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Investigating the Combining Ability and Genetic Constitution of Physiological Indicators of Drought Tolerance in Bread Wheat (*Triticum aestivum* L.) Using GGE Biplot Methods

Ezatollah Farshadfar • Hojjat Hasheminasab*

Department of Agronomy and Plant Breeding, College of Agriculture, Razi University, Kermanshah, Iran

Corresponding author: ***hojathashemi@gmail.com**

ABSTRACT

To study the combining ability and genetic constitution of physiological indicators of drought tolerance in bread wheat using GGE biplot techniques, an eight-parental diallel cross, excluding reciprocals, was grown in a randomized complete block design with three replications under two different water regimes (irrigated and rainfed) in the Agricultural Research Institute of Sararood, Kermanshah, Iran. Significant differences were found for yield potential (Y_p), stress yield (Y_s), relative water content (RWC) and leaf water potential (LWP). The result of biplot analysis showed that the Parent A, F, B, F and E were The best general combiners with positive effects, for improvement of Y, RWC, LWP, RWL and chlorophyll fluorescence **(**CHF) under drought conditions respectively, also parent C exhibited positive GCA for all traits. The crosses (A, C and H) × (B, F and G), (F and D) × (A, C and G), (F and E) × (A, H, C and D), (F, B and E) × (C, G and H) and (F and E) × (A and H) for Y, RWC, LWP, RWL and CHF were heterotic groups with different dominant tolerance genes (D1 and D2), respectively. The polygon view of the biplot indicated combining A × G and F × E produced the best drought tolerance hybrids for all the traits through integrated the four tolerance genes (A1, A2, D1, and D2). G was the best tester in all, as it was very close to the ideal tester. The results showed additive gene effects mainly that control the physiological indicators of drought tolerance. Thus, genetic gain in developing tolerance in bread wheat can be achieved through selection.

Keywords: bread wheat, drought, combining ability, genetic constitution, GGE biplot

Abbreviations: ATC, average tester coordination; **CHF**, chlorophyll fluorescence; **CRD**, completely randomized design; **GCA**, general combining ability; **GGE**, Genotype-by-Environment; **GY**, grain yield; **LWP**, leaf water potential; **RWC**, relative water content; **RWL**, relative water loss; **SCA**, specific combining ability; **Yp**, yield potential; **Ys**, stress yield

INTRODUCTION

Drought is one of the most significant factors among abiotic stresses that limit plant performance, growth and productivity in arid and semi-arid regions, recently global climate change has made this situation more serious. However, in certain tolerant crop plants physiological and metabolic changes occur in response to drought, which contribute towards adaptation to such unavoidable environmental constraints (Blum 1985; Farshadfar *et al*. 2000; Geravandi *et al*. 2011a). Among crop plants, wheat (*Triticum aestivum* L.) is a staple food for more than 35% of the world population and it is also the first grain crop in Iran (Golestani and Assad 1998; Farshadfar *et al*. 2011). Wheat is mainly grown on rainfed land about 35% of the area of developing countries consists of semi-arid environments in which available moisture constitutes a primary constrain on wheat production, so Wheat often experiences drought stress conditions during its growth cycle. Thus, Improvement of wheat productive for drought tolerance is a major objective in plant breeding programs for rainfed conditions (Farshadfar *et al*. 2001; Bayoumi *et al*. 2008). It is essential to understand the mode of inheritance and genes or gene products which are responsible for desired characteristics of drought tolerance at different stages of plant growth (Kaw and Khush 1986; Farshadfar *et al*. 2011b). Knowledge of the physiological and genetic functional relationships among traits would be beneficial to plant breeders in choosing traits for selection in breeding program (Ober *et al*. 2005). Also, concurrent physiological and genetic studies could speed up the process of evaluation of physiological traits (Farshadfar *et al*. 2008b; Khalil *et al*. 2010). Wheat breeding programs mostly involve hybridization, evaluation and selection of desirable genotypes. In addition, the assessment of combining ability and identify heterotic groups are elementary tools for selection of ideal genotypes (Blum 1985; Mall *et al*. 2010). The concept of combining ability was introduced by Sprague and Tatum (1942). Combining ability has a prime importance in plant breeding since it provides information for the selection of parents and also provides information about of involved gene action. The knowledge of genetic structure and mode of inheritance of different characters helps breeders to selection suitable breeding methodology for produced drought tolerance genotypes (Jensen 1970; Kiani *et al*. 2007). Plant breeding programs use different mating systems to study combining ability of quantitative traits. Diallel analysis has been often applied in genetic research to determine combining ability heterotic responses of agronomically more important traits within a set of genotypes (Baker 1978; Farshadfar *et al.* 2011a). There are several methods that can be used for diallel analysis. The mostly used one is the Griffings (1956) method, which partitions the total variance to general combining ability (GCA) variance of parents and specific combining ability (SCA) variance of crosses. Recently Yan and Hunt (2002) suggested the application of GGE biplot techniques for graphical analysis and presentation of diallel. Although the GGE biplot methodology was developed for multi-environment trial (MET) data analysis, but they stated that it should be applicable to all types of two-way data that assume an entry-by- tester data structure (Yan 2001). In MET data, genotypes are entries and environments are tes-

