Quantitative Trait Loci Mapping of Stem ºBrix Content and Stem Diameter in Sorghum Recombinant Inbred Lines Using Genotype-By-Sequencing

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Abstract

Sweet sorghum has the ability to store sugar in its stem. Many sugar content genes have been discovered and through breeding worldwide. However, some of these genes are unstable. This study aimed to detect and validate QTL for stem ^{o}Brix content from sorghum RILs. In two seasons, QTL linked with stem brix content and related traits were examined using 139 F8RILs from a grain and sweet sorghum. A genetic linkage map with 128 SNP markers was created and several QTLs were identified. Phenotypic variation between 6.33 and 14% was identified for a given trait. Over two seasons, four QTLs for stem brix content (*qBrix2-1, qBrix4-1, qBrix4-2*, and *qBrix10-1*) and three QTLs for stem diameter (*qSD1-1, qSD8-1* and *qSD9-1*) were detected. The detected QTL could be useful for improving stem brix content in different growing season. Furthermore, it makes a significant contribution to marker-assisted brix selection and sorghum biofuel improvement.

1. Introduction

Sorghum bicolor (L.) Moench is amongst the most significant crop throughout the semi- arid region of the world, after maize, wheat, rice, and barley (Meena et al., 2020). It is resistance to a variety of biotic and abiotic stress and commonly grown in water –stressed areas (Abebe *et al*., 2020; Badigannavar *et al*., 2018; Boyles *et al*., 2019; Mace *et al.,2020*; Yadav *et al., 2020*; Yang *et al*., 2020). Among its beneficial qualities are its ability to produce high grain yield, stem sugar, and lignocellulosic factors (Chandra *et al.,2012*; He *et al*., 2020).

Sorghum is grown in Ethiopia for food,fodder and feed in both main and off_ season (Tasie and Gebreyes, 2020). After the main season, off-season sorghum is typically plant in verti-soils under soil moister conditions stock up and replanting following the main-season, where both soil and atmospheric drought occur (Samdur *et al*., 2020). In order to meet the growing demand for food in the face of changing climate conditions, progress in the genetic improvement of important traits, such as grain yield and component traits, is necessary (Senapati *et al*., 2019a; Senapati *et al*., 2019b; Torres-Tiji *et al*., 2020). However as most of the off-season sorghum lines, the genetic enhancement of off-season sorghum is at present caught up by lack of genetic multiplicity along with breeding lines (Are *et al*., 2019; Nanaiah and Rakshit, 2020).

Grain yield and sugar related traits are complex characters involving numerous component characters, each of which is regulated by several genes, epistasis, and interactions (Banerjee *et al*., 2020; Disasa *et al*., 2018a; Fu *et al*., 2019). A significant method that has received increasing awareness in plant improvement for commerce with polygenic characteristics is quantitative trait loci (QTL) mapping (Ali *et al*., 2019). DNA markers can be used to dissect polygenic traits that were difficult to influence by conventional plant improvement methods in to individual QTL and these markers used plant developer to establish and go after the many interacting genes that affect complex traits (Ali *et al*., 2019; Cobb *et al*., 2019; Kim *et al*., 2020). In sorghum, many DNA markers such as RFLPs, AFLPs, SSRs and DArTs were developed and helps to construct linkage goups (Rahman *et al*., 2019; Srivastava *et al*., 2019). QTL of sorghum study have manipulated many genomic regions linked with essential agronomic and stem sugar traits, such as plant maturity, plant height, grain yield and related traits (Breitzman *et al*., 2019; Kang *et al*., 2020), and resistance to drought after flowering (Wang *et al*., 2020a), resistance to disease and insects (Jadhav *et al*., 2019), concentration of stem sugar. Building of genetic groups using unique functional genetic markers enables the co-location of genetic markers and QTL to be evaluated and can also improve our consideration of the biochemical pathway and system manipulating stem brix content traits (Disasa *et al*., 2018b; Kajiya-Kanegae *et al*., 2020; Kang *et al*., 2020; Mengistu *et al*., 2020). However, there are not numerous application in sorghum, particularly in off-season sorghum, for the linkage of genetic markers with QTL scheming the concentration of stem sugar and essential agronomic traits.

This would help us better understand the genetics of these traits by discovering QTL that regulate stem brix content and associated properties, as well as elucidating the links between QTL and candidate genes and laying the groundwork for MAS sugar yield in off-season sorghums. The objective of this experiment were to detect and QTL map for stem ^{o}Brix content and stem diameter from sorghum RILs using genotype by sequence data using the creation of a mapping population recombinant inbreed lines (RILs) derived from both grain and sweet sorghum germplasims.

2. Materials And Methods

2.1 Plant material

Mapping populations consisting of 139 Recombinant inbreed lines (RILs) derived from bi-parental population in this experiment. This population was previously produced from the initial, F2 population of a cross between two inbreed lines Gambella (Sweet sorghum as a pollen source) and Sorcoll 163/07 (grain sorghum, as a female parent), through six generations of single seed descent selection. In order to maintain this population for six generations, the first seed collection of the initial F2 population of two inbred lines was used.

