Beni-Suef University Journal of Basic and Applied Sciences

RESEARCH

Open Access

Identification and mapping of QTL associated with some traits related for drought tolerance in wheat using SSR markers

Khaled Adly Mohamed Khaled[1*], Rehab Mohamed Mohamed Habiba[2], Jamila Abdelhafeeth Bashasha[3] and Mohamed Hassan Abd El-Aziz[2]

Abstract

Background: Wheat is the most important crop around the world. Drought stresses affect wheat production and their characterization. Most of the traits that are affected by drought are quantitative traits, so detection of the quantitative trait's loci (QTLs) related to these traits is very important for breeder and wheat producers. In this trend, 285 F2 individuals from crosses between four bread wheat genotypes (*Triticum aestivum* L.), i.e., Sakha93, Sids1, Sakha94, and Gemmiza9, were used for identified QTLs associated with plant height (PH) and leaf wilting (LW). Single marker analysis and composite interval mapping (CIM) were used.

Results: A total of 116 QTLs loci were detected which covered 19 chromosomes out of the 21 chromosomes of wheat. PH and LW had 74 and 42 QTLs loci, respectively. On the other hand, chromosome 7A showed to bear the highest number of QTLs loci (15 loci). While chromosome 1A beard the highest number of QTLs loci related to PH (10 loci), chromosome 2B and 7A beard the highest number of QTLs related LW. We highly recommend our finding to help breeders in wheat breeding programs to improve plant height and leaf wilting.

Conclusion: Our investigation concluded that SSR markers have high efficiency in the identification of QTLs related to abiotic stress; also the CIM method had more advanced priority for QTLs mapping.

Keywords: Wheat, QTLs, Mapping, Composite interval mapping (CIM), Plant height, Leaf wilting, Simple sequence repeats, SSR

1 Background

Wheat is the most important crop that contributes to nutritional and food security around the world. Wheat is one of the strategic crops in Egypt, and the wheat breeding program to produce superior varieties is one of the important breeding programs that many researchers are concerned with. Despite this importance, there is relatively little research in the field of identifying QTLs responsible for some yield-related traits, especially by using the Molecular markers technique. Therefore, this research is an important step to identify the QTLs associated with some drought-affected traits in order to contribute to the development of drought-tolerant wheat cultivars. Although many QTLs related to plant height (PH) were detected in wheat, no QTL related to wilting was detected. On the other hand, abiotic stresses (drought, cold, heat, and salt) affected wheat productivity, while drought stress affects about 1 billion hectares of global agricultural soil including sodic and saline soils [1].

Among the environmental stresses, drought is the important one that affects the development and growth of crops. Drought still to be a major challenge to researchers and breeders. Factors that affect responses of plants to drought stress include genotype, stage of

*Correspondence: Khaled.adly@agr.bsu.edu.eg
[1] Faculty of Agriculture, Beni-Suef University, New Beni Suef City, Beni Suef Governorate, Egypt
Full list of author information is available at the end of the article

growth, duration and stress severity, physiological process of growth, different genes expression patterns, the different activity of respiration patterns and photosynthesis activity, and environmental factors [2–5]. A drought had effects on genes expression, so various responsive genes related to drought were featured [6]. Gene's role could be featured by gene expression to high levels of resistance between varieties (Ouvard et al., 1995). Drought influence plants in levels of protein, production of antioxidant, osmotic adjustment, the composition of the hormone, depth and extension of the root, stomata closing and opening, photosynthesis inhibition, chlorophyll decreasing content, transpiration reduction, and growth inhibition [7–10]. Drought can also cause pollen sterility, loss in grain yield, and abscisic acid accumulation [11].

Recent techniques like molecular methods must be appropriate useful identification tools for some clonal variation, stress tolerance, and genetic stability establishment [12–16].

The main goal of quantitative trait loci (QTL) analysis is to answer the question of whether phenotypic differences are depending on a few loci with quite large effects, or to many loci, each with midget effects. Remington and Purugganan [17] said, "It appears that a substantial proportion of the phenotypic variation in many quantitative traits can be explained with few loci of large effect, with the remainder due to numerous loci of small effect" [17–19].

QTLs can be categorized to constitutive QTL, that detected with most environments (their effects are stable across environmental conditions); and adaptive QTL, that detected with specific conditions of the environment (expression increasing with a level of environmental factor) like QTL that increases drought tolerance [20]. The sensitivity to environmental stress could be explained due to the regulations response (e.g., transcription) of the QTL gene to hint of environment. Meanwhile, response differences may cause by an indirect effect (e.g., larger root systems genotypes will be less affected by water or nutrient deficit, so genes controlling root development may underpin QTLs defined by stomatal conductance, or biomass accumulation). On the other hand, QTLs that caused an alteration in flowering time often affect yield against water or nutrient deficit because the duration of the crop life cycle affects the timing and intensity of the stress experienced by the plants [21]

Many QTLs and molecular markers are related to genes responsible for drought tolerance or sensitivity [22]. Advances in genomic and molecular technologies develop molecular markers which could be useful for QTLs identification. DNA markers based on the polymerase chain reaction (PCR) were the most notable ones among markers that used in studying the genetic characterization of wheat, sequence tagged microsatellite sites (STMSs) and/or simple sequence repeats (SSRs) [23], amplified fragment length polymorphisms (AFLP) [15], and chloroplast simple sequence repeats (cpSSR) [24]. SSR markers had an advantage in wheat molecular studies because it has a co-dominant type of inheritance, a large number of genomes, reproducibility, locus specificity, and high informational content. Moreover, their high polymorphism ratio, chromosome specificity, multiallelic nature, and wide distribution throughout the wheat genome are observed [25, 26].

SSR markers used to identify QTLs related to yield traits such as harvest index and thousand-grain weight [27], to study D genome-based genetic diversity in terms of drought tolerance [28], to study the physiological and genetic characterization wheat genotypes against the drought and temperature tolerance [29], and to detect the quantitative trait loci (QTL) for various traits [30, 31]. The aim of our investigation is to construct QTLs mapping for some traits related to drought tolerance in wheat.

2 Methods

2.1 Wheat materials

A total of 285 F2 individuals from crosses between four bread wheat genotypes (*Triticum aestivum* L.), i.e., Sakha93, Sids1, Sakha94, and Gemmiza9, were used for QTL analysis of four traits related to drought tolerance. The parents were chosen from a previous study [32], as representing a wide range of diversity for several agronomic characters. The parents were supplied by Field Crops Research Institute, Agricultural Research Center, Giza, Egypt. Table 1 presents the Parent's name, pedigree, and drought stress.

