Depiction of Genomic Regions and Genes Related with Drought Tolerance in Sorghum [Sorghum bicolor (L.) Moench]

Habtamu Demelash a*

a Assosa Agricultural Research Center, Ethiopian Institute of Agricultural Research, P.O Box-265, Assosa, Ethiopia.

Author’s contribution
The sole author designed, analysed, interpreted and prepared the manuscript.

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ABSTRACT

The study of quantitative trait loci (QTLs) can bridge the gap between traditional breeding procedures and more efficient genetic improvements. The study of quantitative trait loci (QTLs) can bridge the gap between traditional breeding procedures and more efficient genetic improvements. In this report, we assess progress in mapping quantitative trait loci and genes associated with drought resistance in sorghum. Drought avoidance is linked to a number of morphological and physiological adaptations, including limiting water loss and increasing water absorption. The effects of physiological parameters will be investigated in order to find certain selection criteria that could be relevant in the development of drought-tolerant genotypes. Drought avoidance is linked to a number of morphological and physiological adaptation traits, including in grain sorghum, quantitative trait loci affecting green retention are an important feature for post blooming drought tolerance that have been investigated in various situations and with various genetic backgrounds. The two QTLs remain green (Stg2 and Stg4) of B35 x Tx7000 RILs were entirely matched in both populations, according to QTL analysis performed in the two mapping populations of recombinant inbred lines (RILs). Investigation done on different 44 sorghum lines confirmed that four QTL root nodal root angle discovered in the mapping population. Significant marker–trait association’s delignated within the quantitative chromosome (CI) for root angle (qRA2_5, qRA1_8 and qRA1_10) or closely allied to root angle (qRA1_5). Post-flowering drought response is expressed in sorghum when moisture stress occurs during grain development (GS-3). Three QTLs were detected for flowering time on chromosomes 2, 6, and 9, with log odds values (LOD) ranging from 2.5 to 3.3 and explained phenotypic variance (PVE) values calculated from 6 to 11%.

*Corresponding author: E-mail: habtedeme@gmail.com;
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1. INTRODUCTION

Sorghum grows in a wide range of environments, including different elevations, day lengths, rainfall, and temperatures. It is highly adaptable to the harsh conditions seen in tropical environments [1]. It is a cereal crop grown all over the world due to its unique properties such as drought endurance, water logging, saline, infertile soils, and high temperatures [2].

Drought, or a lack of water in the soil and/or atmosphere, has reduced potential production significantly [3-8]. Water is anticipated to become a limited commodity as a result of increased drought in many parts of the world and a growing population [9]. As a result, as global warming accelerates, the use of enhanced and well-adapted crops in moisture-deficient environments is becoming increasingly important for crop yield [10]. Water is required for plant growth and fulfills a variety of functions, including those of a solvent, a reactant, and a maintainer of cellular turgidity [11]. Water scarcity causes plants to slow cell growth, leaf and stem elongation, and photosynthesis, as well as reduce respiration and turgor, leading to wilting. Drought [11] can influence crop productivity at any stage of plant growth.

According to [12], plants have many physiological ways to cope with moisture stress during the cycles of their life cycle, including escape, avoidance, and tolerance strategies, which they may combine [10]. Plants use a variety of tactics to survive drought and finish their life cycle before they run out of water, and they show developmental plasticity [9]. Plants that are grown in arid and semi-arid agro-ecology intensify their rate of growth by performing high stomatal conductance to complete their life cycle within a short period of time [13]. Utilization of early maturing genotypes as well as date of planting crops was the important strategies crops to escape the drought condition during the development and growth [13]. The use of early maturing genotypes, as well as the date of planting, were essential tactics crops used to avoid drought throughout development and growth [13].