2.2 Experimental design

During the off-season and rainy season for two years (2018 and 2019), field trials were carried out at the Ambo University Guder campus experimental site to test the phenotypic success of the RILs and parents. The research site of Guder is considered to be a midland area At an altitude of 1900 m.a.s..l and situated at 37°46'E, 8° 58'N. The rainfall ranged from 800–3194 mm. Data collection was carried out using the Handheld Geographical Positioning System (GPS). In both experimental seasons, an alpha-lattice design with three replications was utilized. All RILs and both parents were each planted in two plots in a row. Each plot is spaced at 0.75 m with a length of 3.0 m. The space was 2.0 m and 1.5 m between replications and blocks, respectively. At a depth of 5.0 cm, approximately 1.5 grams of sorghum seed were planted. After 25 days of emergence, planting was performed manually following thinning to 0.2 m spacing. Five plants were randomly selected from each row based on the type of characteristics to be evaluated for traits of interest. During planting, the prescribed amount of diammonium phosphate (DAP) was used, while the same amount of urea was added to the split application. All the appropriate agricultural practices have been followed. After flowering, the heads of previously tagged plants were covered with paper bags to protect them from neighboring pollen contamination and bird damage. Based on the sorghum agro-morphological descriptor (IBPGR, 1993) all morphological and yield related data were collected. To test the percentage of stem sugar concentration (Brix), a hand held wireless refracto-meter was used.

2.3 Phenotyping

The flowering date was scored starting from 50% powder set. The date of plant maturity (PM) was 45 days after the flowering date. Three plant maturity stages were described depend on the date of flowering for each recombinant inbreed lines. In order to obtain the plant height (cm), the height of the crop from the ground to the head tip was measured. The length of the crop neck was determined from the flag leaf to the end of the plant neck, excluding the height of the panicle of the plant. The length of the inflorescence was also measured from the inflorescence panicle up to the tip. Measurements of the head diameter were done for each RIL and parents. Between the 4th and 5th nodes of each sampled crop, stalk cylinder were removed. Using a digital caliper, stalk diameter was measured from each stalk cylinder and the mean of the four measurements per plot was used for next experiments. The diameter of the panicle (cm) in the natural position at the widest part was considered. Weight of panicle, grain per plant (gm) and thousand seed weight (gm) were measured using sensitive balance. According to Royal Horticultural Society (RHS) color codes, sorghum leaf midrib color was taken in parenthesis next to the descriptor suites: white (1) and brown (4) and other mid-

rib colors were coded accordingly. Measurements of sugar content in degrees Brix of each RILs and two parents were collected at plant maturity. Between the 4th and 5th node, stack cylinders were cut by each sampled plant. A garlic press was subsequently used to squeeze the stack of juice from each of the four sampled cylinders. To score the soluble sugar present in the stem liquid of each harvest cylinder, a digital refractometer (ATAGO Model-1) was used. In this experiment, the mean of the Brix scored per plot was used for analysis.

2.3.1. Phenotype data analysis

With SAS version 9.3 (SAS Institute, 2009), variance analysis across the progenies was computed. To estimate variance for all characteristics, the PROC GLM Method was used. Using Minitab version 16 statistical tools, the normality and homogeneity of the data for the features for the combined season were calculated (Minitab, 2010). Duncan's multiple range Test was used to perform mean separation. For each couple of character with the PROC CORR procedure, the Pearson correlation coefficient was also determined.

2.4 Genotyping

Seeds of the 139 RIL mapping populations, including two parents (Gambella and Sorcoll 163/07), were planted in greenhouse at the World Agroforestry Center (ICRAF) headquarters, Nairobi, Kenya. Two to three-week-old seedlings were collected from leaf tissues, followed by genomic DNA extraction using the genomic DNA extraction kit (Promega kit). By running on 0.8 percent agarose gel stained with GelRed® (Biotium, USA), the integrity of the genomic DNA was estimated, whereas Qubit®2.0 (Life technologies, Grand Island, NY) was used to quantify genomic DNA.

2.4.1 GBS library construction and SNP calling

Genomic DNA was digested individually with adequate restriction enzymes PstI and MspI.

Briefly, the 96-plex GBS library was constructed. The Illumina Genome Analyzer was used to sequence DNA at Cornell University in the United States. In order to produce polymorphic SNPs across the two parents and their progenies, data filtering, analysis and management were carried out using different tools, including TASSEL v.5. For this analysis, only those SNPs with missing data of less than10% and minor allele frequency greater than 0.05 were selected.

2.4.2 Linkage map

Via the genomic location of the SNP markers determined at the time of SNP call, about 10 constructed groups were allocated. LGs from the same linkage group were fused, and LGs were taken to be unlinked and falled from more grouping with less than five markers. To order all the markers inside LGs, theRECORD (Recombination counting and ORDering) algorithm was used. Using the Kosambi mapping feature, recombination frequencies among markers were converted in to Centi-Morgans. To inspect the markers for duplicate lines, segregation distortion, switched alleles, single and double cross-over (genotyping errors) using the necessary functions, an initial linkage map developed was applied. LGs with a threshold of LOD > 3 were determined and 10 LGs representing all sorghum linkage group were identified. Finally, a linkage map was generated and plotted using the best 128 SNP marker order with the least linkage map distance.

2.4.3 QTL detection

In total, in QTL IciMapping v4.1, 139 RILs with their two parents and 128 filtered SNP markers were used to detect QTL by using BIP features. ICIM-ADD purpose in QTL ICiMapping was chosen as the construction system for detecting QTL. The mapping parameters for ICIM-ADD were set to 1.0 cM and for each mapping method; a probability of 0.05 in stepwise regression was selected. QTL for all traits is designated according to standard nomenclature (Meng *et al.*,

2015). We defined a big QTL as a QTL with a LOD threshold value > 3.0 and a phenotypic difference donation of ~ 10% and we defined a stable QTL as a QTL that demonstrate consequence more than two seasons.