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Table 1 Analysis of variance for the characters under investigation.

S.O.V	**df**	**Mean square**					
		Yp	**Ys**	**RWC**	**RWL**	**CHF**	**LWP**
Replications	2	24.63**	0.47 ^{ns}	37.91^{ns}	0.17**	0.004^{ns}	697.21**
Genotypes	35	21.38**	1.86**	63.29**	0.02^{ns}	0.01ns	120.11*
Error	70	2.10	0.71	12.11	0.01	0.007	71.42
CV %	-	15.2	12.3	3.98	11.9	8.03	18.9

*; ** Significant at the 0.05 and 0.01 probability levels, respectively; ns, non significant.

ters. In diallel data, each genotype is both an entry and a tester (Yan 2002; Yan and Hunt 2002). The GGE biplot technique has also been used for diallel combining ability analysis of bread wheat (Bertoia *et al.* 2006). The objectives of the present investigation were to study (i) GCA and SCA as well as (ii) identification of heterotic groups and (iii) genetic constitution of physiological characters related to drought tolerance.

MATERIALS AND METHODS

Plant material and experimental conditions

The plant material consisted of eight - parent diallel cross excluding reciprocals, was carried out in the Agricultural Research Institute of Sararood, Kermanshah, Iran during year 2004 to 2005 (47° 20′ N latitude, 34° 20′ E longitude and 1351.6 m altitudes). Climate in this region is classified as semi-arid with a mean rainfall of 478 mm. Minimum and maximum temperature in the research station was -27 and 44°C, respectively. The cultivars used were 'Plainsman' (A), 'Regina' (B), 'Capelle desprez' (C), 'Chinese spring' (D), 'Shakha' (E), 'Saberbeg' (F), 'Karchia' (G) and 'Kobomugi' (H). The plant genetic materials (parents and F_1s) were grown in a randomized complete block design with three replications under irrigated and rainfed conditions. Single seeds were sown in 3 m rows and at 3 × 15 cm plant to plant and row to row distances, respectively. From each entry (parents and F1 s), five competitive plants were randomly selected from each replication for recording observations on the following characters:

Grain yield (GY)

GY was recorded under normal (Yp) and stress (Ys) conditions at physiological maturity stage. The physiological maturity stage was considered when 90% of seed changed color from green to yellowish and stopped photosynthetic activity.

Relative water content (RWC)

A sample of 5 leaves were taken randomly from the flag leaves of each genotype and fresh weight (FW) was measured. Then, samples were placed in distilled water for 24 h and reweighed to obtain turgor weight (TW). Leaf samples were oven dried and weight in 70°C for 72 h (DW). RWC was calculated using the following formula (Ober *et al.* 2005):

$$\text{RWC } (\%) = [\text{FW}–\text{DW}/\text{TW}–\text{DW}] \times 100$$

Leaf water potential (LWP)

Leaf water potential was measured on flag leaves of each replication using a pressure chamber (model PMS instrument CO., USA).