Table 1 Names, pedigree, and drought stress response of the parental genotypes used in the study according to previous findings from the maize breeding program in Egypt

No	Genotype	Cross name and pedigree	Drought stress response
1	Sakha93	Sakha 92/TR810328 S.8871-1S-2S-1S-0S	Tolerant
2	Sids1	HD2172/ Pavon "S"//1158.57/ Maya74 "S" Sd 46-4Sd-2Sd-1Sd-0Sd	Tolerant
3	Sakha94	Opata / Rayon // Kauz CMBW90Y3180-0TOPM-3Y-010M-010M -010Y-10M-015Y-0Y-0AP-0S	Sensitive
4	Gemmiza9	Ald"S"/Huac//Cmh74A.630/Sx CGM4583-5GM-1GM-0GM	Sensitive

2.2 Field experiment and drought tolerance assessment

The four parental wheat varieties were sown at the Experimental Farm of Genetics Department, Faculty of Agriculture, Mansura University (31.0449° N, 31.3537° E). Then, these varieties were crossed to produce possible crosses, i.e., Cross 1 (H1) = (Sakha93 × Gemmiza9), Cross 2 (H2) = (Sakha94 × Gemmiza9) , and Cross 3 (H3) = (Sakha93 × Sids1) according to Habiba et al. [32]. F2 and their parents were evaluated for drought tolerance at two drought treatments. They were sown in pots (25 cm.) containing sand and clay (2:1 v/v). Irrigation was given as normal irrigation for control and one irrigation 45 days after planting irrigation, i.e., two irrigations were given through the whole season for drought treatment. Pots were fertilized with P_2O_5, in one dose during soil preparing and Nitrogen was added by ammonia injection in one dose after soil preparing and before 4 days from planting. The trial was arranged in randomized complete blocks design with three replications. The experiment was conducted with 13/11 day/night photoperiod, 20/15 °C day/night temperature, and relative humidity of about 85%. Data were recorded on plant height (PH in cm) and leaf wilting (LW = per day to wilting).

2.3 DNA extraction and SSR markers amplification

DNA extracted from green leaves from each genotype was collected from ten-day seedlings germinated from seeds of each genotype according to Khaled and Esh [33] and Khaled et al. [16]. A set of 143 SSRs from the Wheat database (BARC, CFA, CFD, GWM, WMC, WMSX, BARC, XGWM, XPSP, and XWMC) and new 52 SSRs from the Cotton database (JESPR) involve the 21 chromosomes of wheat (References). Out of the 530 SSR primers, 195 (143 of wheat primers and 52 of cotton primers) have polymorphism to distinguish the genotypes and are used for mapping. Amplification was performed as follows,94 °C for 1 min (one cycle); 94 °C for 20 s, 50–55 °C for 35 s, 72 °C for 45 s (35 cycles), and final extension at 72 °C for 45 s (one cycle). Then hold at 4 °C (infinite). The PCR products were conducted to electrophoresis at 90 V, in 2% agarose gel containing 0.5 µg/ml ethidium bromide for approximately 2 h, using 0.5 × TBE buffer, along with a DNA ladder. The gel was visualized under UV.

2.4 Linkage map and QTLs analysis

Single marker analysis (SMA) and composite interval mapping (CIM) were used to localize the QTL associated with drought tolerance in wheat using 285 plants of an F2 population derived from crosses between four bread wheat genotypes using QTL IciMapping v4.2.5.3 software [34] depending on Kosambi mapping function. The logarithm of odds (LOD) threshold of higher than 3 was used. Segregation ratios of the genotypes classes at each locus were tested using the chi-square test ($p < 0.01$). The linkage mapping was compared with previous maps. The QTL analysis was also performed using IciMapping v4.2.5.3 software by combined analysis of adjusted means of the phenotypic trait value and genotyping data via inclusive composite interval mapping (ICIM) algorithm for additive gene effect with function inbuilt in the software. The walking speed chosen for all QTLs was 1 cM and the LOD threshold was calculated by 1000 permutation and $p = 0.05$.

2.5 Statistical analysis

The collected data were subjected to analysis of variance of the split-plot design and significant differences were estimated according to Bernardo [35]. The analyses of variance (ANOVA) were calculated using SPSS v25 and MS-Excel v365. Values of means, standard deviation, correlation coefficients, and plots showing the distribution of phenotypic data for different traits were determined using SPSS v25 and MS-Excel365. QTLs map was constructed using QTL IciMapping v4.2.5.3 software [34]

3 Results

3.1 Phenotypic evaluation

The phenotypic variations between parents and their hybrids (i.e., Sakha93 (S93), Sids1(Sids), Sakha94 (S94), Gemmiza9 (G9), H1, H2, and H3) were evaluated for plant height (PH) and leaf wilting (LW). Mean, standard error, standard deviation, and coefficient of variance (CV %) are presented in Table 2. Analysis of variance and correlation are presented in Table 3.

Data presented in Table 2 and Fig. 1 illustrated that genotypes (parents and their crosses) exhibited significant variations among studied traits. Due to the results of agronomic traits, Sakha93 and Sids1 were considered drought-tolerant genotypes; and Gemmaza9 and Sakha94 were the sensitive ones. While Sakha93 and Sids1 surpass the others in LW and PH, their cross (H3) was on average. In general, significant variation between tolerant and sensitive genotypes was observed.

Figure 1 and Table 2 reveal that Sakha93 recorded the highest value of PH within parents, while Sids1 surpassed all genotypes and hybrids for their survival against drought treatment (LW value). On other hand, the cross H1 had the highest PH among parents and their crosses, while H1 was in average LW. Variations for all the traits were significantly observed for treatments, genotypes, and genotype × treatments under drought conditions ($p < 0.05$).

The coefficient of variation (CV) was lower for all traits, while LW was the highest among them. Because mean is used in calculating CVs, increasing mean were expected

Table 2 Mean, standard error, standard deviation, and coefficient of variance of parents and their crosses for plant height (PH) and leaf wilting (LW) traits

	Mean		Standard error		Standard deviation		CV%	
	PH	LW	PH	LW	PH	LW	PH	LW
G9	11.737	39.313	1.067	2.313	1.509	3.270	12.856	27.864
S94	12.100	42.500	1.100	2.500	1.556	3.536	12.856	29.219
Sids	32.263	98.813	2.933	5.813	4.148	8.220	12.856	25.478
S93	46.013	90.313	4.183	5.313	5.916	7.513	12.856	16.328
H1 (S93 × G9)	44.605	79.581	4.055	4.681	5.735	6.620	12.856	14.842
H2 (S94 × G9)	29.755	64.635	2.705	3.802	3.825	5.377	12.856	18.071
H3 (S93 × Sids)	48.290	88.152	4.390	5.185	6.208	7.333	12.856	15.186

PH: plant height, and LW: leaf witling

Table 3 Analysis of variance (ANOVA) of plant height (PH) and leaf wilting (LW)

Source of variation	SS	Df	MS	*F*	*p* value	*F* crit
Plant height (PH)						
Genotypes	2864.4790	6.0000	477.4132	121.0000	0.0000	4.2839
Drought treatments	119.2879	1.0000	119.2879	30.2334	0.0015	5.9874
Error	23.6734	6.0000	3.9456			
Total	3007.4402	13.0000				
Leaf wilting (LW)						
Genotypes	6731.0279	6.0000	1121.8380	289.0000	0.0000	4.2839
Drought treatments	250.4372	1.0000	250.4372	64.5159	0.0002	5.9874
Error	23.2908	6.0000	3.8818			
Total	7004.7558	13.0000				