Drought avoidance refers to how plants deal with drought by using one of the known physiological processes to avoid tissue dehydration [9]. This process entails reducing water loss through transpiration while also enhancing water uptake by roots [9]. Excessive deposition of epicuticular wax on the aerial surface of crops, which reduces cuticular transpiration, and the presence of trichomes, which catch and store surface water, allowing foliar water uptake, can both help to reduce crop water loss [10]. Other drought avoidance mechanisms include leaf abscission, dormancy, and leaf rolling to reduce water loss from transpiration. In addition, plants that use C4 photosynthesis have less water loss from transpiration than C3 plants [14]. Furthermore, plants possessing deep, large root systems that can penetrate hard soil layers are often associated with the ability to maintain water supply during low water conditions as well as the ability of the root system to respond to water stress [14]. When plants exposed to water stress they often increased root/shoot ratios, and the root/shoot ratios have been used as a major criterion to identify drought resistance [10].

Drought tolerance is defined as a plant’s ability to maintain a specific level of physiological activity in the face of severe drought stress by regulating thousands of genes and a number of metabolic pathways to decrease or repair stress damage [13]. By lowering tissue water potential, plants use multiple metabolic processes, such as osmotic adjustment and high-level antioxidants, to assist plants develop drought tolerance mechanisms [15]. Both shoots and roots benefit from cytosol because it helps to lower osmotic potential and preserve turgor [15]. Other compounds that plants accumulate compatible solutes such as sugars and sugar alcohols (fructan, trehalose, mannitol, d-ononitol, and sorbitol), ammonium (polyamines, glycinebetaine, b-alanine betaine, dimethyl-sulfonio propionate, and choline-O-sulfate) and amino acids (proline and ectoine) which they store in the cytosol aids in lowering osmotic potential and maintaining the turgor of both shoots and roots [15].

Sorghum has a chromosomal number of $2n = 20$ and a haploid genome size of ca. 760 Mb, and it is closely related to maize with species belonging to the same Andropogoneae tribe. Its tiny genome size ranks second only to rice among the major Poaceae crops. Sorghum has a unique propensity for miRNA expansion, which is increased as the plant grows under dry conditions [16]. The sbi-MIR169 subfamily includes members of the plant nuclear factor Y Faily, which has been linked to Arabidopsis and...
maize developing high drought resistance. Sorghum has a lot of cytochrome P450 domain-holding genes, which are commonly implicated in foraging poisons including those produced in reaction to stress. In sorghum, 328 cytochrome P450 genes have been discovered, whereas rice contains 228 [17].

Physiological variables for leaf greenness (chlorophyll content and chlorophyll fluorescence) are said to be positively connected with grain yield in wheat under normal and drought conditions [18], and QTLs for grain yield in sorghum in combination with drought tolerance or yield components [19]. Plant biologists have had a difficult time understanding the genetic and molecular underpinnings of drought resistance. Stay green quantitative trait loci have been discovered in both sorghum [20] and maize [21]. In order to improve drought tolerance in sorghum and other grass species, researchers need to confirm the constancy of stay green QTLs across different genetic backgrounds.

Drought tolerance is an important target in many plant breeding programs. Due to discrepancies in test settings and interactions between plant growth phases and the environment, drought tolerance selection is difficult. Drought tolerance is a multi-gene trait that is controlled by moisture stress timing and severity. In this review, I discuss recent advancements in mapping quantitative trait loci connected to drought tolerance in sorghum.

2. DROUGHT RESPONSES IN SORGHUM

Drought avoidance and drought tolerance are the two primary groups to which plants have adapted and are resistant to drought [22]. Drought avoidance aids plants avoid drought by lowering water status in tissues by maintaining cell turgor and cell volume while enhancing water intake either by enlarging the root system or by reducing water loss from transpiration and other non-stomatal channels such as the plant cuticle[22].

Plants maintain their metabolism to continue to function even when there is a lack of water. Drought tolerance is influenced by two characters: osmotic adjustment and antioxidant capacity: osmotic adjustment occurs when compatible solutes within cells rise, lowering the osmotic potential and assisting in the maintenance of plant turgor in both shoots and roots [23]. When cells are dehydrated, well-suited solutes are often kept in the cytosol to preserve cell water content despite the decrease in apoplastic water potential. Plant species and genera have varied suitable solutes, such as sugars, organic acids, amino acids, sugar alcohols, or ions [23].