Relative water loss (RWL)

Five leaves were taken randomly from each genotype and weighted (W_1). The leaves were then wilted at 25°C for 2 h and weighed again (W_2). Then the samples were oven dried in 70°C for 72 h and reweighed (W_3). RWL was calculated using the formula suggested by Yang *et al.* (1991).

$$\text{RWL} = [W_1–W_2/W_3]\ [t_1–t_2/60]$$

Chlorophyll fluorescence (CHF)

From each line in each replication, five flag leaves were selected and the quantum yield was recorded after dark adaptation using a MINI-PAM instrument as:

$$\text{QY} = F_v/F_m$$

where F_v and F_m are variable and maximum fluorescence, respectively (Genty *et al.* 1989).

Statistical and genetic analyses

Statistical analysis was performed by SPSS ver. 16.0 (analysis of variance; ANOVA). The GGE biplot software was used to generate biplot figures for drought tolerance indicators and grain yield (Yan and Hunt 2002). Each parent was considered both an entry and a tester. A two-way matrix of entries and testers was generated from the mean values for hybrids, where rows were entries and columns were testers. The biplot model is as follows:

$$\hat{Y}_{ij} – \mu – \beta_j = \lambda_1\, \xi_{i1}\, \eta_{j1} + \lambda_2\, \xi_{i2}\, \eta_{j2} + \varepsilon_{ij}$$

where $\hat{Y}_{ij}$ is genotypic values of the combination between entry i and tester j; μ is the grand mean; β_j is the mean of all combinations involving tester j; λ_1 and λ_2 are the singular values for PC_1 and PC_2, respectively; ξ_{i1} and ξ_{i2} are the PC_1 and PC_2 eigenvectors, respectively, for entry i; η_{j1} and η_{j2} are the PC_1 and PC_2 eigenvectors, respectively, for tester j; and ε_{ij} is the residual of the model associated with the combination of entry i and tester j. When $i \neq j$, the combination is a hybrid.

RESULTS AND DISCUSSION

ANOVA revealed significant differences among parents and hybrids for Y_s, Y_p, RWC and LWP, indicating the presence of genotypic variability, different responses of genotypes to water stress condition and possible selection of drought tolerant genotypes under water deficit (**Table 1**). According to the results suggested that significant heterosis among parents and hybrids (Rastogi *et al.* 2010). Breeding for drought tolerance by selecting solely for grain yield may not be successful, because the heritability of grain yield under drought conditions is low (Golestani and Assad 1998; Geravandi *et al.* 2011). Several physiological criteria have been proposed for selecting resistant genotypes. RWC, RWL, STI, LWP and WUE were shown as screening techniques for discrimination of drought tolerance genotypes in bread wheat (Ober *et al.* 2005; Farshadfar *et al.* 2011c). In fact the development of any plant breeding program is dependent upon the existence of genetic variability, the efficiency of selection and expression of heterosis in the plant population (Farshadfar and Sutka 2002; Butorac *et al.* 2004; Ahmad *et al.* 2009).

Grain yield

The biplot for GY explained 65.3% (38.2 and 27.1% by PC1 and PC2, respectively) of the total variation, which, in conventional analyses (**Fig. 1**). The general combining ability (GCA) and specific combining ability (SCA) effects of the crosses (entries) were examined by drawing an average tester coordinate (ATC) view for entries (**Fig. 1A**). The small circle represents an average tester, which is defined by the average PC1 and PC2 values of all testers. The line

