Detection of drought tolerance-related QTL in the Plainsman V./Cappelle Desprez doubled haploid wheat population

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Abstract
Drought stress is one of the major abiotic factors that significantly reduces wheat grain yield. Improving drought tolerance is a challenge that plant breeders are facing nowadays. In this study, our goal was to identify quantitative trait loci (QTL) in the Plainsman V./Cappelle Desprez doubled haploid (DH) population under drought induced as decreased irrigation (ds) and well-watered (ww) conditions in glasshouse. In total, 54 QTL were detected across the three years in two water regimes linked to 10 drought tolerance-related agronomic traits. Out of the detected QTL regions several have been previously reported. The QTL on chromosome 1A (wPt-744613-wPt-8016) related to thousand grain weight was detected in both ds and ww conditions, explaining the 12.7–17.4% of the phenotypic variance. QTL for grain yield was detected on chromosomes 1A, and 6B in the ds treatment. Numerous QTL was identified under both irrigation levels.

Keywords Drought · Wheat · QTL · Grain yield

Introduction
Wheat is one of the most widely grown cereal species all over the world (El-Feki et al. 2018). Nowadays, the climate change has strong influence on the productivity of wheat. Adequate soil moisture is essential for proper growth and development of crop species, which ultimately leads to optimum productivity (Kadam et al. 2012). Drought stress is the major abiotic factor that reduces wheat grain yield (Dashti et al. 2007; Safar-Noori et al. 2018).

Drought tolerance is a complex quantitative character comprising of several physio and biochemical processes at the cellular and molecular level at different stages of the plant development (Kadam et al. 2012). Drought tolerance is controlled by multiple genes, with each gene having a relatively small effect (Zhang et al. 2013). Most of the drought-related traits are also quantitative (Teulat et al. 2003). Plants adapt to drought stress in many ways, including enhanced water uptake by developing large root system, reduced water loss by increasing stomatal resistance, and adaptation to water shortage by accumulation of cellular osmolytes (Rampino et al. 2006; Tavakol et al. 2016).

Breeding varieties with improved drought tolerance is one of the most important goals for plant breeders. This could be enhanced by the understanding the genetic and molecular bases of drought tolerance (Zhang et al. 2011; Sinha et al. 2018). Genomics-assisted improvement of abiotic stress tolerance of crops is relying on the QTL approach (Collins et al. 2008). The QTL analysis based on high-density molecular linkage maps has become a useful tool to understand the genetic background of drought tolerance. Diversity Array Technology (DArT, Kilian et al. 2012) has been used in previous QTL studies of wheat, providing high-density genotypic map by detecting large number of DNA variants (El-Feki et al. 2018). In wheat, drought stress QTL mapping has been applied at different plant developmental stages and was carried out at several morpho-physiological traits in different mapping populations. Most of the reported QTLs for drought tolerance in wheat were identified for yield or yield components under limited water conditions (Nasseer et al. 2018).
F1 generation followed the protocol of Pauk et al. (2003). DH population was developed from the anther culture of the drought-tolerant Plainsman V. (Pl) and the drought-sensitive品种. This population consisted of 135 DH lines derived from a cross between the Plainsman V. (Pl) and the Cappelle Desprez (CD). The DH lines were developed using the protocol of Pauk et al. (2003). Grain yield in wheat can usually be described by yield components, the spikes per plant, the grain number per spike, and the thousand kernel weight, and the plant number per given area. The yield component traits are also influenced by several physiological traits like plant height (PH) and biomass (BM) in different populations (Guan et al. 2018; Pouri et al. 2019). Furthermore, PH could be a suitable trait to model the dissection of drought tolerance (Zhang et al. 2011). Flowering time is another important trait in drought tolerance (Bennet et al. 2012b). Root systems are crucial to plants for adaptation to suboptimal conditions (Liu et al. 2013). Underwater stress conditions, plants often develop deep and extensive root systems as an adaptive strategy (Li et al. 2014). Extensive root systems were positively associated with higher grain yield in the case of rice under drought stress (Lafitte et al. 2004).