3. THE SORGHUM BICOLOR GENOME

Sorghum and maize shared a common ancestor around 12 million years ago (Myr), when polyploidization and repetitive DNA propagation contributed considerable genome complexity to maize. The sorghum genome is estimated to be roughly 730 megabases, 60 percent larger than rice but only 14 percent of maize [24]. Sugarcane, on the other hand, is more closely related to sorghum phylogenetically (approximately 5 Myr of divergence) and has a genome larger than maize with 4-fold redundancy of most genes [25]. Sorghum has a tiny diploid genome and low levels of gene duplication. The genome of Sorghum bicolor was recently sequenced, adding to our understanding of grass genome evolution [26], and the gene order and density are similar to that of grass genomes, the gene order and density are similar to those of rice. Retrotransposon accumulation explains the ~75% larger genome size of sorghum compared with rice total, DNA transposons constitute 7.5% of the sorghum genome, between maize (2.7%) and rice (13.7%) among 34,496 sorghum gene models, 27,460 bona fide protein-coding genes have been found [24].

Sorghum is similar to Arabidopsis and rice in terms of size, number of genes, and gene families. Though gene and repetitive DNA distributions have remained relatively constant since palaeopolyploidization 70 million years ago, several of the most duplicated gene sets lost one member before the sorghum–rice split [27]. One duplicated chromosomal section performs as if it is only a few million years old [26]. Nearly 24% of genes are grass-specific, 7% are sorghum-specific, recent genes, and micro RNA duplications may explain for sorghum's drought tolerance.

4. TRAITS PROVIDING TOLERANCE TO DROUGHT

One of the most significant areas in plant science is understanding water stress responses at a physiological/molecular level [10]. Studying the effects of physiological factors will aid in the development of drought-tolerant genotypes by
establishing some selection criteria. Several investigations have been conducted to identify physiological indicators linked to drought tolerance [28]. A review of the literature revealed that morpho-physiological traits such as leaf area [29], root dry matter [30], and whole-plant transpiration rate [18] had been widely used as selection parameters for screening of water stress tolerant crop plants, and that genomics and molecular biology had been used to elucidate the mechanisms of drought response of several agronomically important plant species.

5. STAY-GREEN TRAIT IN SORGHUM

The term 'stay green' has been used to characterize the drought tolerance response of sorghum after flowering [31]. Stay-green is a physiological process that causes foliar senescence to be delayed or rendered ineffective [31]. Stay-green has been studied extensively in several crops, including sorghum [32,33] and wheat [34]. The expression of stay-green in sorghum under normal and stress conditions is a complex physiological process, and stay-green genotypes maintain transpiration under stress conditions, which is beneficial if sufficient water reserves are available at the end of the crop cycle; otherwise, it will cause severe stress [31].

Despite being a perennial plant, sorghum will perish as a result of drought stress during grain loading [35]. Stay green sorghum plants can withstand post-flowering drought stress, delaying leaf and plant death [31]. Drought tolerance was developed as a result of the persistence of green stems and top leaves when water was scarce during grain filling. When crop growth is favorable prior to flowering, followed by significant moisture stress, particularly during the grain-filling stage, post-flowering symptoms become more obvious [31].

Sorghum genotypes with a high level of stay green continue to fill their grain normally under drought conditions and have higher resistance to charcoal rot and lodging [36, 37]. Because grain output and lodging are so closely linked, the stay green trait should provide a significant direct advantage to sorghum growers by minimizing moisture stress-type lodging, which causes premature leaf and stalk death. In automated agriculture, such as in the United States, lodging frequently results in full grain loss from lodged plants. Stay-green genotypes showed greater harvest index and grain production than non-stay-green lines, according to research published in [38].