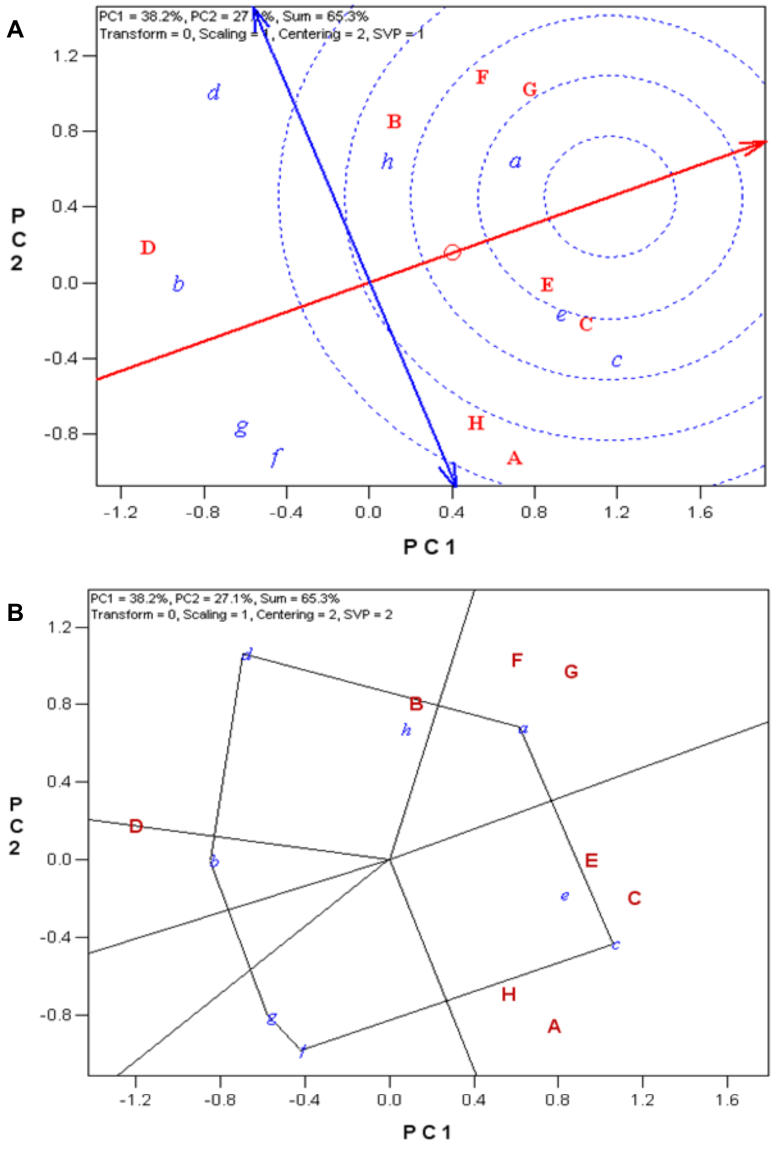

Fig. 1 Biplot showing (**A**) average tester coordinate (ATC) view and (**B**) polygon view of eight parents for grain yield in rainfed condition. Uppercase letters are testers and lowercase letters are entries of eight parents. Parents are: Plainsman (A), Regina (B), Capelle desprez (C), Chinese spring (D), Shakha (E), Saberbeg (F), Karchia (G) and Kobomugi (H).