More than 500 QTLs related to grain yield and its components have been previously reported on all chromosomes of the wheat genome under drought stress conditions (Zhang et al. 2010). Bennet et al. (2012b) reported grain yield (GY)-related QTLs on 1A, 1B, 2A, 2B, 2D, 3A, 4D, 6D, 7A chromosomes. In addition, Kadum et al. (2012) detected QTL regions on 2D, 3D, 4B, 5A chromosomes which were associated with GY. Mathews et al. (2008) reported QTLs related to GY on 1A, 1B, 2A, 2B, 3A, 4A, 4B, 5A, 6B, 7A, 7B chromosomes of wheat. Detected regions can be used in breeding and pre-breeding to increase its efficiency through marker-assisted selection (Pinto et al. 2010; Gao et al. 2016). In addition, phenotyping plays a crucial role in gene discovery and in understanding the complex interactions between genes, genetic background, and environment (Lopes et al. 2013). The goal of the present study was to identify QTL regions in the Plainsman V. (Pl)/Cappelle Desprez (CD) DH population under drought stress and optimal irrigation conditions in glasshouse experiments.

**Materials and methods**

**Plant material**

The winter wheat DH population, used in this study, consisted of 135 DH lines derived from a cross between the drought-tolerant Plainsman V. (Pl) and the drought-sensitive Cappelle Desprez (CD) varieties (Gallé et al. 2009). The DH population was developed from the anther culture of the F1 generation followed the protocol of Pauk et al. (2003). PI (year of release, 1974) is an American hard red winter wheat with high protein content and has excellent drought tolerance. CD (year of release, 1946) producing high yield in intensive farming conditions, but sensitive to drought, was bred in France (Gallé et al. 2009).

**Glasshouse experiments**

The experiments were carried out in 2014, 2015, 2016, under glasshouse conditions in Szeged. The one-week-old seedlings were vernalized at 4 °C in a cold chamber, under continuous dim light for 6 weeks. The seedlings of DH lines were planted in February. The pots contained soil mixture (526 g peat soil, and 1340 g dry sandy soil) and 4 g controlled release fertilizer (Osmocote Exact, Scotts Company, Marysville, Ohio, including N16 + P9 + K12 + 2,5MgO). Each DH line was planted in two pots/treatment and two (2014) or three (2015, 2016) plants/pot. The experiment was carried out from the end of February till mid-June, in controlled conditions using the standard glasshouse wheat growing program. Prior to the experiment, the water capacity of the used soil mixture was determined (Cseri et al. 2013). At the time of potting, the wheat plants were watered with 100 ml water/pot to ensure the adaptation of seedling.

Pots were irrigated twice weekly. The well-watered (ww) plants were irrigated to the 60% of the soil water capacity. Five ww Pl and five CD pots weight was measured by a computer-controlled balance (GSE model 350, 6.000 ± 1 g), which gave the average irrigation norm. In the ww treatment each plant during the experiment got 1575 ml water in 2014 (the 2015 experiment has been previously reported Nagy et al. 2017), and 1025 ml water in 2016. In the drought stress (ds) treatment, the plants were irrigated to the 20% of the soil water capacity in the same way as in the ww treatment. During the growing season the stressed plants got 575 ml in 2014, 475 ml water in 2016.

**Recorded traits**

The days from sowing to heading (HT heading time) were registered individually for each plant when the spike left the leaf sheath completely. The plant height was measured from the ground to the top of the spike. The whole plants were harvested and dried in drying cabinet at 40 °C to the constant weight and the aboveground biomass (BM), spike length (SL), non-threshed spike weight (SW), number of grains/ mean ear (GNE), and total grain yield/plant (GY), thousand grain weight (TGW) were measured.