Stay green genotypes also have higher levels of cytokinins [39] and basal stem sugars [40] than senescent genotypes. Increased soluble sugar accumulation in stay green types was linked to a larger functional leaf area during grain filling, reducing their reliance on stored assimilates from the stem [39]. Stay green is an important characteristic for both grain and fodder production in dual-purpose sorghums because a higher concentration of stem sugars boosts the digestible energy content of the Stover [41].

6. MAPPING QTLS ASSOCIATED WITH THE STAY-GREEN TRAIT IN SORGHUM

Stay green is an important post-flowering drought tolerance feature in grain sorghum [31], with QTLs influencing it across diverse environmental conditions and genetic backgrounds [31]. The QTL areas or markers that show strong epistatic interaction in the expression of the stay green trait have been found. In sorghum, stay green may be controlled and is highly reliant on grain yield [42]. Drought responses have been investigated in particular, and heritable traits that may be transferred by traditional breeding procedures have been identified. The stay green trait appears to be dominant in F1 hybrids in certain lines (B35), but recessive in others (R9188) [35]. In addition, trials utilizing the cross combination B35 (stay green inbred line) x Tx7000 (non-stay green inbred line) revealed that significant genes for this feature were dominant [35].

The study of QTL analysis the two RIL mapping populations (Fig.1) shown that two QLLs are completely consistent between both populations. Although these findings observed QTLs of Stg2 and Stg4 obtained from RIL population of B35 x Tx7000 Stg A and Stg J respectively. The highest percentage of phenotypic variation were shown on both population stg2.there is also Stg3 of the B35 x Tx7000 population was close to the Stg D2 of [43]. Even though, QTL analysis using interval mapping did not identify Stg1 in the B35 x Tx430 with in population, single-marker analysis shown that markers linking this QTL in the B35 x Tx7000 population were highly associated with the stay green scores in the B35 x Tx430 population. Tx430 donates favorable alleles for the stay green trait at two QTL regions, Stg B and Stgl.1. The two QTLs Stg G and Stgl.2 were not aligned in the B35 x Tx7000 population.
Table 1. Quantitative trait loci for stay-green rating and chlorophyll content under post-flowering drought stress in sorghum RILs of the cross B35 x Tx7000

<table>
<thead>
<tr>
<th>Trait and location</th>
<th>Flanking markers</th>
<th>Linkage groups</th>
<th>Interval length</th>
<th>QTL position</th>
<th>Additive effects</th>
<th>Peak LOD score</th>
<th>% explained</th>
<th>Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>SG97DLL</td>
<td>RZ323-A12RFLP</td>
<td>A</td>
<td>2.2</td>
<td>2</td>
<td>0.0838</td>
<td>2.65</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td></td>
<td>UMC5-UMC116</td>
<td>D</td>
<td>5.5</td>
<td>2</td>
<td>0.0728</td>
<td>1.9</td>
<td>10.7</td>
<td></td>
</tr>
<tr>
<td></td>
<td>UMC85-TXS644</td>
<td>E</td>
<td>7.2</td>
<td>4</td>
<td>0.0821</td>
<td>2.22</td>
<td>13.6</td>
<td></td>
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<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>6.48</td>
<td>32.6</td>
<td></td>
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<tr>
<td>SG98HW</td>
<td>NPI414-BNL15.20</td>
<td>A</td>
<td>4.4</td>
<td>2</td>
<td>0.0205</td>
<td>3.18</td>
<td>15.4</td>
<td></td>
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<tr>
<td></td>
<td>WG889-TXS584</td>
<td>A</td>
<td>12.8</td>
<td>6</td>
<td>0.2677</td>
<td>3.66</td>
<td>19.9</td>
<td></td>
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<tr>
<td></td>
<td>BNL15.40-PSB605</td>
<td>D</td>
<td>7.2</td>
<td>0</td>
<td>0.185</td>
<td>1.91</td>
<td>9.1</td>
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<tr>
<td><strong>Total</strong></td>
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<td></td>
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<td></td>
<td></td>
<td>6.86</td>
<td>30.1</td>
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<tr>
<td>SG3478</td>
<td>NPI414-BNL15.20</td>
<td>A</td>
<td>4.4</td>
<td>3.2</td>
<td>0.0205</td>
<td>3.61</td>
<td>18.1</td>
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<td></td>
<td>WG889-TXS584</td>
<td>A</td>
<td>12.8</td>
<td>5.5</td>
<td>0.0703</td>
<td>5.52</td>
<td>29.2</td>
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<tr>
<td></td>
<td>TXS1307-UMC5</td>
<td>D</td>
<td>0.7</td>
<td>0</td>
<td>0.0573</td>
<td>3.49</td>
<td>17.5</td>
<td></td>
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<tr>
<td></td>
<td>Txes387-CSU166C</td>
<td>J</td>
<td>14.8</td>
<td>0.3</td>
<td>0.0305</td>
<td>1.81</td>
<td>9.4</td>
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<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>53.5</td>
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<td></td>
</tr>
<tr>
<td>CHL34</td>
<td>CSU143-dhn6</td>
<td>A</td>
<td>7.1</td>
<td>5.9</td>
<td>-2.0755</td>
<td>3.67</td>
<td>16.9</td>
<td></td>
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<tr>
<td></td>
<td>WG889-TXS584</td>
<td>A</td>
<td>12.8</td>
<td>2.3</td>
<td>-5.2845</td>
<td>5.44</td>
<td>22.6</td>
<td></td>
</tr>
<tr>
<td></td>
<td>TXS1307-UMC5</td>
<td>D</td>
<td>0.7</td>
<td>0.7</td>
<td>-4.4913</td>
<td>2.8</td>
<td>12.4</td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
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<td></td>
<td></td>
<td></td>
<td>8.56</td>
<td>34.6</td>
<td></td>
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</tbody>
</table>