passing through the biplot origin and the average tester, with an arrow pointing to the average tester, is called the ATC abscissa. The GCA effects of the entries are approximated by their forecasted on to the ATC abscissa (Yan 2001). As seen in **Fig. 1A**, entries a, c, e and h were on the positive side of the ATC abscissa suggesting that they had positive GCA effects and exhibited higher drought tolerance hybrids while entries b, d, g and f had negative GCA effects. Based on the distance between entry and ATC abscissa, entry a had the highest GCA effects and entries h and b had the lowest GCA effects (Malla *et al.* 2010). A higher GCA rate indicates that additive gene action was important and parents differed in the level of the tolerance to drought they contributed to the progeny (Butorac *et al.* 2004). The GCA effects of the entries are in the order of: a > c ≈ e > h > d > f > g ≈ b. According to Yan and Kang (2003), to explain the differences in GCA can be assumed that entries h and d (Group 2) had an additive gene for drought tolerance (A1) relative to entries f, g and b (Group 1), also entries a, c and e (Group 3) had an additional gene (A2) relative to Group 2. Baker (Baker 1978) reported that, when combining ability ratio approaches unity, GCA alone can predict the performance of the parents. The Biplot also displayed the SCA effects of the entries. The SCA effects of the entries were estimated based on the projection of the entries on the ATC ordinate (Yan 2001). Testers F, H and A, had the highest projected on the ATC ordinate from the biplot origin, so they had large SCA effects compared to other testers (**Fig. 1A**). Based on SCA, testers can be divided in two heterotic groups: testers B, F and G as one group and A, C and H as the other. Testers D and E falls between groups 1 and 2 and has a short vector. If it is assumed that heterosis arises from the accumulation of different dominant genes, then two groups must have different dominant drought tolerance genes that are designated as D1 and D2 (Farshadfar *et al.* 2011c). These results clearly indicated heterosis in crosses (A, C and H) × (B, F and G). The heterotic effect might be due to over dominance or epistatic effect of different dominant genes present in these parents (Farshadfar *et al.* 2008a; Khalil *et al.* 2010). The biplot (**Fig. 1B**) shows the polygon. It provided the best way to demonstrate the interaction patterns between entries and testers (Yan and Hunt 2002). The biplot was divided into six sectors, with entries a, b, c, d, f and g as the vertex entries, and are referred to as sector a, sector b, sector c, sector d, sector f and sector g, respectively. The biplot indicated that entry a was the best mating partners for F and G. Since the tester A was not in the sector a, all crosses between genotype A with F and G were heterotic (Rastogi *et al.* 2010). Entry d and b were the best mating with B and D respectively. Since tester D was not in sector d and tester b was not in the sector b, hybrid D × B exhibited higher tolerance than D × D and B × B (B and D