At the end of the experiment root dry mass was measured in 2015. Harvest index (HI) was calculated as the ratio between harvestable yield and aboveground biomass, as reported by Donald (1962), and Passioura (1983).
Broad sense heritability ($h^2$) was calculated with the following formula: 
\[ h^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{ge}^2}{n} + \frac{\sigma^2}{nr}} \]
where $\sigma_g^2$ is the genotypic effect, $\sigma_{ge}^2$ is the genotype by environment effect, $\sigma^2$ is the residual error, $n$ is the number of genotypes and $r$ is the number of errors (Guan et al. 2018).

### Statistical analysis

The normality of data was checked with Kolmogorov–Smirnov test by IBM SPSS statistics 22 software. Analyses of the collected data were made by IBM SPSS Statistics 22 software ‘Descriptive statistics’ function to calculate means, minimum and maximum values, percentiles, standard deviation (heading time, plant height, grain yield, aboveground biomass, non-threshed spike weight and root dry mass).

The ‘General Linear Model’ (GLM) function was used to perform the two-way ANOVA, investigating the genotype-by-treatment interactions. Correlation analysis was performed for each treatment separately (ww, ds) on the population average of the three years using IBM SPSS Statistics 22 software ‘Pearson Correlation’ function.

### DNA isolation and molecular markers

DNA was isolated from seedling leaf tissue according to the CTAB method (Rogers and Bendich 1985). The quality and quantity of DNA were measured with a NanoDrop 1000 Spectrophotometer (Thermo Scientific, USA).

To map the Pl/CD population, a database of 897 DArT markers was used. The DArT marker data were provided by the Australian Diversity Arrays Technology Pty Ltd (Lv. D, Bldg. 3, University of Canberra, Bruce ACT 2617, Australia).

### Molecular mapping and QTL analysis

Linkage groups were constructed by using JoinMap® 3.0 software (Van Ooijen and Voorrips 2001), and interval mapping was carried out with MapQTL® 5 software (Van Ooijen 2004). Interval mapping (IM) was carried out with the average of each trait. The permutation tests (determined by 1000 iterations) indicated minimum LOD scores between 1.5 and 2.1 at P=0.05 significance level (Van Ooijen 1999).

### Results

In the experiments, 135 DH lines of the Plainsman V./Cap­pelle Desprez population were tested in glasshouse under ds and ww conditions for three years. Yield-related agronomic traits, plant height and root dry mass were measured; HI was calculated.

**Phenotypic results**

The two parental varieties and 135 DH lines were grown in pots for the phenotyping of drought-responsive traits for three years. In the experiments, all traits showed lower values under stress condition than under ww condition (S1.). The phenotype results of the 2015-year experiment have been reported earlier (Nagy et al. 2017). Within the experiments significant variation between the tested DH lines was measured. Pl had less GY under ww conditions compared to CD. On the other hand, under ds conditions Pl had less yield depression compared to CD. In the experiments 2014, 2016 the highest $h^2$ value was found for HT and PH, the lowest value was for GY (S1.)

Significant correlations were found between traits (data not shown). The PH, HT, BM traits were positively correlated with each other under both conditions. GY under ww conditions positively correlated with BM ($r = 0.573$), SW ($r = 0.439$), GNE ($0.360$) at the 0.01 probability level.

A different result was observed under ds conditions, namely GY positively correlated with PH ($r = 0.175$) at the 0.05 probability level. Furthermore, negative correlation was observed between GY and HT ($r = -0.185$) at the 0.05 probability level. Also, positive correlation was found between GY and BM ($r = 0.428$), SW ($r = 0.758$), GNE ($r = 0.540$) under ds conditions at the 0.01 probability level.

### Marker analysis and map construction

The total marker dataset included 897 DArT markers. The created 36 linkage group consisted of 810 DArT markers and represented the 21 chromosomes covering a genetic distance of 1317 cm. The D genome had the lowest map distance and number of markers. For chromosome 1D- 11, 4D- 2, 5D- 2, and 6D- 5 markers were mapped. The average map length was 62.5 cm/chromosome.