Table 2. Single marker analysis summary (p values) for the level of association between markers in the four nodal root angle QTL regions and grain yield in subsets of the RIL population in three different hybrid combinations

<table>
<thead>
<tr>
<th>Trait</th>
<th>QTL</th>
<th>Chr</th>
<th>Peak position</th>
<th>Confidence interval</th>
<th>QTL start</th>
<th>QTL end</th>
<th>LOD</th>
<th>PVE</th>
<th>Additive effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Flowering Time</td>
<td>qFT2.1</td>
<td>2</td>
<td>96.8</td>
<td>91.3–103.9</td>
<td>S2_63084956</td>
<td>S2_62976360</td>
<td>3.1</td>
<td>6</td>
<td>-0.51</td>
</tr>
<tr>
<td></td>
<td>qFT6.1</td>
<td>6</td>
<td>49.6</td>
<td>43.7–76.3</td>
<td>S6_1402697</td>
<td>S6_40763291</td>
<td>2.5</td>
<td>11</td>
<td>0.27</td>
</tr>
<tr>
<td></td>
<td>qFT9.1</td>
<td>9</td>
<td>94.8</td>
<td>91.5–104.5</td>
<td>S9_7580762</td>
<td>S9_4719436</td>
<td>3.1</td>
<td>6</td>
<td>0.81</td>
</tr>
</tbody>
</table>

NS not significant; *P>0.1; **P<0.1; ***P<0.01
In general, the complete analysis demonstrates that all of the significant QTLs of the B35 x Tx7000 population are consistent with those of the B35 x Tx430 population (Fig. 1). The Stg2 QTL, which was consistently recognized in two genetic backgrounds and in all of the environments tested, was found to be the most relevant QTL and should be the subject of further investigation. Furthermore, this research marks the beginning of a phase in which this Stg2 QTL region will be targeted for the discovery of genes that control remain green [31]. The QTL analysis was started using pooled mean data on remain green rating over seven environments, and the map of the B35 x Tx7000 population [20] was enlarged by the addition of 91 additional markers. In the B35 x Tx430 population, the information on remain green QTLs came from [43], while in the B35 x Tx7078 population, it came from [44]. In the B35 x Tx7000 and B35 x Tx7078 populations, a partial linkage map was found in linkage groups A and B, respectively. The dotted lines indicate the location of the QTL in different populations. Stay green QTL terminology, such as Stg1, Stg2, Stg3, and Stg4, was adopted from [20].

