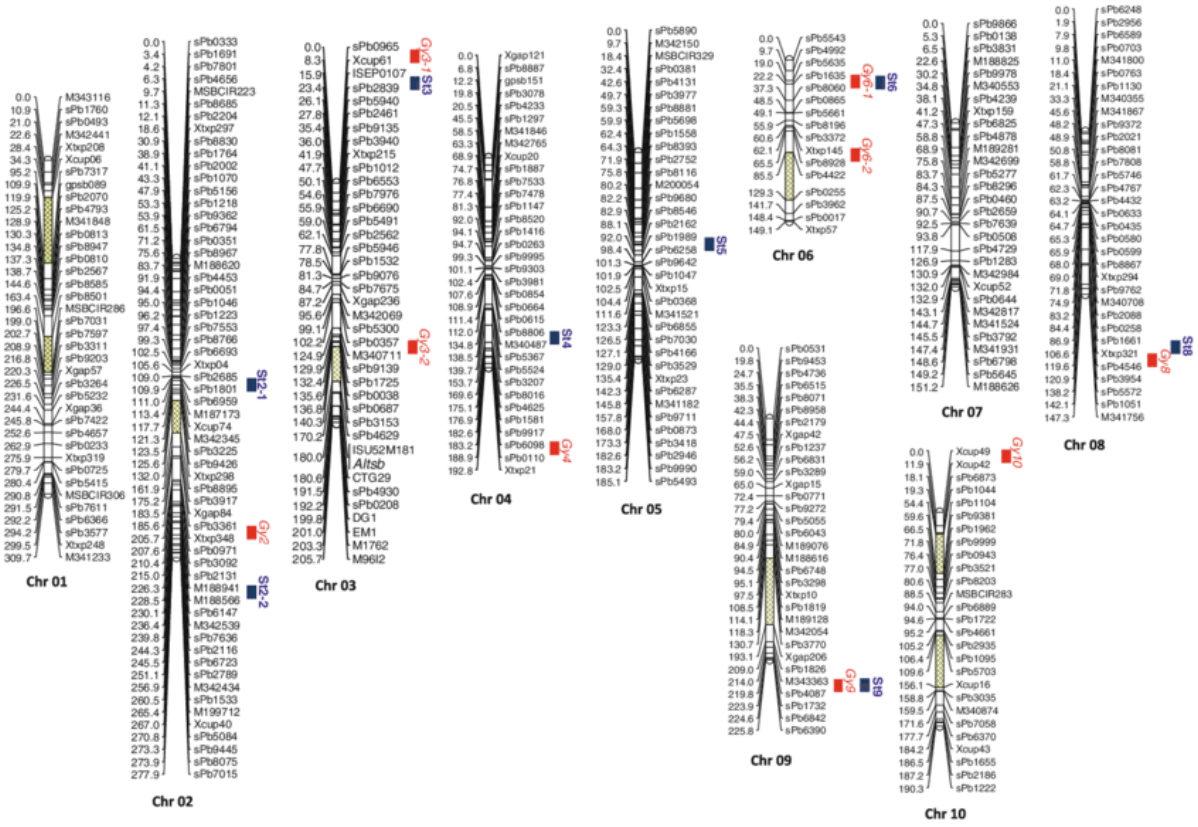

Figure: The positions for QTL influencing grain yield (Gy, in blue) and stay green (St, in red) (Source: Sabadin *et al.*, 2012)

Disease Resistance

Grain mould incidence was observed to be influenced by five QTL, each accounting for the phenotypic variance between 10 % and 23 % (Klein *et al.*, 2001). **Foliar Diseases:** QTL for resistance to sorghum anthracnose was mapped. A major QTL on SBI-06 between SSR markers, Xtxp95- Xtxp57 (Klein *et al.*, 2001) influencing resistance against various unrelated pathogens causing foliar diseases, was consistently detected with the phenotypic variation ranging from 32 % (bacterial leaf blight, zonate leaf spot) to 55 % (anthracnose), indicating involvement of a key gene for disease resistance. Four major QTL for **rust** resistance on SBI-01, SBI-02, SBI-03, and SBI-08 explaining 16 % - 42 % of trait variation were reported using a population of 160 RILs (Tao *et al.*, 1998). The major QTL on SBI-08 accounting 42 % of trait variation was found to host the key rust R-gene homologue of Rp1-D from maize and sugarcane (McIntyre *et al.*, 2005).

Charcoal Rot: Two major QTL for lodging were reported on LG 9 between Xtxp176-Xtxp312 and Xtxp274-Xabt29 explaining 12 % - 20 % variation. Similarly, major QTL for length of infection and number of internodes crossed were also reported on LG 2. Four major QTL for percent **ergot** infection (SBI-01 11.8 % near sPb-8261, SBI-06 14.1 % near sPb-1543, SBI-08 11 % near AGG þ CAG6, and SBI-09 19.5 % near Sb4-32) and one major QTL each for pollen quantity (SBI-06 19.9% near AAG þ CTT6) and pollen viability (SBI-07 12.5 % near sPb-5594) were detected besides the co-localization of QTL, signifying the clustering of genes with related function. It was also observed that the major QTL for percent ergot infection on SBI-06 was co-located with QTL for a number of diseases, including grain mould, anthracnose, zonate leaf spot, and bacterial leaf spot (Mohan *et al.*, 2010).

Striga Resistance: A single recessive gene controls low striga germination stimulant (lgs) activity, a well-known resistance mechanism in sorghum. Satish *et al.*, (2012) precisely mapped and tagged the lgs gene on SBI-05 between two tightly linked microsatellite markers SB3344 and SB3352 at a distance of 0.5 and 1.5 cM, respectively, using 354 RILs derived from SRN39 (low stimulant) and Shan Qui Red (high stimulant) lines.

Terminal Drought Resistance: B35 (BTx642) has been a useful source of stay-green. Four major QTL, namely Stg1 (SBI-03) and Stg2 (SBI- 03), Stg3 (SBI-02) and Stg4 (SBI-05), which together accounted up to 53.5 % phenotype variance.

Cold Resistance: Genetic mapping of cold tolerance using a population of 153 RILs from a cross Shan Qui Red (cold-tolerant) SRN39 (cold-sensitive) detected two QTL for germination, one on SBI-03 contributing 12 % and 15 % of variation under both cold and optimal temperatures, whereas the second QTL on SBI-07 showed greater significance only under cold temperature accounting 10 % trait variation (Knoll *et al.*, 2008).

Sweet Sorghum: QTL were identified for all sugar traits and were generally co-located to five locations (SBI-01, SBI-03, SBI-05, SBI-06, and SBI-10) (Ritter *et al.*, 2008).

CONCLUSION

Several studies have been identified major QTLs for many traits and integration of linkage maps resulted in saturated consensus maps. Several of these QTL have been validated in different genetic backgrounds and are therefore ready for application through MAS in sorghum. Plant breeders should integrate MAS into their conventional breeding schemes for higher genetic gains in sorghum.

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