### QTL analysis

In total 54 QTL regions were detected across the three years and two water regimes with 10 traits in the Pl/CD DH population (Table 1). The QTL distribution was balanced between the two water regimes. In total 22 QTL were detected under ds conditions; another 19 QTLs were found in the ww treatment. Furthermore, 13 QTL were detected under both conditions. In addition, 2 QTL were detected in all years and water regimes associated with PH on chromosome 4B, 6B. The QTL frequency was the highest on the B genome (55.5%), on the A genome 23 QTL were detected (42.5%). Only 1 QTL was identified on the D genome (1.8%). The highest
Table 1 The detected QTLs for agronomic traits of the Plainsman V/Cappelle Desprez DH population under two water regimes (ww; ds) for three years (2014–14; 2015–15; 2016–16) in glasshouse

| Trait | Environment | CHR | Marker interval | cM    | LOD  | A   | R²  |
|-------|-------------|-----|-----------------|-------|------|-----|-----|
| PH    | 15ww, 16ww  | 1A  | wPt-5367-wPt-8016 | 51.6–57.3 | 2.82 | −2.47 | 9.2 |
|       | 15ds        | 2B  | wPt-7715-wPt-9978 | 51.83–54.48 | 2.07 | −1.70 | 7.0 |
|       | 14ww,14ds   | 3B  | wPt-6043-tPt-6487 | 96.1–106.9 | 3.30 | −2.48 | 9.9 |
| all   | 4B          | 5B  | wPt-743712-wPt-9666 | 13.22–27.15 | 2.84 | 1.85  | 9.2 |
| all   | 6B          | 7D  | wPt-663764-wPt-2175 | 40.21–47.04 | 2.22–3.07 | −2.39 | 7.3–17 |
| HT    | 15ww, 16ww,15ds,16ds | 1B  | wPt-3950-wPt-1973 | 0.0–11.81 | 2.56–3.18 | −1.49 | 8.5–10.1 |
|       | 15ds        | 2B  | wPt-5250-wPt-744643 | 57.78–60.23 | 2.40 | 1.27  | 7.9 |
|       | 14ww, 16ww  | 3B  | wPt-9826-wPt-741322 | 41.4–45.24 | 2.08–4.07 | −0.26 | 6.9–16.3 |
| BM    | 14ww,15ww   | 3B  | wPt-6376-wPt-9514 | 110.9–115.1 | 7.97 | −3.79 | 23.8 |
|       | 14ds        | 5B  | wPt-743712-wPt-9666 | 13.22–27.15 | 2.84 | 1.85  | 9.2 |
| SW    | 13ds        | 1A  | wPt-664698-wPt-734301 | 96.5–99.17 | 3.07 | 0.04  | 21.8 |
|       | 14ww,15ww   | 1B  | wPt-3266-wPt-2597 | 134.3–145.0 | 2.92 | 0.07  | 9.3 |
|       | 14ww,16ww,15ds,16ds | 3B  | wPt-9826-wPt-741322 | 41.4–45.24 | 2.08–4.07 | −0.26 | 6.9–16.3 |
|       | 16ww        | 5B  | tPt-8942-wPt-0963 | 38.09–53.71 | 2.52 | −0.05 | 8.2 |
| SL    | 14ww,14ds,15ww,16ww | 1A  | wPt-741357-wPt-6280 | 0.0–16.74 | 3.97 | −0.39 | 12.7 |
| GNE   | 15ww        | 2A  | wPt-1722-wPt-731381 | 0.00–9.82 | 2.66–2.97 | −0.38 | 8.6–11.1 |
|       | 14ds,16ds   | 2B  | wPt-6511-wPt-5759 | 58.91–68.53 | 2.88 | 0.33  | 9.4 |
|       | 14ww,16ww,14ds | 3B  | wPt-11218-wPt-0212 | 76.66–82.62 | 2.99 | 0.36  | 10.6 |
|       | 16ww        | 5B  | wPt-5092-wPt-1304 | 105.88–142.75 | 3.30 | −0.10 | 10.6 |
|       | 15ww,16ww   | 6A  | wPt-666773-wPt-5654 | 105.97–117.11 | 2.29–3.44 | −0.34 | 7.5–11.0 |
|       | 15ww,16ww, 14ds | 6B  | wPt-656999-wPt-0432 | 59.3–62.6 | 2.82 | −0.06 | 12.8 |
|       | 15ww,14ds,15ds,16ds | 6B  | wPt-666773-wPt-6696 | 105.97–118.24 | 3.24–4.96 | 3.04 | 10.5–15.7 |
|       | 14ww,15ww   | 7A  | wPt-5949-wPt-3992 | 73.12–107.32 | 3.64–3.67 | 0.38  | 12.5 |
|       | 15ww        | 1A  | wPt-744613-wPt-8016 | 40.5–57.34 | 3.36–4.66 | −1.78 | 12.7–17.4 |
|       | 15ds        | 1B  | wPt-2575 | 185.10–191.02 | 2.37 | 1.40  | 7.7 |
| RDM   | 15ds        | 1A  | wPt-9938-wPt-669499 | 51.61–59.35 | 3.81 | 0.077 | 12.0 |
|       | 15ds        | 2A  | wPt-1772-wPt-743211 | 0.00–15.52 | 2.28 | 0.005 | 7.5 |
number of QTL was detected with the TGW (9), the less with BM (2).