7. ROOT-ANGLE TRAIT IN SORGHUM

The ability of a plant to approach soil water is determined by its root system, and its structure can influence adaptation to water-stressed situations [1]. Because of the nature of the root system of the plant under crucial crop adaptation, plants can determine how much water is used in the soil [10]. This is especially important for species like sorghum (Sorghum bicolor L. Moench.) and maize (Zea mays L.), which have evolved to thrive in such conditions. Increased roots and water taking out at a distance have been linked to improved drought adaption in both sorghum [45] and wheat [46,47], on the other hand, demonstrated the precise nature of drought adaptation provided by deep rooting, pointing out that increased root length density at depth was especially advantageous in upland rice, but offered little advantage in on season lowland rice where, subsoil restraints can limit rooting depth. The capacity of a crop to receive water can be determined by the nodal root angle on the spatial delivery of the root system of a plant that is towards the end of its life cycle. Plants acclimated to drought stress are severely hampered in terms of grain output, with each additional mm of water available during grain filling increasing grain yield by 50–60 kg ha⁻¹ in wheat [48] and 30 kg ha⁻¹ in sorghum [49]. By managing the environment variables that are favourable to more vertical root systems, such as high plant densities and locations with deep soils in maize [50], nodal root angle might influence root system dissemination, and hence could have a crucial effect on drought adaptation. In disparity, a wide nodal root angle could adequately influence to access soil water in controlling conditions where, a more horizontal root system would be advantageous to extract water from inter-row spaces [49].

8. MAPPING QTLS ASSOCIATED WITH THE ROOT-ANGLE TRAIT IN SORGHUM

The association-mapping study [33] indicated that the four QTL for nodal root angle discovered in the mapping population were validated using a set of 44 different lines. All four nodal root angle QTL had significant marker—trait relationships, either within the CI (for qRA2 5, qRA1 8, and qRA1 10) or closely connected to (qRA1 5). The potential for extra genomic areas to be elaborated in the genetic control of this characteristic was also specified by the association mapping analysis. However, because of the limited sample size, the extra six significant marker—trait relationships discovered in the association mapping analysis should be treated with care [33]. Three of the four nodal root angle QTL found in the mapping population had similarity with previously discovered root angle Root angle in rice and maize, as characterized through basic local alignment sequencing tool (BLAST) analysis 50, of flanking markers. This homology with previously identified QTL for root angle in diverse species additional supports the findings of the current study.

[33] found two significant QTL for nodal root angle, both of which were found on SBI-05, with qRA2 5 being highly significant (LOD of 4.96) and qRA1 5 being significant (LOD of 3.69). On SBI-08 and SBI-10, two suggestive QTL were also noted. For nodal root angle, the four QTL explained 58.2 percent of the phenotypic variance. Only the first QTL (qRA1 5) had a positive additive effect (Table 2); indicating that its alleles came from the narrow angled parent B923296. The negative additive effects of the other three nodal root angle QTL (qRA2 5, qRA1 8, and qRA1 10), on the other hand, revealed that their alleles were derived from the SC170-6-8 wide angled parent. From the data, (Lopez et al. 2017b) identified seven QTLs across multiple contexts. Only 2.6 percent of the variation in root
angle was explained by a QTL on chromosome three (qRA3;). Contrary to popular belief, overlapping QTLs on chromosome 6 (qDM6 and qLN6) explained 25.69 and 57.74 percent of the observed phenotypic variation in days to maturity and leaf number, respectively [51].

The goal of [32]'s study was to uncover a probable link between grain yield and nodal root angle for a subset of the RIL population, using a hybrid combination of three different tester lines to conduct SMA. In the mapping population employed in the study, markers within variance in yield performance were found in general [33]. The single market study revealed that there were significant connections between grain yield and three of the four nodal root angle QTL when considering a putative link between grain yield and nodal root angle. Correlation has recently been discovered in maize [30] between a significant QTL that influences root characteristics and leaf ABA concentrations, root-ABA1, and grain yield and other agronomic variables, which the authors think is likely due to pleiotropy. Three of the four nodal root angle QTL were significantly linked with grain yield (Table 2) across two hybrid combinations.