3. Results

3.1 Phenotypic trait analysis

Table 1 presents the phenotypic trait study of the RIL population with two controls for eleven traits over two consecutive years, 2018 and 2019, with three replications throughout the rainy season. In addition, Table 2 presents phenotypic trait analyses of the combined season. Important differences were observed in the RIL population for three characteristics, stem diameter, maturity date and panicle neck length; i.e., the value calculated for Gambela was considerably superior to that of Sorcoll 163/07 at ($P < 0.0001$). The concentration of stem ^{o}brix content scored for Gambela was considerably higher ($P < 0.05$) than that of Sorcoll 163/07. However, there was no substantial variation ($P > 0.05$) flank by the two parents with RILs during both seasons in traits such as plant height, flowering date, stem diameter, panicle length, panicle diameter, stem diameter, panicle weight, grain per plant and thousand seed weight 1000. Stem ^{o}brix content, maturity date and panicle neck length phenotypic value demonstrate permanent difference crosswise the progeny (RILs) over two years and was frequently spread through a mild kurtosis and skewness value (Supplementary data: Table 1).

The descriptive characteristics examined in this experiment have been summarized in Table 2 in general. According to Royal Horticultural Society color codes, the mid-rib color was graded, i.e. 4 (brown mid-rib color) from the parent Gambella and 1 (white mid-rib color) from the parent Sorcoll 163/07. Similarly, 62 RILs of the 139RIL population showed brown mid-rib color associated with the parent Gambella, and 77 RILs showed white mid-rib color associated with the parent Sorcoll 163/07 (Supplementary Table 3). Among the RILs, the highest (21.8) and lowest (3.8) stem brix content were registered during the off-season and main season, respectively (Supplementary data Table 2).

Table 1
Mean analyses for yield, yield components, sugar and sugar related traits Combined season (Off-season and Rain-season)

Traits	Parents		RILs							
	Gambela	Sorcoll 163/07	mean	Variance	Std.error	skewness	kurtosis	Min.	Max.	P-value
SBC	22.15	3.2	9.95	10.9	18.785	4.315	0.47	3.8	21	0.03
FD	97.5	117.5	108.95	102.9	48.095	6.915	-0.79	80	117.5	0.545
MD	127.5	137.5	133.75	129.8	36.2	6.055	-0.04	105	155	0.00
PH	220	231.5	209.25	210.3	1436.2	37.895	0.27	72.5	310	0.375
PNL	15.5	15	15.56	18.95	48.31	6.925	1.91	2.5	45.5	0.00
PL	17	28.5	23.37	23.38	28.49	5.315	-0.45	14	37	0.62
SD	14.2	13.7	13.305	13.3	7.48	2.715	0.1	8.595	21.4	0.195
PD	70.2	88.9	75.1	75.38	152.05	12.31	0.9	47.35	122	0.435
PW	103	81.5	73.69	74.4	380.3	19.5	-0.16	26	136.5	0.84
GPP	69.7	60	56.31	56.6	376.15	19.395	0.21	22	89.15	0.295
TSW	34.45	30.25	30.255	30.28	25.7	5.085	0.105	19.45	43.1	0.33

SBC: Stem brix content (Brix %); FD: Flowering date (days); MD: Maturity date (days); PH: Plant height (cm); PNL: Panicle Neck Length (cm); PL: Panicle length (cm); PD: Panicle diameter (mm); PW: Panicle weight (gm); SD: Stem diameter (mm); GPP: Grain/plant (gm); TSW: Thousand seed weight (gm)

3.2 Comparison of stage of sorghum for stem brix content

The juice extracted from each stage of the sorghum had different mean values for stem oBrix content, according to the results of mean separation study (Table 2). Following that, the juice derived from the sorghum maturity stage had a significantly higher mean oBrix percentage than the flowering stage (p 0.05). As a result, the maturity stage was used to extract juice for ^{o}Brix measurement in this experiment, resulting in a high mean value of stem ^{o}Brix content.

Table 2
The mean values of stem brix content varies among stage of the sorghum

Stage of sorghum	^{o}Brix of Gambela (%)	^{o}Brix of Sorcoll 163/07 (%)	^{o}Brix of RILs (%)
Flowering stage	8	0.6	6.9
Dough stage	16	1.6	14.6
Maturity stage	22.5	3.2	21
Significantly different at $P \leq 0.05$			

3.3. Correlation of morphological traits

The dates of flowering correlated strongly through all the traits. Flowering date and maturity date had the largest positive connection (r = 0.67), followed by stem diameter (r = 0.46) and panicle length (r = 0.36). The significant negative relation sheep was discovered between stem sugar concentration and panicle weight (r = -0.29). An important yet weaker relationship with plant height (r = 0.181) was shown by flowering dates. All parameters were favorably and

substantially linked with stem brix contents, with thw exception of a negative non-significant association with panicle weight and a mild significant negative association with panicle length.

Moderate and the highest association between the concentrations of stem sugar and mid rib color (r = 0.94) and stem diameter (r = 0.64) was observed (Supplementary data: Table 3).