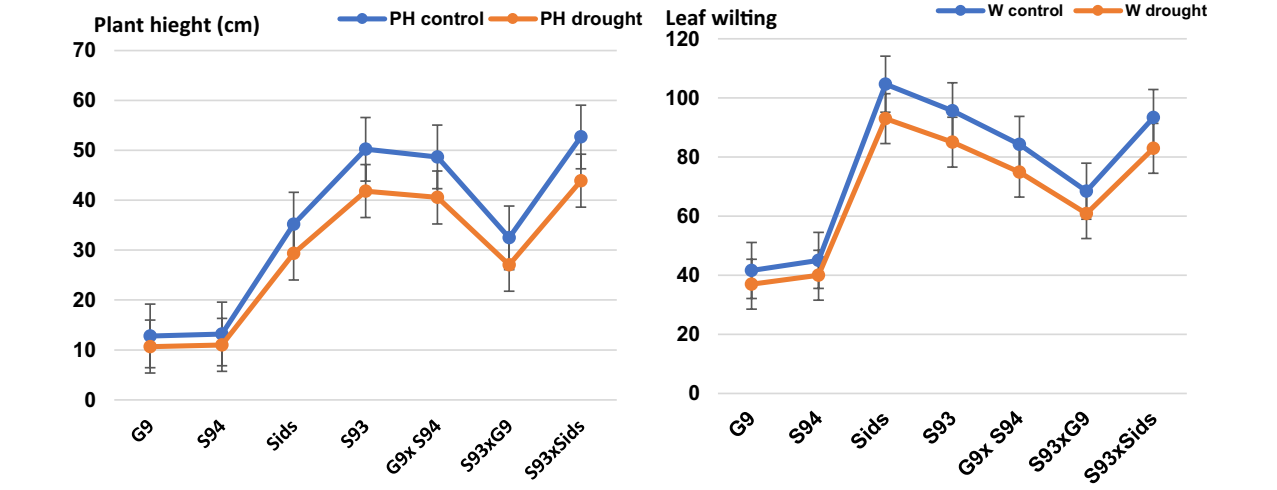

Fig. 1 Response of different parental genotypes to drought stress, i.e., the effect of drought on plant height (cm) and leaf wilting (days) of Wheat genotypes

to produce smaller coefficients of variation. Phenotypic correlations ranged widely among traits under drought conditions and control. Correlations were significantly positive ($p < 0.05$) between genotypes and both PH and LW.

3.2 Construction of linkage map

A genetic map was constructed for plant height and leaf wilting using 195 SSR markers of that 79 SSRs on A chromosomes were mapped, 69 SSRs on B chromosomes, and 47 SSRs on D chromosomes. Chromosomes 1A and 2B beard highest markers that coverage of 19 SSRs, and the chromosome 7D had the lowest one that 3 SSRs coverage it. The genetic length that the linkage map covered was 5057.4858 cM and the average inter marker distance was 25.9358 cM (Fig. 2).

The number of QTLs covered by each chromosome is presented in Tables 4, 5, and 6. Data in Table 4 revealed that QTLs related to plant height (PH) and leaf wilting (LW) were distributed among all chromosome sets except chromosomes 20 and 21.

The nineteen chromosomes were shown to bear 116 QTLs where plant height had 74 QTLs loci and 42 loci for leaf wilting. Out of the observed 116 QTLs, chromosome 19 (7A = 15) beard the highest QTLs number for both the studied traits, followed by chromosome 5 (2B = 14) and chromosome 1 (1A = 13). Among the two traits (plant height and leaf wilting), chromosome 1(1A) exhibited the highest number of QTLs that related to plant height trait (= 10) followed by chromosome 3 (1D) and 19 (7A) which recorded 7 QTLs loci, while chromosomes 5 (2B) and 19 (7A) showed the highest number of QTLs related to leaf wilting.

4 Discussion

Traits such as plant height and leaf wilting, historically, have been subjected to strong selective natural and artificial pressure, to improve the adaptation of bread wheat to different climatic conditions and to increase the grain yield [36–39]. However, these same traits are not only important for increasing crop yield potential, but they are also useful in determining the adaptation to climate change [40]. In the present work, the genetic control of two traits was investigated to identify associated QTLs. Variations for all the traits were significantly observed for treatments, genotypes, and genotype × treatments under drought conditions ($p < 0.05$). The coefficient of variation (CV) was lower for all traits, while LW among them was the highest. Because mean used in calculating CVs, increasing mean were expected to produce smaller coefficients of variation. Phenotypic correlations ranged widely among traits under drought conditions and control. Correlations were significantly positive ($p < 0.05$) between genotypes and plant height, similarly between plant height and LW. However, significant negative correlations ($p < 0.05$) were exhibited between LW and genotypes. This was consistent with previous reports in wheat and also in other cereal species such as rice and barley, indicating a high response to selection of these traits [41–43]. Continuous distribution or absence of discrete segregating classes for PH and LW suggested that its inheritance is either determined by a large number of genes with small effects or by a few major genes with substantial environmental effects. The presence of transgressive segregants in all traits investigated suggested that each of the parental cultivars had desirable and undesirable alleles in various proportions for loci governing these traits.

A total of 530 high-quality SSR markers were used to build the genetic map, and as expected, most of them were placed on genomes A and B, in line with previous results [44, 45]. Wen et al. [46] showed that the D genome had fewer markers than the A and B genomes in the high-density consensus map in common wheat. A total of 28 and 10 QTLs were found in the F2 populations. The comparative QTL analysis of genomes A and B between F2 populations showed that 55 QTLs for PH could be considered to be adjacent and nearly overlapping. Pearson rank between the assessed traits revealed that PH was correlated with the LW, in agreement with Rabbi and Hisam [45], Bilgrami et al. [47], and Mecha et al. [48]. In our study, several QTLs for PH and LW co-localized on the same chromosome, suggesting that they were not distributed evenly in the wheat genome, but they tended to cluster in particular chromosome regions (Table 4).

5 Conclusions

Most of the traits that are affected by drought are quantitative traits, so detection of the QTLs related to these traits is very important for breeder and wheat producers. In this trend, QTLs for plant height (PH) and days to wilting (W) were studied. A total of 116 QTLs loci were detected which covered 19 chromosomes out of the 21 chromosomes of wheat. Chromosome 7A showed to bear the highest number of QTLs loci (15 loci). While chromosome 1A beard the highest number of QTLs loci related to PH (10 loci), chromosome 2B and 7A beard the highest number of QTLs related to surviving (days to wilting). We highly recommend our finding to help breeders in wheat breeding programs to improve plant height and survival (days to wilting). SSR markers are useful for the detection of QTLs related to abiotic stress like drought. Liu et al. [49] detected seven QTLs related to PH on chromosomes 1B, 4B (two regions), 6A (two regions), 6D and 7A; on the other hand, Wang et al. [50] identified two major QTLs related to PH on chromosomes 4B and 6D.