In hybrid combination (with the tester R995248), markers within qRA1 5 were substantially (P < 0.05) related with grain yield, and suggestive (P = 0.0696) in a second hybrid combination (with the tester R986087-2-4-1). The direction of the effect in both cases revealed that the presence of the narrow root angle allele of the qRA1 5 QTL improved yield. In hybrid combinations with two tester genotypes (R995248 and R986087), markers within qRA1 10 were substantially (P < 0.05) linked with grain yield [33], while the same hybrid combinations showed suggestive relationships with grain yield for markers within qRA1 8.

Fig. 1. Sorghum linkage groups exhibiting the consistency of remain green QTLs in RIL populations B35 x Tx7000, B35 x Tx430, and B35 x Tx7078
9. FLOWERING TRAIT IN SORGHUM

Flowering period is an adaptation feature that impacts the extent of a crop's spread under various climatic circumstances, as well as its reproductive success and breeding methodology[52]. Grain sorghum is a photoperiod-sensitive plant that was initially a short-day plant [53]. Sorghum contains several maturity loci (Ma1 through Ma6) that are linked to flowering timing and maturity [53]. Under extended day circumstances, Ma1 and Ma6 operate as a repressor of flowering. 54. PRR37, a pseudo-response regulator protein, is encoded by Ma1 [54]. The photoperiod sensitivity of the plant is determined by Ma2, Ma4, and Ma5 (Quinby 1974). Ma3 is responsible for the production of Phytochrome B, a photoperiod-sensing light receptor that regulates maturity[53]. Ma5 and Ma6 are large-effect maturity loci [55].

10. PRE-FLOWERING DROUGHT RESISTANCE

Diverse sorghum lines with distinct phenotypic responses to both pre-flowering and post-flowering drought conditions were investigated, and better bases of for each type of stress were discovered. Crops grown before to flowering, particularly those at the stage of panicle differentiation to flowering (GS-2), described the pre-flowering response under severe moisture stress. The panicle size, grain number, and grain yield are all affected by this type of stress. Six genomic areas related with pre-flowering drought tolerance, as well as eight additional regions generally linked with yield or yield components in fully watered conditions, were identified by [56].

Using a SC56 Tx7000 hybrid in sorghum, four significant QTLs responsible for preflowering drought were also discovered in linkage groups C, E, and F [57].

11. POST-FLOWERING DROUGHT RESISTANCE

When moisture stress occurs during the grain development stage in sorghum, the plant responds with a post-flowering drought response (GS-3). When water is scarce during the grain-filling period, rapid premature leaf death is common. Premature leaf senescence results in
charcoal rot, stem lodging, and a considerable reduction in production. Drought stress increases senescence in many plant species by driving several physiological processes in the same direction as natural senescence [58]. Chlorophyll loss and a progressive decline in photosynthetic capacity generally characterize senescence. Senescence impacts absorption and grain filling in agricultural plants at an early stage. More than 80% of commercial sorghum hybrids in the United States are grown without irrigation, and while most exhibit pre-flowering drought tolerance, many do not have strong post-flowering drought resistance.

Variations in plant physiological parameters, particularly carbon and water exchange, have been linked to pre-flowering or post-flowering tolerance to water stress in sorghum, yielding a number of genes or cDNA clones that are genuinely implicated in drought resistance [32]. The majority of these genes are involved in either plant water regulation or photosynthetic processes.

Three QTLs affecting flowering time were discovered in chromosomes 2, 6, and 9, with LOD scores ranging from 2.5 to 3.3 and PVE values ranging from 6 to 11 percent, according to [42]. (Tables 3 and Fig.4). QTL was found on chromosome 2 in both normal and stressful settings, with a peak location of roughly 100 cM [42]. The QTL in chromosome 2 was discovered with a PVE of 10% in 2008, while the QTL in chromosome 6 was discovered with a PVE of 11 percent in 2009.

