Mapping QTLs for yield and yield components under drought stress in bread wheat

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ABSTRACT

A mapping population of 118 F2:7 recombinant inbred lines from a cross between a drought tolerant Iranian landrace, Tabassi, and a non-drought tolerant European wheat variety, Taifun, was grown in three drought stress environments: under natural post anthesis drought stress in Iran, under a rain shelter in Hungary, and under post anthesis drought stress induced by a chemical desiccant in Austria. QTLs were identified for yield and yield components, based on a linkage map of 202 SSR markers.

INTRODUCTION

Bread wheat is the most important crop in Iran, providing half of the food supply. Of its production area 60% is located in arid and semi-arid regions. Under this condition, wheat is permanently challenged by drought, along with nutrient deficiency of the soil and other kinds of biotic and abiotic stresses. This challenge results, if not always but frequently, in a partial to drastic reduction of yield.

During the last two decades, several studies in wheat, mostly utilizing inter-varietal substitution lines, revealed some of the major chromosomal regions controlling plant response to drought and other abiotic stresses. These fundamental findings would help to better understand the genetic basis of crop performance (yield) under stress (Cattivelli et al. 2002). On the other hand, due to the complexity of this trait and the difficulties of field evaluation under stress conditions, very few studies were carried out targeting QTLs for yield and particularly yield under drought stress. Quarrie et al. (2005) evaluated a population of 96 DHs from a cross between Chinese Spring and SQ1 (a high ABA-expressing breeding line) at 24 location-treatment-year combinations, including nutrient, drought and salt stress treatments. Seventeen clusters of QTLs were identified on all seven chromosome groups of wheat. In a most recent study (Kuchel et al. 2007), a population of 192 DH lines from a cross between two Australian wheat varieties differing in yield was used to dissect QTLs for yield and its components, at 18 site-year combinations. They found 3 clusters of QTLs on chromosomes 1B, 4D, and 7D. This study and the one by Quarrie et al. (2005) can be considered to be the most valuable QTL studies for yield, regarding the number of location-year combinations, including drought stress conditions. The main objective of the present study was the identification of potential QTLs controlling yield and yield components under drought stress conditions (Kordenaeej 2008).

MATERIALS AND METHODS

Two spring wheat genotypes, contrasting in all agronomic and morphological traits of interest, a typical Iranian drought tolerant landrace, ***Tabassi,*** and a highly bred and non-drought-tolerant European wheat variety, ***Taifun***, were crossed to develop a mapping population, consisting of 118 F2:7 recombinant inbred lines (RILs), by single seed descent method (Kordenaeiij 2008). Field experiments were conducted in three locations: Tulln-Austria, Ilam-Iran (IRN), and Szeged-Hungary (HUN). Fifty seeds of each F2:7 line were planted 2007 at the recommended time for spring wheats at each location, in double rows with 17 cm between the rows and 30 cm between the double rows, with a plant distance of 5 cm within the rows. To determine the experimental error, five check varieties: the two parents, Tabassi and Taifun, the varieties Kärntner Früher, the German spring wheat variety Trappe, and one local variety were included in four replications, randomized, representing an augmented experiment, based on a randomized complete block design with four blocks. The experiments in Hungary were conducted in two environments. One was grown under rainfed conditions, the other under an electro automated shelter, preventing plants to receive any rain (HUN-Str), providing a controlled drought stress, starting after tillering. Moreover, to simulate post anthesis drought, which is the dominant drought stress in Iran, in a separate experiment in Tulln, Austria, potassium iodide (KI) was applied two weeks after anthesis. Phenotypic data for grain yield per ten spikes (Yld), grain number per ten spikes (Gps), 1000-kernel weight (Tkw), spike length (Sln), spikelet per spike (Sps), plant height (Pht), and ear emergence time (Eet) were collected. A linkage map, based on 202 polymorphic SSR markers and three morphological traits, i.e. *awnedness*, *spike pubescence* and *flag leaf waxyness* was constructed using JoinMap version 3.0 (Stam 1993). Broad sense heritability (H^2) for all agronomic traits was calculated by regression of the F2:7 means on the mid-parent values (Falconer and Mackay 1996). QTL analysis was done by composite interval mapping (CIM; Zeng 1993) using Windows QTL Cartographer version 2.5 software (Wang et al. 2007). A permutation test (Doerge and Churchill, 1996) was performed at a significance level of $P<0.05$, resulting in an average value of LR=14 to reach a minimum LOD threshold of 3. Forward and backward regression was employed to select cofactors for CIM. The p (F_{in}) and p (F_{out}) thresholds were 0.05, and the maximum number of 20 cofactors was used according to the formula 2(ÿ*n*) – 2, where *n* is the population size (Piepho, 2001). CIM model 6 was used with a 10-cM window size and 1-cM walk speed. A QTL was declared when the LOD score was greater than 3. Graphical maps of chromosomes were generated using MapChart version 2.1 software (Voorrips, 2002).