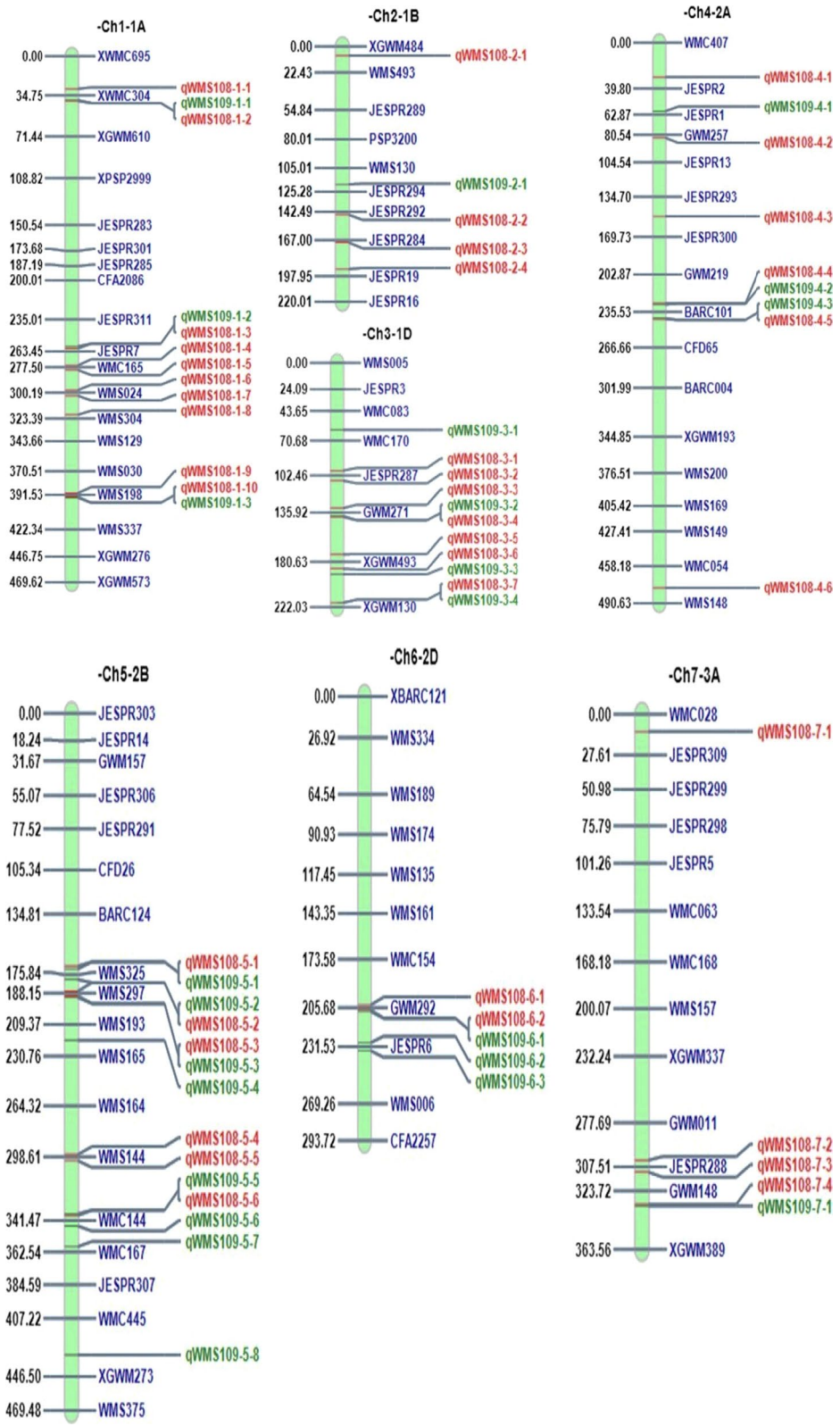

Fig. 2 Linkage maps revealed the position and distribution the QTLs related to plant height and leaf wilting among Wheat chromosomes. QTL name on the right side and centimorgan (cM) distance on the left. A colored bar represents the CI (confidence interval) of QTL identified through single-locus analysis