During the experiments 10 agronomic traits were measured. QTL related to HT were identified on chromosome 1B (wPt-6376-wPt-1975), 2B (wPt-5250-wPt-744643), 3B (wPt-6376-wPt-9514), 5B (wPt-5250-wPt-0935). The 1B QTL was detected under both conditions in 2016, the 2B QTL was localized in ds conditions in 2015, the 3B and 5B QTL was found in ww conditions (Table 1, Fig. 1). The HT QTL explained the 7.9–23.8% of the phenotypic variance.

On chromosome 1A, 2B, 3B, 4B, 5B, 6B, 7D, PH-related QTL were detected (Table 1, Fig. 1) In addition, two QTL were identified in all years and treatment, which were localized on chromosome 4B (wPt-5334-wPt-5497) and 6B (wPt-663764-wPt-2175), the first one explained the 9.7–37.3% of the phenotypic variance, the other one had smaller effect, 7.3–17%. QTLs were identified on chromosome 3B under ww conditions and on chromosome 6B for ds treatment related to BM.

During the experiments five yield-related traits were measured and in total 30 QTL were identified for them. QTL on chromosome 1A (ds), 1B (ww), 3B (ww, ds), 5B (ww) were detected with SW and they explained from 6.9 to 21.8% of the phenotyping variance. Another seven QTL was located with SW on chromosome 1A (ww, ds), 2A (ww, ds), 2B (ds), 3B (ww, ds), 5B (ww), 6A (ww), 7A (ww), explaining the 8.5–12.7% of the phenotyping variance (Table 1). The GNE QTL was located on chromosome 2A (ww), 3B (ww, ds), 6A (ww, ds). In total seven QTL was detected for GY, accounting for 8.6 to 24.0% of the phenotypic variation. None of them was identified for both water supply level. The RDM QTL explained from 7.5 to 15.6% of the phenotypic variance (Table 1).

The RDM was measured only in one-year 2015 and seven QTL were detected with this trait. The QTL were located on chromosome 1A, 2A, 2B, 3A, 3B, 4B, and 7A (Fig. 1). None of them was identified under both water supply level. The RDM QTL explained from 7.5 to 15.6% of the phenotypic variance (Table 1).