3.4 Genotypic trait analysis

3.4.1 Linkage maps

Among the screened SSR markers, sixteen percent (128 out of 1082) revealed polymorphism between the two parents. Genotyping 139 RILs mapping populations using 128 polymorphic markers helped to construct linkage map. The majority of the 128 markers utilized in this study had a decent segregation pattern that did not differ considerably from the expected 1:2:1 segregation ratio. Ten linkage groups were used to create a genetic association group. More or less the distribution of markers appears to be distributed evenly across the ten groups of linkages. The total genetic map length was 1291.2 cM with 128 SSR markers spread over 10 linkage groups (Fig. 1). The mean and maximum distances were 2.25 and 29.8 cM respectively, between the two individual markers.

3.4.2 QTL detection

For QTL detection, eleven quantitative traits were grouped and analyzed using 3.0 LOD thresholds to state a QTL in ICiMapping software. In general, seven QTL were identified through two traits, ^{o}Brix and Stem Diameter, which were evaluated in the combined two seasons under the Ethiopian environment (Rain and Off-season) then summarized in Table 4 and Fig. 3. These QTL were spread over five linkage group; 1, 2, 4, 8 and 9 out of ten sorghum linkage groups with one or more QTL (Table 3) and 6.33 to 14.00 percent of the phenotypic variation was individually identified. Generally, the amount of QTL discovered appeared to be superior in main-season planting relative to the off- season.

Table 3
Linkage groups of quantitative trait loci detected at the Guder campus related to stem brix content and stem diameter traits (rainy season and Off-season)

Season	L G	QTLs	Position	Left marker	Right marker	LOD	PVE (%)	Add
Rain-season	SBI-2	*qBrix2-1*	246	74935854	76231234	6.00	14.00	-2.39
	SBI-4	*qBrix4-1*	156	51449056	53284525	3.03	6.33	-1.66
	SBI-4	*qBrix4-2*	266	65678951	67406111	4.55	9.33	-1.96
	SBI-10	*qBrix10-1*	38	57036699	55748280	4.00	8.14	-1.85
	SBI-2	*qSD2-1*	243	74935854	76231234	3.66	10.70	2.38
	SBI-4	*qSD-4-1*	262	65678951	67406111	3.11	9.02	2.18
Off-season	SBI-2	*qBrix2-1*	237	74935854	76231234	3.86	9.08	-1.94
	SBI-3	*qBrix3-1*	126	54459901	41419135	3.31	7.85	-1.83
	SBI-4	*qBrix4-1*	158	51449056	53284525	4.53	10.20	-2.11
	SBI-6	*qBrix6-1*	150	50392560	51205301	4.02	8.19	-1.81
	SBI-6	*qSD6-1*	127	49236398	50392560	3.23	9.9551	-1.41

3.4.2.1 Stem brix content (^{O}Brix %)

Four QTLs (*qBrix2-1, qBrix4-1, qBrix4-2* and *qBrix10-1)* for Brix content termination through rain-season were distinguished. The phenotypic variance ranged from 6.33 percent to 14.00 percent for these QTLs and the LOD score ranged from 3.03 percent to 6.00 (Table 3). The LOD score was distributed between the three linkage groups (SBI-2, SBI-4 and SBI-10) with an additive effect of -2.39, -1.66, -1.96 and − 1.85 respectively (Table 3). For alleles contributed by the parent sweet variety (Gambella), both additive effects were important. In addition, three QTLs (*qBrix-2-1, qBrix3-1, qBrix4-1and qBrix6-1*) were detected through off-season and spread over four linkage groups (SBI-2, SBI-3, SBI-4and SBI-6) with additive effects of -1.94, -1.83 and − 2.11 and − 1.81, respectively. Two stable QTLs (*qBrix-2-1 and qBrix4-1*) were observed in the combined season for the Brix trait and distributed at positions 238 and 25, respectively, on linkage groups of SBI-2 and SBI-4. All most 7.79 and 12.33% of the overall phenotypic variance is clarified by these QTLs, respectively. In addition, the LOD score ranged from 3.18 to 5.00. The additive effects of these QTLs detected were − 0.45 and − 0.43, respectively (Table 4). Negative signs were the additive results for all QTLs; this suggests that the parent one derived these alleles; high sugar sweet sorghum variety (Gambella).

3.4.2.2 Stem diameter

Two additive QTLs (*qSD2-1 and qSD4-1*) were identified during the rainy season for the stem diameter trait. In addition, the LOD score distributed over two linkage groups (SBI-2 and SBI-4). The LOD score ranged from 3.11 to 3.66 (Table 3). The phenotypic variance was ranged from 9.02 to 10.70 percent for the characteristics of stem diameter. Only one QTL (*qSD6-1*) was correspondingly reported with phenotypic variation 9.96 percent for the traits of stem diameter in the off-season (Table 3). In total, in the combined season three stable QTL (*qSD1-1* and *qSD9-1*) were detected for the stem diameter trait. The phenotypic variance ranged from 7.90 to 10 percent for these QTLs and from 3.26 to 4.16 for LOD scores (Table 4).

In general, the LOD score of maturity date, flowering date, grain yield per plant, thousand seed weight, plant height, panicle length, panicle diameter, panicle weight and panicle neck length were scored under LOD threshold we used. Because of this, the result of these traits couldn't discussed under QTL detection. Plant season has a major effect on stem brix content from phenotypic data analysis, which may again reflect on the detection of QTL for Brix in this experiment.