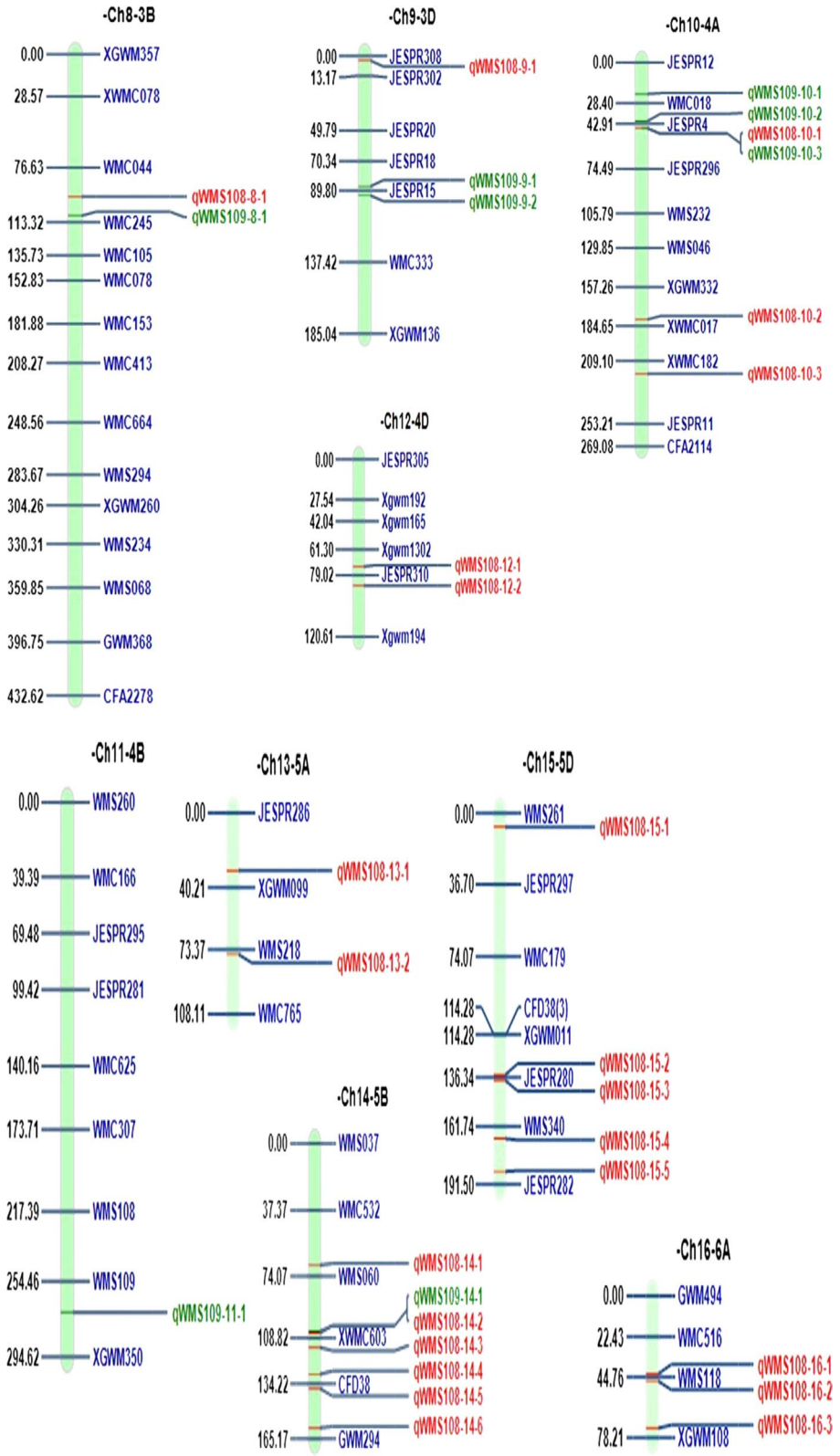

Fig. 2 continued

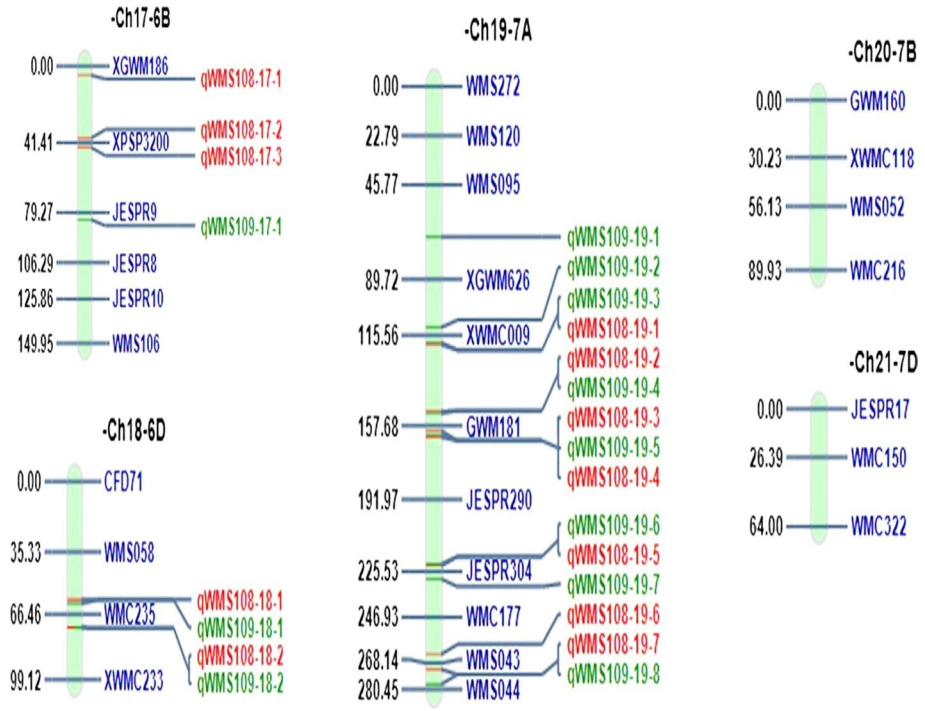

Fig. 2 continued

Table 4 Chromosomes ID and their QTLs loci related to plant height and leaf wilting for nineteen chromosomes out of twenty-one wheat chromosomes

Chrom. ID	QTLs			
	Plant height	Leaf wilting	Total	Mean
-Ch1-1A	10	3	13	8.67
-Ch2-1B	4	1	5	3.33
-Ch3-1D	7	4	11	7.33
-Ch4-2A	6	3	9	6.00
-Ch5-2B	6	8	14	9.33
-Ch6-2D	2	3	5	3.33
-Ch7-3A	4	1	5	3.33
-Ch8-3B	1	1	2	1.33
-Ch9-3D	1	2	3	2.00
-Ch10-4A	3	3	6	4.00
-Ch11-4B	0	1	1	0.67
-Ch12-4D	2	0	2	1.33
-Ch13-5A	2	0	2	1.33
-Ch14-5B	6	1	7	4.67
-Ch15-5D	5	0	5	3.33
-Ch16-6A	3	0	3	2.00
-Ch17-6B	3	1	4	2.67
-Ch18-6D	2	2	4	2.67
-Ch19-7A	7	8	15	10.00
Mean	3.89	2.21	6.11	4.07
Total	74	42	116	

Table 5 Position, characters, and distribution the QTLs related to plant height among nineteen chromosomes out of twenty-one wheat chromosomes

Chromosome	Position	Left marker	Right marker	LOD	PVE (%)	Add
-Ch1-1A	29	XWMC695	XWMC304	34.4606	0.9496	0.0102
	40	XWMC304	XGWM610	33.8512	0.9572	0.0055
	261	JESPR311	JESPR7	38.0261	0.8465	−0.0055
	276	JESPR7	WMC165	33.7177	0.8451	−0.0010
	280	WMC165	WMS024	36.4749	0.843	0.0041
	298	WMC165	WMS024	36.085	0.8498	0.0311
	303	WMS024	WMS304	38.5963	0.8532	0.0293
	320	WMS024	WMS304	34.9425	0.8486	0.0031
	390	WMS030	WMS198	40.7933	0.8392	−0.0085
	393	WMS198	WMS337	40.1553	0.8495	−0.0067
-Ch2-1B	8	XGWM484	WMS493	27.2976	0.9367	−0.0055
	145	JESPR292	JESPR284	36.5342	0.8558	0.0052
	169	JESPR284	JESPR19	40.0445	0.8551	0.0010
	192	JESPR284	JESPR19	36.1952	0.9561	−0.0163
-Ch3-1D	98	WMC170	JESPR287	36.2982	0.9524	−0.0011
	107	JESPR287	GWM271	39.0537	0.9532	−0.0001
	132	JESPR287	GWM271	41.4678	0.951	0.0050
	140	GWM271	XGWM493	41.6785	0.9556	0.0004
	174	GWM271	XGWM493	34.5048	0.9617	−0.0220
	187	XGWM493	XGWM130	33.928	0.9609	−0.0238
	218	XGWM493	XGWM130	39.2011	0.9562	−0.0153
-Ch4-2A	30	WMC407	JESPR2	24.0876	0.9642	−0.0172
	83	GWM257	JESPR13	35.7785	0.8563	−0.0446
	152	JESPR293	JESPR300	32.2305	0.9634	−0.0264
	228	GWM219	BARC101	30.7708	0.9618	0.0200
	242	BARC101	CFD65	26.2169	0.953	0.0276
	477	WMC054	WMS148	26.4074	0.9607	0.0042
-Ch5-2B	170	BARC124	WMS325	34.6034	0.9596	0.0364
	187	WMS325	WMS297	46.0389	1.0697	0.0773
	190	WMS297	WMS193	48.4367	1.0739	0.0825
	297	WMS164	WMS144	51.8691	1.1331	0.0507
	301	WMS144	WMC144	52.1626	1.1341	0.0486
	338	WMS144	WMC144	43.3711	1.1476	−0.0264
-Ch6-2D	204	WMC154	GWM292	41.742	0.8497	0.0142
	207	GWM292	JESPR6	39.0355	0.8485	0.0139
-Ch7-3A	12	WMC028	JESPR309	24.3793	0.9536	−0.0136
	303	GWM011	JESPR288	33.0059	0.9451	−0.0024
	311	JESPR288	GWM148	29.471	0.8896	0.0093
	333	GWM148	XGWM389	28.0939	0.9657	0.0016
-Ch8-3B	96	WMC044	WMC245	28.7844	0.9661	−0.0006
-Ch9-3D	3	JESPR308	JESPR302	41.7766	1.0162	−0.0162
-Ch10-4A	46	JESPR4	JESPR296	48.1947	1.2901	−0.0150
	180	XGWM332	XWMC017	34.6088	0.9524	−0.0102
	218	XWMC182	JESPR11	25.6417	0.9619	−0.0001
-Ch12-4D	73	Xgwm1302	JESPR310	21.3911	0.8453	−0.0044
	86	JESPR310	Xgwm194	25.5533	0.9638	−0.0022
-Ch13-5A	31	JESPR286	XGWM099	23.3193	0.9656	−0.0195
	76	WMS218	WMC765	36.0515	0.8476	0.0000