Discussion

Phenotypic results, correlation analysis

The effect of ds on wheat DH lines was evaluated in pot experiments using two different water regimes (ww = 60% of the soil water capacity, ds = 20% of the soil water capacity) for three years (2014–2016) in glasshouse. The average yield of the DH population was reduced by 50.5%, 65.8%, and 70.8% under ds conditions, respectively, compared to ww conditions in the experiments. Varga et al. (2015) reported similar results in their glasshouse experiment. Czyczylo-Mysza et al. (2018) measured 10–70% yield loss in their drought tolerance experiment.

Many drought tolerance research focused on GY and its relation to other traits. Medium strength positive correlation was found in the experiments between GY and PH under ds conditions. In agreement with the result Kumar et al. (2018) and El-Feki et al. (2018) reported positive correlation between the two traits. On the other hand, Khan et al. (2005) reported negative correlation. The yield-related traits (GNE, TGW) showed positive correlation with GY under both conditions. These results were like those, Khan et al. (2005); El-Feki et al. (2018); Kumar et al. (2018); Wang et al (2018), who reported strong positive correlation between the traits.

QTL mapping

QTL distribution

In total, 54 QTL regions were detected across the three years and two water regimes with 10 traits in the Pl/
CD DH population. The QTL distribution was balanced between the two water regimes. Twenty-three QTLs were detected only under ds conditions; another 18 QTLs were found only in the ww treatment. Furthermore, 11 QTLs were detected under both conditions. In addition, 2 QTLs were detected in all years and water regimes associated with PH on chromosome 4B, and 6B. The occurrence of QTL was the highest on the B genome (55.5%). On the A
genome 23 QTLs were detected (42.5%). Only 1 QTL was identified on the D genome (1.8%). The highest number of QTLs was detected with the TGW (9), the less with BM (2).

**Agronomic traits**

Heading time-related QTL was detected on 2D, 7D chromosome (Bogard et al. 2013, S 2.), 2D (Verma et al. 2004). On the contrary, none of those QTLs were localized in our
glasshouse experiment. The heading time QTL detected on chromosome 3B under ww conditions was previously reported by Marza et al. (2006) and McCarteney et al. (2005).

Many QTL were identified related to plant height, on 3B (Bennet et al. 2012a), 6A (Bennet et al. 2012b), 2B, 4B, 5D (Lopes et al. 2013), 4B, 4D (Gao et al. 2015), 2A (Edhaie et al. 2016). With the PI/CD DH population under ds conditions six QTL regions were identified, which were located on 2B, 3B, 4B, 5B, 6B and 7D chromosomes. The PH QTL on the 2B chromosome was reported by Marza et al. (2006), Mathews et al. (2008), Pinto et al. (2010), Thamasebi et al. (2017), El-Feki et al. (2018). The 3B PH QTL was reported by Marza et al. (2006), Shukla et al. (2014). The QTL on 4B chromosome was identified in all our experiments and was reported previously by Cadalen et al. (1998); Huang et al. (2004), Marza et al. (2006).

QTL regions on chromosome 2D and 5D were reported by Osipova et al. (2016) related to BM in drought stress treatment. Shukla et al. (2015) detected QTL on chromosome 3B, 3D, and 3A under drought stress conditions with BM. In addition, Xu et al. (2017) localized QTL region on the 1B chromosome with the same trait. On the other hand, none of the above-mentioned QTL was identified in our experiments. QTL on the 6B chromosome was detected under ds conditions and on 3B under ww conditions and was identified with the Plainsman V./Cappelle Desprez DH population in glasshouse.

Yield, Yield-related traits

QTL regions related to grain yield and its related traits have been reported previously by numerous authors. Dashti et al. (2007) reported GNE QTL regions on chromosome 1B, 4A, 5B in ww treatment and on chromosome 5B, and 7A under ds conditions. GNE-related QTL regions on chromosome 1A (Huang et al. 2004), 3B (Marza et al. 2006; Shukla et al. 2014), and 6B (Huang et al. 2004; Marza et al. 2006; Kuchel et al. 2007) have been identified with the Plainsman V./Cappelle Desprez DH population too.