Table 4
Linkage classes, location and neighboring markers of quantitative trait loci detected at the Guder campus related to stem brix content and stem diameter (Combined season)

L G	QTLs	Position	Left marker	Right marker	LOD	PVE (%)	Add
SBI-1	*qBrix1-1*	4.00	73782812	72351563	4.03	9.48	-0.46
SBI-2	*qBrix2-1*	238	74935854	76231234	3.18	8.74	-0.45
SBI-4	*qBrix4-1*	25.00	1595489	3909059	3.32	7.79	-0.43
SBI-4	*qBrix4-2*	234	63340633	64663157	5.00	12.33	-0.52
SBI-1	*qSD1-1*	215	26030629	18963538	3.75	8.99	-1.51
SBI-8	*qSD8-1*	123	22836746	6672443	3.26	7.90	-1.42
SBI-9	*qSD9-1*	188	56521967	56112618	4.16	10.00	-1.61

4. Discussion

Sugar and sorghum grain yield can be influenced by season and crop maturity traits. The present study shows that the most important feature among the sugar component traits of sorghum is the leaf mid rib color and stem diameter to

increase the sugar yield per plant unit. We observed that Gambella parent also produced high sugar yield in response to brown mid rib color, but Sorcoll 163/07 reacted to white mid rib color and did not produce higher sugar yield than Gambella parent. The result showed the importance of mid-rib color to increase the yield of sugar in sorghum, particularly during the main-season. In addition, our correlation study of RILs showed that leaf mid rib color is strongly associated with sugar yield, implying that brown mid rib color will also result in an increase in sugar yield. In other way, grain yield was found to be positively associated with panicle number, panicle size and thousand seed weight. This result revealed the mitigate of increasing grain yield through these yield component traits. Most kernel number/panicle with kernel size is produced as the grain yield increases. It was also observed that the number of panicles and the size of panicles had a highly significant positive association with themselves. In producing advanced yielding sorghum cultivars with grain yield, each of these traits may be equally essential. These two independent qualities could be controlled simultaneously or individually in the selection of sorghum with high grain yield. Our data showed that compared to the off-season, more kernels were produced in the main season. This outcome may be attributed to a greater chance of moisture during the main season. Few QTLs were discovered for each characteristic in this study, due to the quantitative character of the traits, divergence in parents for most of the characteristics, and performance of the RILs. In the present study many traits of this RIL population were discussed in phenotype characterization but not detected in QTL mapping because of many traits were under LOD threshold used. Many variables, such as quality performance, physiological efficiency, marker density, population numbers, and expanding environments, may contribute to the power of QTL detection in QTL analysis. In terms of data quality, evidently good data, such as a little number of missing plot, would be adequate to detect more QTL (Barbeira et al., 2020; Tong et al., 2020). Plots that were not present in our overall plot count were not scored. Aside from the restricted number of missing plots, field agronomic performance by genotype is also important in detecting QTLs.

This argument may be justified by the identification of more QTLs with our better performing experimental area. From phenotypic data analysis, QTLs were identified for stem brix content and stem diameter traits in the least performing environment. It could be argued that more QTLs were also substantially identified by other data structures rather than more phenotypic output scored for stem brix content and stem diameter. In addition to phenotypic data, the power of QTL detection is an important problem of genotypic data. Relatively genetic maps constructed from different markers were used in the present experiment. In addition to marker size, the number of QTL detected could be influenced by population size (Kiranmayee *et al*., 2020; Wang *et al*., 2019; Wang *et al*., 2020b). Identifying QTLs associated with the concentration of sorghum stem brix and its component traits was considered. Stem diameter is crucial in achieving high stem brix content in sorghum, as defined in phenotypic data analysis, and hence, as previously discussed by different authors (Knoll and Ejeta, 2008; Li and Huang, 2017), the discovery of strong QTLs linked to this feature is of special interest. These findings support our quantitative collected data and point to the importance of stem diameter QTL in sorghum development for stem brix concentration stabilization in a variety of growth situations. In phenotypic data analysis, as demonstrated by the small frequency difference between two seasons for this trait, we observed that the climate has little effect on stem diameter. Additionally, our findings showed that QTLs were more stable during the combined season for stem brix content than stem diameter. The findings were consistent with the previous observations in sorghum. In conclusion, our findings show that although the concentration of stem sugar is complex, QTL that significantly contributes to the concentration of stem sugar could be established and used for higher sugar yield in breeding sorghum.

Declarations

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Contributions

All authors contributed to the study conception and design. Material processing and data collection and analysis were performed by Abera Takele. He also wrote the first draft of the manuscript, and all writers provided input on the previous edition. The final manuscript was read and accepted by all contributors.

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Ethics declarations

Conflict of interest

There are no conflicts of interest declared by the writers.

Ethics Approval

Not applicable.

Consent to participate

All coauthors indicate their motivation to contribute in this research.

Consent for publication

All coauthors have read and have the same opinion to submit the manuscript.