Table 5 (continued)

Chromosome	Position	Left marker	Right marker	LOD	PVE (%)	Add
-Ch14-5B	68	WMC532	WMS060	29.1324	0.9597	0.0092
	106	WMS060	XWMC603	38.4724	0.8466	−0.0050
	114	XWMC603	CFD38	38.8464	0.9508	−0.0107
	129	XWMC603	CFD38	39.614	0.9535	−0.0209
	137	CFD38	GWM294	39.7165	0.8489	0.0013
	159	CFD38	GWM294	36.638	0.9537	−0.0016
-Ch15-5D	7	WMS261	JESPR297	32.7536	0.9607	0.0148
	135	XGWM011	JESPR280	39.4811	0.8469	0.0009
	138	JESPR280	WMS340	39.8181	0.8478	−0.0070
	168	WMS340	JESPR282	33.824	0.95	−0.0080
	185	WMS340	JESPR282	32.8221	0.9507	0.0030
-Ch16-6A	43	WMC516	WMS118	37.929	0.8452	0.0030
	47	WMS118	XGWM108	40.1389	0.8504	−0.0023
	73	WMS118	XGWM108	38.4625	0.9541	−0.0014
-Ch17-6B	5	XGWM186	XPSP3200	38.204	0.9564	−0.0190
	39	XGWM186	XPSP3200	36.8637	0.8546	−0.0215
	44	XPSP3200	JESPR9	36.7797	0.8585	−0.0235
-Ch18-6D	59	WMS058	WMC235	29.0349	0.9574	0.0221
	73	WMC235	XWMC233	27.5574	0.9571	0.0188
-Ch19-7A	120	XWMC009	GWM181	35.1153	0.9549	−0.0035
	151	XWMC009	GWM181	31.242	0.9585	0.0080
	160	GWM181	JESPR290	31.5985	0.8614	0.0412
	163	GWM181	JESPR290	31.6545	0.9482	0.0114
	223	JESPR290	JESPR304	32.1148	0.8729	0.0646
	264	WMC177	WMS043	152.458	6.5384	1.0027
	271	WMS043	WMS044	144.937	6.5372	1.0032

Table 6 Position, characters, and distribution the QTLs related to leaf wilting among nineteen chromosomes out of twenty-one wheat chromosomes

Chromosome	Position	Left Marker	Right Marker	LOD	PVE (%)	Add
-Ch1-1A	39	XWMC304	XGWM610	17.4069	1.4801	0.0521
	259	JESPR311	JESPR7	25.6445	1.4736	−0.0308
	394	WMS198	WMS337	28.8588	1.4826	−0.0584
-Ch2-1B	119	WMS130	JESPR294	15.5173	1.4733	0.0358
-Ch3-1D	61	WMC083	WMC170	19.5631	1.5356	−0.0081
	139	GWM271	XGWM493	24.2811	1.4685	0.0499
	192	XGWM493	XGWM130	16.9353	1.5755	0.0080
	218	XGWM493	XGWM130	22.9043	1.4934	0.0029
-Ch4-2A	60	JESPR2	JESPR1	21.0829	1.4521	−0.0257
	229	GWM219	BARC101	20.7341	1.5709	0.0967
	241	BARC101	CFD65	16.8518	1.5776	0.1122
-Ch5-2B	172	BARC124	WMS325	48.1412	2.165	0.1868
	179	WMS325	WMS297	40.9734	2.179	0.1843
	191	WMS297	WMS193	26.859	1.5677	0.1432
	220	WMS193	WMS165	30.6749	1.9623	0.1286
	337	WMS144	WMC144	25.9318	1.513	0.0143
	345	WMC144	WMC167	23.2376	1.4579	0.0052
	359	WMC144	WMC167	22.3533	1.4586	−0.0399
	432	WMC445	XGWM273	17.488	1.7303	0.0011
-Ch6-2D	208	GWM292	JESPR6	23.6446	1.4494	−0.0133
	229	GWM292	JESPR6	24.7027	1.4517	−0.0232
	234	JESPR6	WMS006	26.735	1.4583	−0.0281
-Ch7-3A	334	GWM148	XGWM389	11.8946	1.5697	−0.0263
-Ch8-3B	109	WMC044	WMC245	21.0153	1.4801	−0.0107
-Ch9-3D	87	JESPR18	JESPR15	17.3147	1.4543	−0.0231
	93	JESPR15	WMC333	23.7691	1.4605	−0.0264
-Ch10-4A	22	JESPR12	WMC018	18.9897	1.5582	0.0009
	41	WMC018	JESPR4	27.6101	1.9431	0.0079
	46	JESPR4	JESPR296	38.4845	1.9785	0.0033
-Ch11-4B	271	WMS109	XGWM350	8.3317	1.5451	0.0391
-Ch14-5B	105	WMS060	XWMC603	22.9912	1.4643	0.0136
-Ch17-6B	83	JESPR9	JESPR8	20.0978	1.4532	−0.0056
-Ch18-6D	61	WMS058	WMC235	16.8681	1.5493	0.0933
	73	WMC235	XWMC233	19.853	1.5985	0.0760
-Ch19-7A	70	WMS095	XGWM626	16.0521	1.618	−0.0311
	112	XGWM626	XWMC009	21.471	1.4436	−0.0188
	119	XWMC009	GWM181	24.079	1.4653	−0.0075
	152	XWMC009	GWM181	22.432	1.5547	0.0712
	162	GWM181	JESPR290	22.8931	1.5316	0.0929
	222	JESPR290	JESPR304	26.2245	1.5366	0.1215
	229	JESPR304	WMC177	26.1425	1.5501	0.1487
	278	WMS043	WMS044	81.141	5.268	0.9462

Abbreviations
AFLP: Amplified fragment length polymorphisms; CIM: Composite interval mapping; cM: Centimorgan; $_{CP}$SSR: Chloroplast simple-sequence repeats; CV: Coefficient of variance; DNA: Deoxyribonucleic acid; ICIM: Inclusive composite interval mapping; LOD: Logarithm of odds; LW: Leaf wilting; PCR: Polymerase chain reaction; PH: Plant height; QTLs: Quantitative trait loci; SMA: Single marker analysis; SSR: Simple-sequence repeats; STMS: Sequence-tagged microsatellite; TBE: Tris-borate-EDTA.

