



Drought resistance of wheat alien chromosome addition lines evaluated by membership function value based on multiple traits and drought resistance index of grain yield



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ABSTRACT

Drought is the single greatest abiotic stress leading to yield loss of wheat worldwide. The long-term domestication and selective breeding in artificial environments may have reduced the drought resistance of wheat. Wheat alien chromosome addition lines, with chromosomes derived from wild species, may possess drought resistant genetic potential and could serve as a bridge for transferring those traits to wheat. The drought resistance of 82 wheat alien chromosome addition lines along with their common parent Chinese Spring were evaluated for 10 agronomic traits under both well-watered and water-stressed conditions. Spike length was the most stable trait while biomass plant⁻¹ was the most sensitive trait when subjected to drought stress. Evaluation of heritability and correlations with yield plant⁻¹ suggested that plant height, peduncle length, distance between spike and flag leaf, grain number spike⁻¹ and thousand-grain weight could be used as indicators of drought resistance. The membership function value of drought resistance (MFVD) based on those traits and grain yield plant⁻¹, indicated 26 of the 82 wheat addition lines expressed high drought resistance. Higher MFVD was observed in the *Agropyron elongatum* 3E addition line in two years, and it was considered as the most drought resistant material. Analysis of the yield plant⁻¹ suggested that the drought resistant addition lines identified by MFVD were drought resistant but not very high-yielding, thus they could be used to improve germplasm with high-yield potential but low drought resistance. The drought resistance index (DI) based on yield plant⁻¹ indicated that 10 addition lines included both drought resistance and greater grain yield, which could be used in moderate stressed areas for improving drought resistance. Among them, addition lines with *Aegilops peregrina* 4SV and *Ae. peregrina* 3UV chromosome showed excellent performance and could be further investigated in drought resistance studies or breeding programs.

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1. Introduction

Wheat (*Triticum aestivum* L.) is a major staple food worldwide. The fast-growing global population and the resultant growth in food consumption is increasing demand for wheat production.

Abbreviations: CS, Chinese Spring; WW, well-watered; WS, water-stressed; PH, plant height; PL, peduncle length; DSL, distance between spike and flag leaf; SL, spike length; TN, tiller number; SN, spikelet number; GNS, grain number spike⁻¹; TGW, thousand-grain weight; BP, biomass plant⁻¹; YP, grain yield plant⁻¹; ANOVA, analysis of variance; H², broad sense heritability; DC, drought-tolerant coefficient; MFVD, membership function value of drought resistance; DI, drought resistance index.

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However, with global climate change, the stability and productivity of wheat are affected by various abiotic stresses with drought being the most serious factor affecting global wheat production. Although irrigation can minimize the losses caused by drought, in the 12 distinct mega-environments recognized by CIMMYT where wheat is produced, only a small area can be irrigated (Rajaram et al., 1993; Braun et al., 1996). In addition, periodic drought will also be a problem even in normally favorable environments. Thus, development of high-yielding wheat varieties that can perform in water-limited environments is the most viable solution to stabilize and increase wheat production under current and future climatic conditions.

Domestication and selective breeding has limited the genetic diversity of wheat, leading to cultivars adapted to artificial environments which has resulted in reduced resistance to drought stress (Kumar et al., 2008; Budak et al., 2013). To produce new drought resistant cultivars, plant breeders must identify germplasm with

increased drought resistance. One opportunity is presented by the exploitation of wild germplasm of wheat. *Triticum dicoccoides* is an important source of drought-related genes and is highly suitable as a donor for improving drought resistance in cultivated wheat species (Peleg et al., 2008; Peng et al., 2013); several drought tolerance genes of *T. dicoccoides* have been identified and characterized (Lucas et al., 2011a,b; Kuzuoglu-Ozturk et al., 2012). It seemed that the interspecies variations are more profound than intraspecies variations. For example, *Aegilops tauschii* is more drought tolerant than *Triticum* and wild emmer wheat (Ashraf et al., 2009; Nevo and Chen, 2010). Wheat alien chromosome addition lines created with individual chromosomes derived from wild germplasm, have been used to study the effect of individual chromosomes. By studying a set of wheat-rye disomic addition lines, Mohammadi et al. (2003) found that most of the genes controlling drought tolerance were located on chromosomes 7R, 5R and 3R. A wheat translocation line with an alien chromosome segment (7DL) from *Agropyron elongatum* was found to have improved water stress adaptation and higher root and shoot biomass compared with the control genotypes (Placido et al., 2013). The presence of the 1RS translocation in spring cultivar “Pavon” increased root biomass and was more tolerant to field environmental stresses than Pavon (Ehdaie et al., 2003). These studies indicate that alien chromosome addition lines are promising sources of drought-related genes that could be used in wheat improvement programs.