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Figures

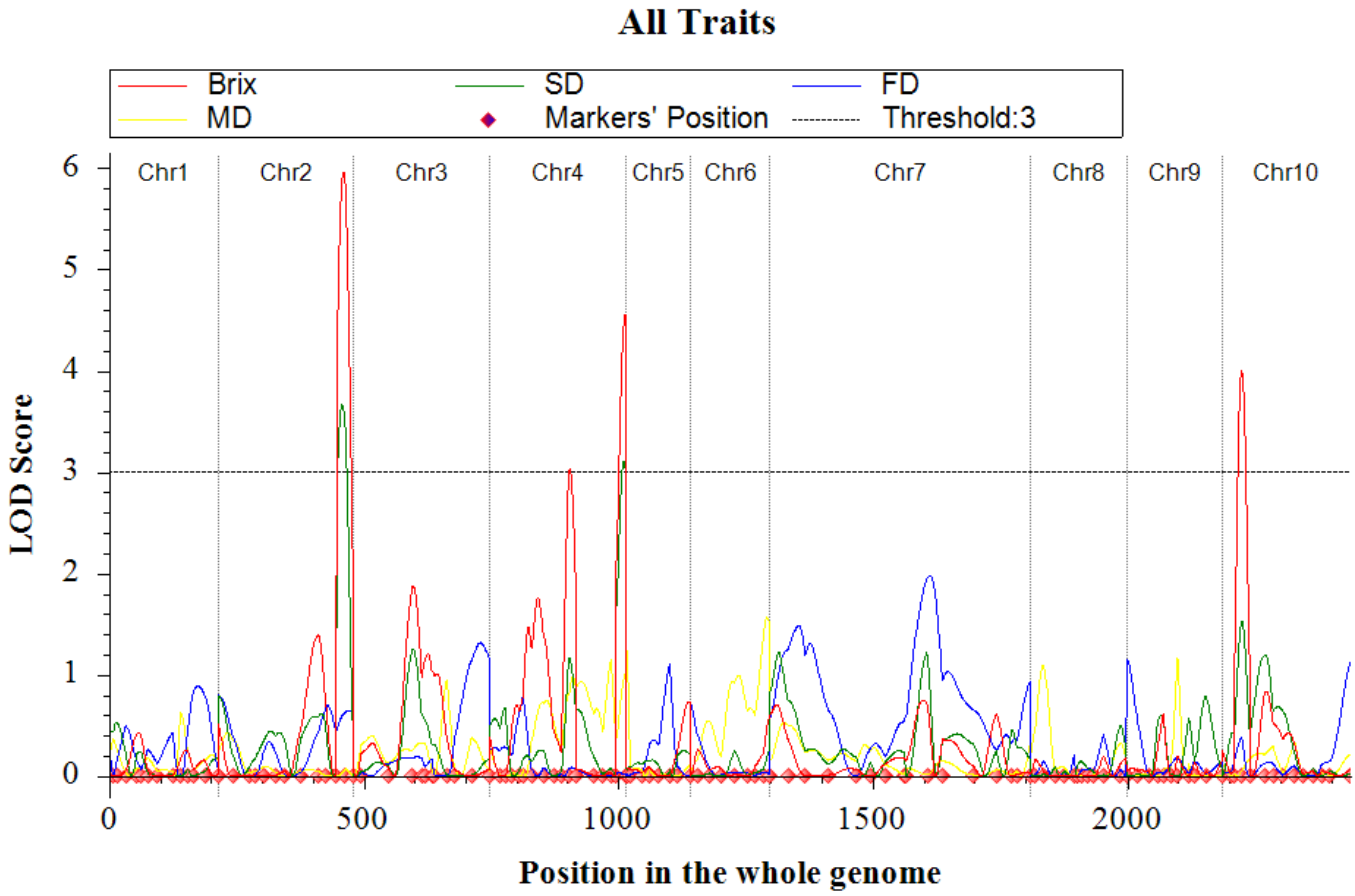

Figure 1

Detected quantitative trait loci for Stem diameter and stem brix content traits in sorghum at LOD threshold 3 (Rain-season)