RESULTS AND DISCUSSION

Under drought stress Tabassi, as a drought tolerant landrace, appears superior to Taifun, a non-drought tolerant cultivar, in total yield and 1000-kernel weight. These advantages are mainly due to the clear differences between the two genotypes in (1) root mass and development, as a major constitutive trait, (2) early emergence, as a phenological event, and (3) the difference in plant height. All these characteristics allow Tabassi to have a significantly higher and more stable yield under drought stress, compared to Taifun. From this point of view, Tabassi and the RIL- and a BC2F4 population developed from the cross with Taifun are valuable genetic sources for further studies on drought stress tolerance. Moreover, due to its geographic origin, Tabassi has already been used in salinity and heat tolerance studies, therefore, this genotype can also be of great value to investigate the genetics of these traits as well. Finally, the material may enter practical breeding programs targeting tolerance of drought, salinity and heat stresses.

For QTL detection a relatively sparse map, consisting of evenly spaced markers, is adequate (Collard et al. 2005). Our present study supports this idea. For example, chromosome 3B with the highest number of markers (18) carried 0.8 QTLs per marker. Chromosome 4B, with 10 markers and the smallest average genetic distance between its marker loci (6 cM), had only 0.3 QTL per marker. In contrast, chromosome 4D with 8 markers and an average map distance of 13.1 cM contained the highest number of QTLs per marker (2.4). Out of the 202 linked SSR-loci on the map, 32.7% showed significant association with the QTLs. This observation also indicates that genes are not evenly distributed in the wheat genome. Uneven distribution was observed too for parental QTLs within and between the genomes. Normal distribution of yield and yield components among RILs in each of the five experiments, and significant RILs x environment interaction showed the polygenic inheritance of yield and its components, involving several QTLs. The high estimates of heritability strengthen the validity of the QTLs. A total of 46 major QTLs were identified for seven traits (an average of 6.6 QTLs per trait). Major QTls for Yld were located on chromosomes 3B, 4D, 6D and 7B, for Gps on chromosomes 3B, 4A, 5B, 7A and for Tkw on chromosomes 3D, 4D, 5A, 5B, 5D and 7B. Chromosome 4D can be introduced as a very gene-rich region, containing QTLs detected mainly under drought stress. It contributes the highest number of QTLs (19), with an average of 1.8 QTL per 10cM. Indeed, out of 19 QTLs, 14 were identified under drought stress, i.e. 3 QTLs for Yld and 2 for Gps in IRN and under KI, one for Tkw and Sln each, both in IRN, 5 QTLs for Pht in IRN and HUN-Str, and 2 QTLs for Eet in IRN. The positions of these QTLs, as found in the present study, are in complete synteny with the same QTLs identified by McCartney et al. 2005. The distance between the common marker, *Xgwm194,* and the common QTLs for Yld, Tkw, Pht and Eet is nearly the same in the two maps (Kordenaeij 2008).

The KI-experiment has proven very successful to provide conditions for studying the effect of post-anthesis drought, simulating closely the natural drought condition in Iran. Moreover, it was very efficient in QTL detection with respect to their number and synteny to those found under natural stress condition in Iran.

In addition to the importance of chromosome 3A for QTLs for agronomic traits, we emphasize the importance of 3B, along with 3A, as the main region for spike length, and together with 3D, as the main region for grain per spike (Kordenaeiij 2008). The significance of 7A showing QTLs for yield under stress and 7B under non-stress condition is in complete agreement with results reported by Quarrie et al. (2006).

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