Drought resistance is a quantitative trait with a complex phenotype affected by the plant's developmental stage, thus making the assessment or evaluation more difficult. During the last decades, progress has been made from empirical breeding, which has taken yield as the main trait for selection in target environments (Araus et al., 2008). But yield, a quantitatively inherited trait, is characterized by low heritability and a high genotype-by-environment (GE) interaction (Jackson et al., 1996), which makes the process very time-consuming (Blum, 1988). An alternative approach is phenotype based selection in which lines are selected on the basis of specific traits determined to be beneficial under water deficient conditions (Bidingger and Witcombe, 1989). Then selection for drought resistance could be simplified by identifying morphological or physiological characters that are closely linked to yield in water-limited environments. For a secondary trait to be useful, it must comply with at least three requirements, significant genetic correlation with yield under drought stress, higher heritability than yield and genetic variability within the species (Bänziger et al., 2000; Araus et al., 2002; Lafitte et al., 2003; Royo et al., 2005). Studies showed that morphological traits such as number of tillers, number of grains spike⁻¹, fertile tillers plant⁻¹, 1000-grain weight, peduncle length, awn length, plant height, spike length and grain weight spike⁻¹ were drought sensitive and that these traits have been proposed as important selection criteria for drought resistance (Blum, 2005; Nouri-Ganbalani et al., 2009; Aminzadeh, 2010). However, both drought screening and selection gains have indicated that different selection criteria based on secondary traits may vary significantly with populations and germplasm used. Therefore, it is still necessary to evaluate different selection criteria using more diverse germplasm (Lu et al., 2011).

This study evaluated the drought resistance of 82 wheat alien chromosomes addition lines along with their common parent, Chinese Spring, for major agronomic traits under both well-watered and water-stressed conditions. The objectives of this study were to evaluate the use of multiple phenotypic traits as secondary traits for drought resistance assessment; and to identify wheat alien chromosome addition lines with high drought resistance for possible utilization in wheat improvement program.

2. Materials and methods

2.1. Plant materials

A total of 82 previously identified wheat disomic alien chromosome addition lines ($2n=44$) and their common parent, Chinese Spring (*T. aestivum* L., $2n=42$), were used as materials in this study. These addition lines were kindly provided by Prof. Tsujimoto Hisashi, Arid Land Research Center, Tottori University, Japan. The alien chromosomes of 39 addition lines were derived from the wild genus *Aegilops*, 13 lines from *Leymus*, 11 lines from *Agropyron*, 6 lines from *Hordeum*, 5 lines from *Secale*, 5 lines from *Elymus* and 3 lines from *Psathyrostachys*.

2.2. Rain-out shelter experiments

The experiments were conducted for two wheat growing seasons (October 2012 to June 2013, and October 2013 to June 2014) in the rain-out shelter of the Institute of Water Saving Agriculture in Arid Regions of China, Northwest A&F University, Yangling, Shaanxi, China (34°16' N, 108°04' E, elevation 526 m). The materials were evaluated under two water treatments, including well-watered (WW) and water-stressed (WS) regimes. Wheat addition lines were arranged in a randomized complete block design with two replications. Each line was planted in two rows, 1.50 m in length and 25 cm apart. Seeds were sown by hand with an interval of 6.70 cm between seeds.

Both the WW and the WS plots were irrigated to enhance germination before sowing. The average gravimetric soil moisture content (0–100 cm in depth) was 15.67% when planting in 2012–2013 and 16.05% in 2013–2014. For each growing season, the WW and WS treatment was given a total of 210 mm and 120 mm irrigation, respectively. Both the WW and WS treatments were given an equal irrigation of 40 mm at tillering (Zadoks stage: Z20, Zadoks et al., 1974), stem elongation (Z30) and booting (Z39), respectively. After the booting stage, irrigation (30 mm per event) was only applied to the WW treatment at heading (Z55), flowering (Z65) and grain-filling (Z73). The rain-out shelter was open during growing seasons, and it was closed when there was rain. At maturity (Z92), the average gravimetric soil moisture content (0–100 cm in depth) measured under the WW and WS treatment was 12.31% and 10.48%, 12.81% and 10.92% after 2012–2013 and 2013–2014 growing seasons, respectively.

2.3. Agronomic traits assessment

Plant height (PH), peduncle length (PL), distance between spike and flag leaf (DSL), spike length (SL), tiller number (TN), spikelet number (SN) and grain number spike⁻¹ (GNS) were determined at maturity (Z92). PH was measured as the distance from the soil surface to the top of the spike (awns excluded) of the main tiller. PL was determined as the length between the base of spike and the first internode from the top. DSL was the distance from spike base to flag leaf ligule. SL was measured from the base of the spike to the tip excluding awns. The number of productive tillers was counted to determine TN per individual plant. SN and GNP were counted using the spike of the main tiller. Five individuals were measured for each genotype in every replication.

At harvest, 10 individual plants of each replication were hand-cut at ground level. Samples were air-dried at 35°C for three days and weighed before and after threshing as the above-ground biomass and grain yield. Then biomass plant⁻¹ (BP) and grain yield plant⁻¹ (YP) were calculated. One thousand grains of each genotype in every replication were weighed and the values were averaged as TGW.

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