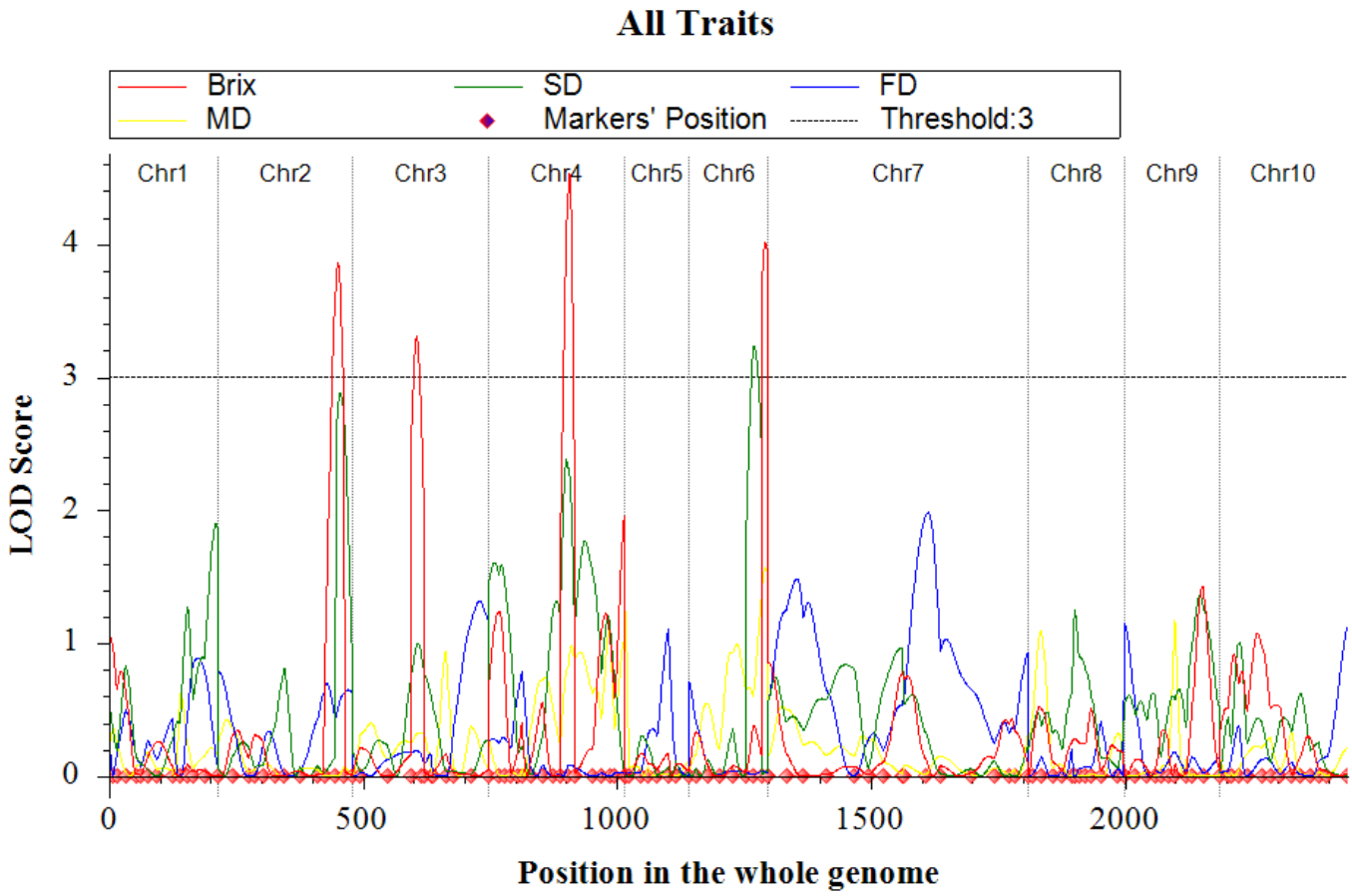

Figure 2

Detected quantitative trait loci foe stem diameter and stem brix content traits in sorghum at LOD threshold 3 (Off-season)