Acknowledgements
The work was carried out and supported by the Genetic department, faculty of Agriculture, Beni-Suef University and the Genetic department, faculty of Agriculture, Mansoura University.

Authors' contributions
All authors were involved in conceptualization and methodology; KAMK, MHA, and RMMH helped in application of drought treatments and DNA extraction from all samples; KAMK contributed to PCR and bioinformatics analysis; writing—original draft preparation; MHA, RMMH, and JAB were involved in review and editing. All authors have read and approved the final manuscript.

Funding
Not applicable.

Availability of data and materials
The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interest.

Author details
[1]Faculty of Agriculture, Beni-Suef University, New Beni Suef City, Beni Suef Governorate, Egypt. [2]Faculty of Agriculture, Mansoura University, Elgomhouria St., Mansoura City 35516, Egypt. [3]Horticulture Department, Faculty of Agriculture, Benghazi University, Benghazi, Libya.

Received: 5 August 2021 Accepted: 10 February 2022
Published online: 16 March 2022

References

1. FAO. State of Food and Agriculture (2020) Overcoming water challenges in agriculture. Rome. https://doi.org/10.4060/cb1447en
2. Anjum SA, Ashraf U, Tanveer M, Khan I, Hussain S, Shahzad B, Zohaib A, Abbas F, Saleem MF, Ali I, Wang LC (2017) Drought induced changes in growth, osmolyte accumulation and antioxidant metabolism of three maize hybrids. Front Plant Sci. https://doi.org/10.3389/fpls.2017.00069
3. Eftekhari A, Baghizadeh A, Yaghoobi MM, Abdolshahi R (2017) Differences in the drought stress response of DREB2 and CAT1 genes and evaluation of related physiological parameters in some bread wheat cultivars. Biotechnol Biotechnol Equip 31:709–716. https://doi.org/10.1080/13102818.2017.1316214
4. El-Moneim DA, Alqahtani MM, Abdein MA, Germoush MO (2020) Drought and salinity stress response in wheat: physiological and TaNAC gene expression analysis in contrasting Egyptian wheat genotypes. J Plant Biotechnol 47:1–14. https://doi.org/10.5010/JPB.2020.47.1.001
5. Itam M, Mega R, Tadano S, Abdelrahman M, Matsunaga S, Yamasaki Y, Akashi K, Tsujimoto H (2020) Metabolic and physiological responses to progressive drought stress in bread wheat. Sci Rep 10:1–14. https://doi.org/10.1038/s41598-020-74303-6
6. He C, Du Y, Fu J, Zeng E, Park S, White F, Zheng J, Liu S (2020) Early drought-responsive genes are variable and relevant to drought tolerance. G3 10:1657–1670. https://doi.org/10.1534/g3.120.401199
7. Lawlor DW, Cornic G (2002) Photosynthetic carbon assimilation and associated metabolism in relation to water deficits in higher plants. Plant Cell Environ 25:275–294. https://doi.org/10.1046/j.0016-8025.2001.00814.x
8. Szegletes ZS, Erdei L, Tari I, Cseuz L (2000) Accumulation of osmoprotectants in wheat cultivars of different drought tolerance. Cereal Res Commun 28(4):403–410. https://doi.org/10.1007/bf03543622
9. Yordanov I, Velikova V, Tsonev T (2000) Plant responses to drought, acclimation, and stress tolerance. Photosynthetica 38:171–186. https://doi.org/10.1023/A:1007201411474
10. Zhu JK (2002) Salt and drought stress signal transduction in plants. Annu Rev Plant Biol 53:247–273. https://doi.org/10.1146/annurev.arplant.53.091401.143329
11. Xuemei Ji, Shiran B, Wan J, Lewis DC, Jenkins CLD, Condon AG, Richards RA, Dolferus R (2010) Importance of pre-anthesis anther sink strength for maintenance of grain number during reproductive stage water stress in wheat. Plant Cell Environ 33:926–942. https://doi.org/10.1111/j.1365-3040.2010.02130.x
12. Al-Taweel SK, Abdel-Aziz RM, Rabea KM, Khaled KAM (2019) Studying cDNA SCoT in response to salinity stress in *Stevia rebaudiana* Bertoni. SABRAO J Breed Genet 51:281–294
13. Al-Taweel SK, Azzam CR, Khaled KA, Abdel-Aziz RM (2021) Improvement of Stevia (*Stevia rebaudiana* Bertoni) and steviol glycoside through traditional breeding and biotechnological approaches. SABRAO J Breed Genet 53:88–111
14. Bennici A, Anzidei M, Vendramin GG (2004) Genetic stability and uniformity of *Foeniculum vulgare* Mill. regenerated plants through organogenesis and somatic embryogenesis. Plant Sci 166:221–227. https://doi.org/10.1016/j.plantsci.2003.09.010
15. Khaled KA, El-Arabi NI, Sabry NM, El-Sherbiny S (2018) Sugarcane genotypes assessment under drought condition using amplified fragment length polymorphism. Biotechnology 17:120–127. https://doi.org/10.3923/biotech.2018.120.127
16. Khaled KA, El-Demardash IS, Amer EAM (2015) Genetic polymorphism among some sugarcane germplasm collections as revealed by RAPD and ISSR analyses. Life Sci J 12:159–167. https://doi.org/10.7537/marslsj120315.21
17. Remington DL, Purugganan MD (2003) Candidate genes, quantitative trait loci, and functional trait evolution in plants. Int J Plant Sci 164:S7–S20
18. Mackay TFC (2004) The genetic architecture of quantitative traits: lessons from Drosophila. Curr Opin Genet Dev 14:253–257
19. Roff DA (2007) A centennial celebration for quantitative genetics. Evolution 61:1017–1032
20. Vargas M, van Eeuwijk FA, Crossa J, Ribaut JM (2006) Mapping QTLs and QTL × environment interaction for CIMMYT maize drought stress program using factorial regression and partial least squares methods. Theor Appl Genet 112:1009–1023
21. Reynolds M, Tuberosa R (2008) Translational research impacting on crop productivity in drought-prone environments. Curr Opin Plant Biol 11:171–179
22. Budak H, Hussain B, Khan Z, Ozturk NZ, Ullah N (2015) From genetics to functional genomics: improvement in drought signaling and tolerance in wheat. Front Plant Sci 6:1012. https://doi.org/10.3389/fpls.2015.01012
23. Prasad M, Varshney RK, Roy JK, Balyan HS, Gupta PK (2000) The use of microsatellites for detecting DNA polymorphism, genotype identification and genetic diversity in wheat. Theor Appl Genet 100:584–592. https://doi.org/10.1007/s001220050077
24. Tomar RSS, Deshmukh RK, Naik KB, Tomar SMS (2014) Development of chloroplast-specific microsatellite markers for molecular characterization of alloplasmic lines and phylogenetic analysis in wheat. Plant Breeding 133:12–18. https://doi.org/10.1111/pbr.12116
25. Ahmed HGMD, Kashif M, Rashid MAR, Sajjad M, Zeng Y (2020) Genome wide diversity in bread wheat evaluated by SSR markers. Int J Agric Biol 24:263–272. https://doi.org/10.17957/IJAB/15.1433
26. Mwadzingeni L, Shimelis H, Rees DJG, Tsilo TJ (2017) Genome-wide association analysis of agronomic traits in wheat under drought-stressed and non-stressed conditions. PLoS ONE 12:e0171692. https://doi.org/10.1371/journal.pone.0171692