Flowering time QTLs were discovered in chromosome 6 using a variety of approaches, including year-by-year analysis, grouped analysis of six environments, and distinct environment analysis. In a combined examination of the data, the QTL in chromosome 9 was discovered. In a combined analysis of data from six normal environments, three environments in 2009, and the Ottawa environment in 2008, was detected [42].

In the current study, flowering time QTLs were found on chromosomes 2, 6, and 9 in RIL testcrosses. Flowering time QTLs (qFT6.1) were discovered in chromosome 6 between 43.7 and 76.3 cM (Chr6: 1,402,697 to 40,763,291), and individual environment analysis revealed flowering time QTLs in the same region. Flowering time locus Ma1 was discovered in chromosome 6 [59] in previous studies. Under long day circumstances, Ma1 is a flowering time repressor gene [54]. The physical position Chr6: 40,265,943 to 40,266,766 was determined using a BLAST search of the PRR37 (Ma1) gene sequence from NCBI on the phytozome sorghum browser. In sorghum, the Ma6 maturity locus is also found on chromosome 6 [42]. Another flowering time locus, Ma5, was discovered in chromosome 2 between 91.3 and 103.9 cM (Chr6: 63,084,956 to 62,976,360) under normal and drought conditions. Previous research have

![Fig. 3. Post-flowering drought](image-url)
Table 3. QTLs detected for traits of 188 RIL testcrosses grown under six normal environments in 2008 and 2009. Least square means from six environments were used, LOD is the logarithm of odds, and PVE is the phenotypic variation explained by QTLs

<table>
<thead>
<tr>
<th>QTL</th>
<th>LG</th>
<th>RIL/hybrid combinations</th>
<th>LOD</th>
<th>PVE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>R995248</td>
<td>R986087</td>
<td>R986087</td>
</tr>
<tr>
<td>qRA1_5</td>
<td>SBI-05-II</td>
<td>0.0228*</td>
<td>NS</td>
<td>0.0696*</td>
</tr>
<tr>
<td>qRA2_5</td>
<td>SBI-05-III</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
</tr>
<tr>
<td>qRA1_8</td>
<td>SBI-08-II</td>
<td>0.0602*</td>
<td>0.0780?</td>
<td>NS</td>
</tr>
<tr>
<td>qRA1_10</td>
<td>SBI-10</td>
<td>0.0087**</td>
<td>0.0415?</td>
<td>NS</td>
</tr>
</tbody>
</table>

Additive effect: positive values indicate contribution by Tx436 and negative values by 00MN7645; ‡ CovFT, flowering time added as a covariate in analysis; § QTL detected consistently in 2008, 2009, and 201

Fig. 4. QTLs detected from a combined analysis of data collected on 188 RIL testcrosses grown under six normal environments in 2008 and 2009: B flowering time

discovered flowering time locus Ma5 in chromosome 2 between 91.3 and 103.9 cM (Chr6: 63,084,956 to 62,976,360). (Kim 2003). Several other research have revealed blooming time QTLs on chromosome 9 [59], and earlier studies have also reported QTLs for plant height on chromosome 9, which are generally associated features [3].

12. CONCLUSION

In a water-stressed sorghum environment, mapping QTL associations is critical for finding genomic areas linked to days to flowering, root angle, and stay green. In water-scarce situations, understanding the genetic basis of these morphological and physiological features is critical for crop improvement. Understanding the interplay of these QTL with other loci and the environment would require molecular approaches that identify plants with numerous favorable alleles for a certain environment.

NOTE

The review of this paper complies with the current laws of Ethiopia

COMPETING INTERESTS

Author has declared that no competing interests exist.

REFERENCES


41. Van Oosterom E, Whitaker M, Weltzien E. Integrating genotype by environment interaction analysis, characterization of drought patterns, and farmer preferences to identify adaptive plant traits for pearl millet; 1996.