In the experiments in ww conditions five TGW QTL have been identified (1A, 3B, 4B, 6B, and 7A). The 4B QTL have been previously reported by Nezhad et al. (2012). In addition, Dashti et al. (2007) in ww treatment detected QTL on chromosome 2A, 4A, and 7A. In the ds treatment ten TGW QTL regions have been detected with the Plainsman V./Cappelle Desprez DH population. The QTL on chromosome 2B (Kordenaee et al. 2008; Maccaferri et al. 2008); 3B (Kordenaeej et al. 2008; Pinto et al. 2010; Shukla et al. 2014), 5B (Maccaferri et al. 2008), 6B (Maccaferri et al. 2008), and 7A (2012; Huang et al. 2004) QTLs have been previously reported. The QTL on 1A chromosome, which was identified in both conditions in the experiments, haven’t been previously reported.

Yield-related QTL regions were identified on the following chromosomes under drought stress conditions: 1A (Bennet et al. 2012b), 1B (Pinto et al. 2010; Lopes et al. 2013), 2D (Hamza et al. 2017; El-Feki et al. 2018), 3A (Hamza et al. 2017), 3D (Kuchel et al. 2007), 4A (Kirwgi et al. 2007; Pinto et al. 2010; Lopes et al. 2013; Shukla et al. 2014; Tahmasebi et al. 2017), 4B (Pinto et al. 2010; Lopes et al. 2013), 4D (Pinto et al. 2010; Lopes et al. 2013), 5A (Hamza et al. 2017; El-Feki et al. 2018), 5B (Kuchel et al. 2007; El-Feki et al. 2018), 5D (Kadam et al. 2012), 6B (Pinto et al. 2010; Lopes et al. 2013), 6D, 7A (Hamza et al. 2017), 7B (Kuchel et al. 2007; El-Feki et al. 2018) 7D (Pinto et al. 2010; Lopes et al. 2013). From the above-mentioned QTL the 1A, and 6B QTL were identified under ds conditions in the glasshouse experiments.

HI-related QTL region was identified on chromosome 1A, 3B and 6A with the Plainsman V./Cappelle Desprez DH population under ww conditions. In addition, on chromosome 1A HI-related QTL was identified in ds conditions. Kadam et al. (2012) reported QTL with HI on chromosome 1B, 2D, 4B, and 5A in drought treatment. On the other hand, Shukla et al. (2014) identified QTL with this trait under drought conditions on chromosome 2B, 3B, 3D, 4D (Pinto et al. 2010; Lopes et al. 2013), 5D (Hamza et al. 2017; El-Feki et al. 2018), 6B (Pinto et al. 2010; Lopes et al. 2013), 6D, 7A (Hamza et al. 2017), 7B (Kuchel et al. 2007; El-Feki et al. 2018) 7D (Pinto et al. 2010; Lopes et al. 2013). From the above-mentioned QTLs the 1A, and 6B QTL were identified under ds conditions in the glasshouse experiments.

Root dry biomass

Zhang et al. (2014) reported QTLs associated with root length on chromosome 5A. Liu et al. (2013) reported that genotypes with the greater root vigor under drought conditions showed the lowest yield reductions under severe water stress and also detected QTL associated with root length on 1A chromosome. Edhaie et al. (2016) found that root system traits have positive effects on wheat grain yield, particularly in drought conditions. They detected QTL on 2D, and 3A related to total root biomass. Kadam et al. (2012) reported QTL region on chromosomes 2D and 4B with RDM under drought stress. QTLs were identified under ds conditions with the PI/CD DH population on the 2A, 2B, 3B, 4B, and 7A chromosomes related to RDM in our experiments. Christopher et al. (2013) reported QTL with RDM in the same position on the 3B chromosome.

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