27. Golabadi M, Arzani A, Maibody SM, Tabatabaei BS, Mohammadi SA (2011) Identification of microsatellite markers linked with yield components under drought stress at terminal growth stages in durum wheat. Euphytica 177:207–221. https://doi.org/10.1007/s10681-010-0242-8
28. Faheem M, Mahmood T, Shabbir G, Akhtar N, Kazi AG, Mujeeb-Kazi A (2015) Assessment of D-genome based genetic diversity in drought tolerant wheat germplasm. Int J Agric Biol 17:4. https://doi.org/10.17957/IJAB/14.0018
29. Ramya P, Jain N, Singh PK, Singh GP, Prabhu KV (2015) Population structure, molecular and physiological characterisation of elite wheat varieties used as parents in drought and heat stress breeding in India. Ind J Genet Pl Breed 75:250–252. https://doi.org/10.5958/0975-6906.2015.00038.3
30. Kumari S, Jaiswal V, Mishra VK, Paliwal R, Balyan HS, Gupta PK (2018) QTL mapping for some grain traits in bread wheat (*Triticum aestivum* L.). Physiol Mol Biol Plants 24:909–920. https://doi.org/10.1007/s12298-018-0552-1
31. Liu RX, Wu FK, Xin YI, Yu LIN, Wang ZQ, Liu SH, Mei DENG, Jian MA, Wei YM, Zheng YL, Liu YX (2020) Quantitative trait loci analysis for root traits in synthetic hexaploid wheat under drought stress conditions. J Integr Agric 19:1947–1960. https://doi.org/10.1016/S2095-3119(19)62825-X
32. Habiba R, El-Adl A, El-Mageed A, Gomaa K (2018) Effect of genotypes and polyethylene glycol on immature embryo culture in wheat. J Agric Chem Biotechnol 9:175–180. https://doi.org/10.21608/JACB.2018.35237
33. Khaled AMK, Esh AMH (2008) High quality genomic DNA impurities-free from sugar crops and other plant tissue. In: Proceedings of international conference (IS-2008), Al Arish, Egypt
34. Meng L, Li H, Zhang L, Wang J (2015) QTL IciMapping: integrated software for genetic linkage map construction and quantitative trait locus mapping in biparental populations. Crop J 3:269–283. https://doi.org/10.1016/j.cj.2015.01.001
35. Bernardo R (2002) Breeding for quantitative traits in plants, vol 1. Stemma Press, p 369
36. Law CN, Worland AJ (1997) Genetic analysis of some flowering time and adaptive traits in wheat. New Phytol 13:19–28. https://doi.org/10.1046/j.1469-8137.1997.00814.x
37. Lewis S, Faricelli ME, Appendino ML, Valárik M, Dubcovsky J (2008) The chromosome region including the earliness per se locus Eps-A m1 affects the duration of early developmental phases and spikelet number in diploid wheat. J Exp Bot 59:3595–3607. https://doi.org/10.1093/jxb/ern209
38. Richards RA (1988) A tiller inhibitor gene in wheat and its effect on plant growth. Aust J Agric Res 39:749–757. https://doi.org/10.1071/AR9880749
39. Sanchez-Garcia M, Bentley AR (2019) Global journeys of adaptive wheat genes. In: Miedaner T, Korzun V (eds) Applications of genetic and genomic research in cereals, 1st edn. Elsevier, Amsterdam, pp 183–200. https://doi.org/10.1016/B978-0-08-102163-7.00009-0
40. De Vita P, Taranto T (2019) Durum wheat (*Triticum turgidum* ssp. durum) breeding to meet the challenge of climate change. In: Al-Khayri JM, Jain SM, Johnson DV (eds) Advances in plant breeding strategies: cereals. Springer, pp 471–524
41. Abinasa M, Ayana A, Bultosa G (2011) Genetic variability, heritability and trait associations in durum wheat (*Triticum turgidum* L. var. durum) genotypes. African J Agric Res 6:3972–3979
42. Iqbal M, Navabi A, Salmon DF, Yang RC, Murdoch BM, Moore SS, Spaner D (2007) Genetic analysis of flowering and maturity time in high latitude spring wheat: genetic analysis of earliness in spring wheat. Euphytica 154:207–218. https://doi.org/10.1007/s10681-006-9289-y
43. Shrimali J, Shekhawat AS, Kumari S (2017) Genetic variation and heritability studies for yield and yield components in barley genotypes under normal and limited moisture conditions. J Pharmacogn Phytochem 6:233–235
44. Berkman PJ, Visendi P, Lee HC, Stiller J, Manoli S, Lorenc MT, Lai K, Batley J, Fleury D, Šimková H et al (2013) Dispersion and domestication shaped the genome of bread wheat. Plant Biotechnol J 11:564–571. https://doi.org/10.1111/pbi.12044
45. Rabbi A, Hisam SM (2017) Genetics of drought tolerance in hard red spring wheat in the Northern United States of America. Ph.D. Thesis, North Dakota State University, Fargo, ND, USA
46. Wen W, He Z, Gao F, Liu J, Jin H, Zhai S, Qu Y, Xia X (2017) A high-density consensus map of common wheat integrating four mapping populations scanned by the 90k SNP array. Front Plant Sci 8:1–14. https://doi.org/10.3389/fpls.2017.01389
47. Bilgrami SS, Ramandi HD, Shariati V, Razavi K, Tavakol E, Fakheri BA, Mahdi Nezhad N, Ghaderian M (2020) Detection of genomic regions associated with tiller number in Iranian bread wheat under different water regimes using genome-wide association study. Sci Rep 10:1–17. https://doi.org/10.1038/s41598-020-69442-9
48. Mecha B, Alamerew S, Assefa A, Dutamo D, Assefa E (2017) Correlation and path coefficient studies of yield and yield associated traits in bread wheat (*Triticum aestivum* L.) genotypes. Adv Plants Agric Res 6:1–10. https://doi.org/10.15406/apar.2017.06.00226
49. Liu DC, Gao MQ, Guan RX, Li RZ, Cao SH, Guo XL, Zhang AM (2002) Mapping quantitative trait loci for plant height in wheat (*Triticum aestivum* L.) using a F2:3 population. Yi Chuan Xue Bao 29(8):706–711
50. Wang Z, Hu H, Jiang X, Tao Y, Lin Y, Wu F, Hou S, Liu S, Li C, Chen G, Liu Y (2020) Identification and validation of a novel major quantitative trait locus for plant height in common wheat (*Triticum aestivum* L.). Front Genet 11:602495. https://doi.org/10.3389/fgene.2020.602495

Publisher's Note