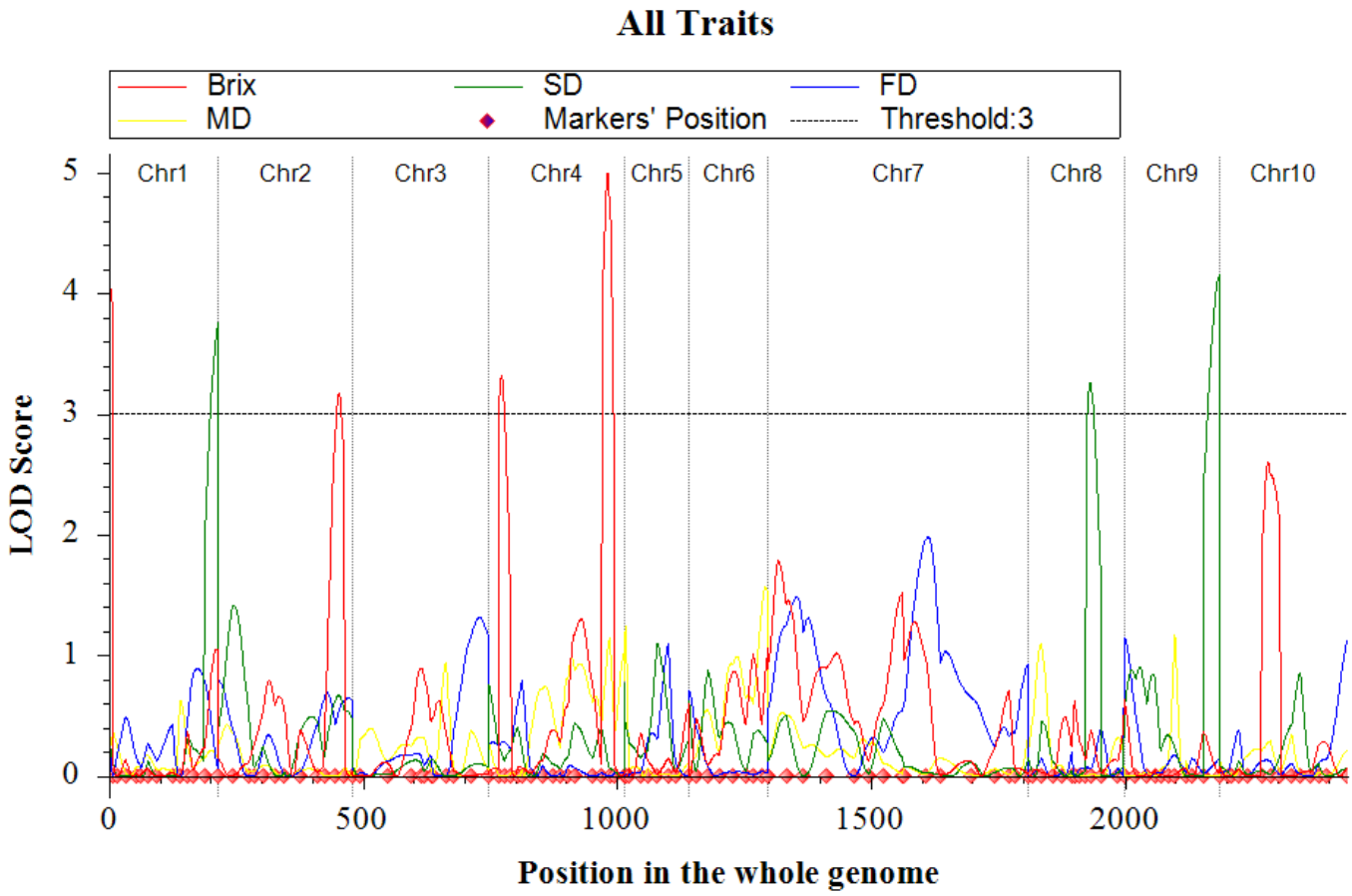

Figure 3

Detected quantitative trait loci for stem-diameter and stem brix content in sorghum at LOD threshold 3 (Combined-season)

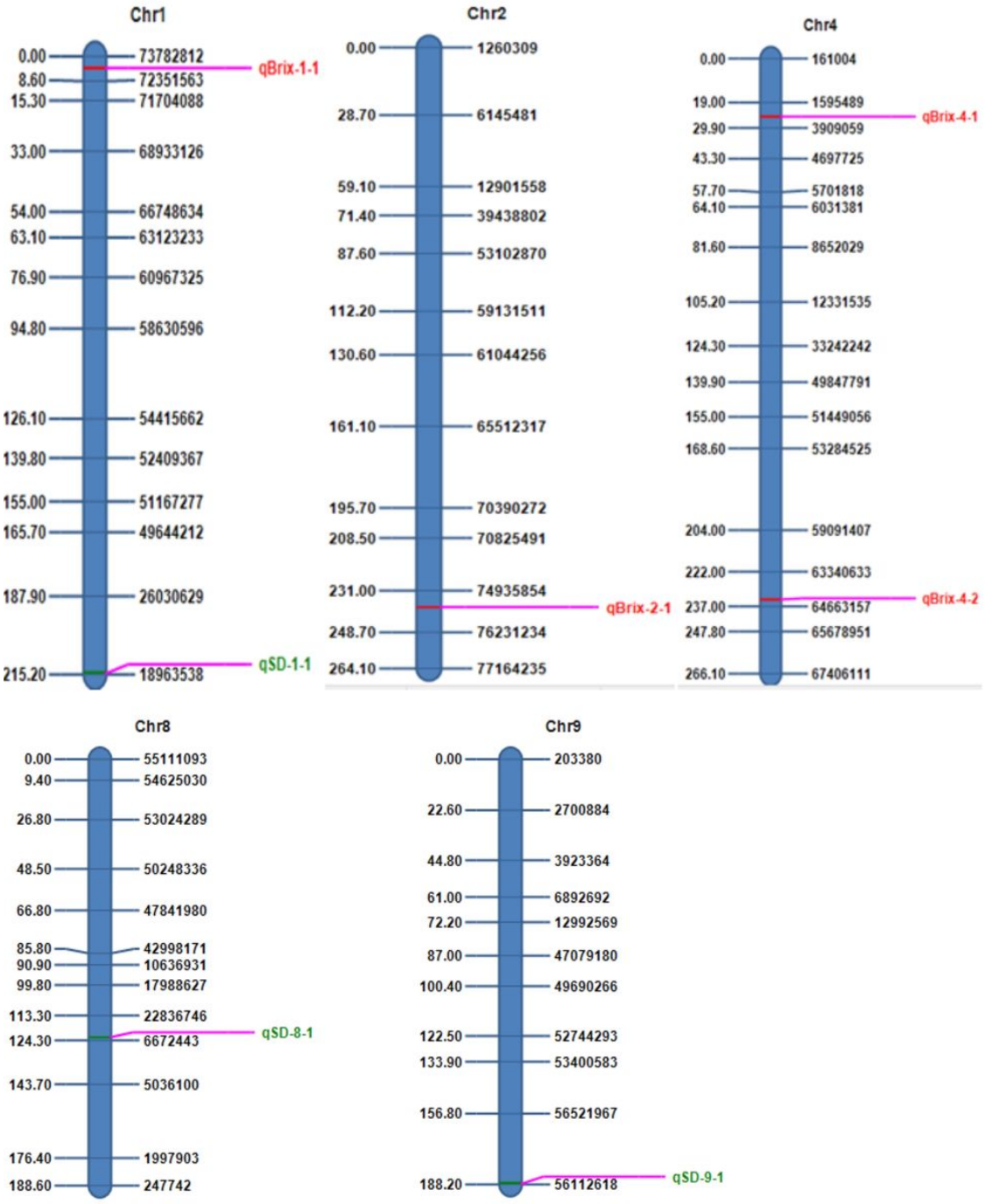

Figure 4

Significant QTL linked with stem brix content and stem diameter of 139 RILs and their parents cultivated under rain and off-season are shown on a genetic linkage map. The QTL is abbreviated as q=QTL, followed by the trait's abbreviation name: SD stands for stem diameter, and Brix stands for stem brix content.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- SupplementarydataQTL.docx