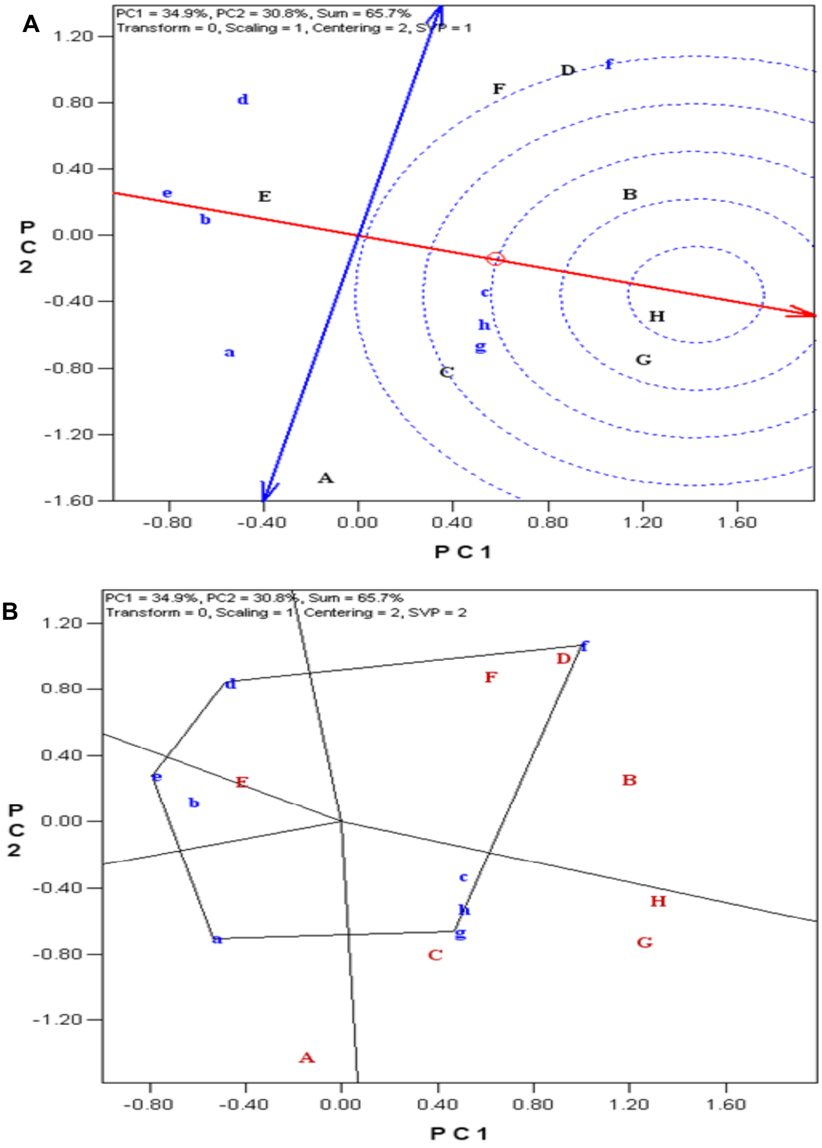

Fig. 2 Biplot showing (**A**) average tester coordinate (ATC) view and (**B**) polygon view of eight parents for Relative water content (RWC) in rainfed condition. Uppercase letters are testers and lowercase letters are entries of eight parents. Parents are: Plainsman (A), Regina (B), Capelle desprez (C), Chinese spring (D), Shakha (E), Saberbeg (F), Karchia (G) and Kobomugi (H).

pure lines). The biplot showed entry c produced best hybrids with tester C, A, E and H, Since C was in the sector c, all crosses between genotype C with A, E and H were not heterotic. Thus, the combination C × C (Pure line C) is the best among all crosses involving C. The biplot indicated no tester fell in the, g and f sectors, suggesting that these entries produced the poorest hybrids with some or all of the testers (Bertoia *et al*. 2006). Therefore, the best combination for improved drought tolerance were: seven hybrids involving C × C, C × A, C × E, C × H, A × F, A × G and D × B. The hybrids between C with A and H were the best hybrids relative to drought tolerance because they each integrated the four tolerance genes (A1, A2, D1, and D2). Also the crosses C × C and C × E might be have the four drought tolerance genes (A1, A2 and D2). In the **Fig. 1A**, the concentric circles are drawn to identify the best tester for assessing GCA of parents with hypothesized ideal tester at the center (Yan and Kang 2003). Clearly, tester E was the best tester in this data set, as it was very close to the ideal tester. Whereas, D was the poorest tester, as it is the least representative of all testers.

Relative water content

RWC is the appropriate physiological indicators for drought tolerance which related to water status and water potential in plant leaves (Ober *et al*. 2005; Geravandi *et al*. 2011). Maintenance of higher relative water content has been suggested as screening criterion for drought resistance (Blum 1985; Ahmad *et al*. 2009). The biplot for RWC explained 65.7% (34.9 and 30.8% by PC1 and PC2, respectively) of the total variation (**Fig. 2**). Entries f, g, h and c had positive GCA whereas a, b, e and d had negative GCA effects. The expression of positive GCA in these entries reveals the advantage of additive gene action (Baker 1978; Farshadfar *et al*. 2008a). The GCA effects of the entries are in the order of: f > c ≈ g ≈ h > a > b ≈ d > e. Based on the results can be assumed that entries f, g, h and c had an additive gene (A1) relative to entries a, b, e and d (**Fig. 2A**). Farshadfar *et al*. (2011a) reported that compared to other types of gene effects, highly additive gene effects for RWC trait will increase the success of selection for it. Entries a, g, f and d have the greatest distance from the ATC ordinate, so they had large SCA effects as compared to other entries (**Fig. 2A**). The biplot clearly indicates heterosis in crosses (F and D) × (A, C and G). If we assume that heterosis arises from the accumulation of different dominant genes, then the two groups must have different dominant drought tolerance genes that are designated as D1 and D2. These heterotic crosses can be easily exploited through heterosis breeding, while, in segregating generation, the transgressive segregates can be exploited through recurrent breeding and

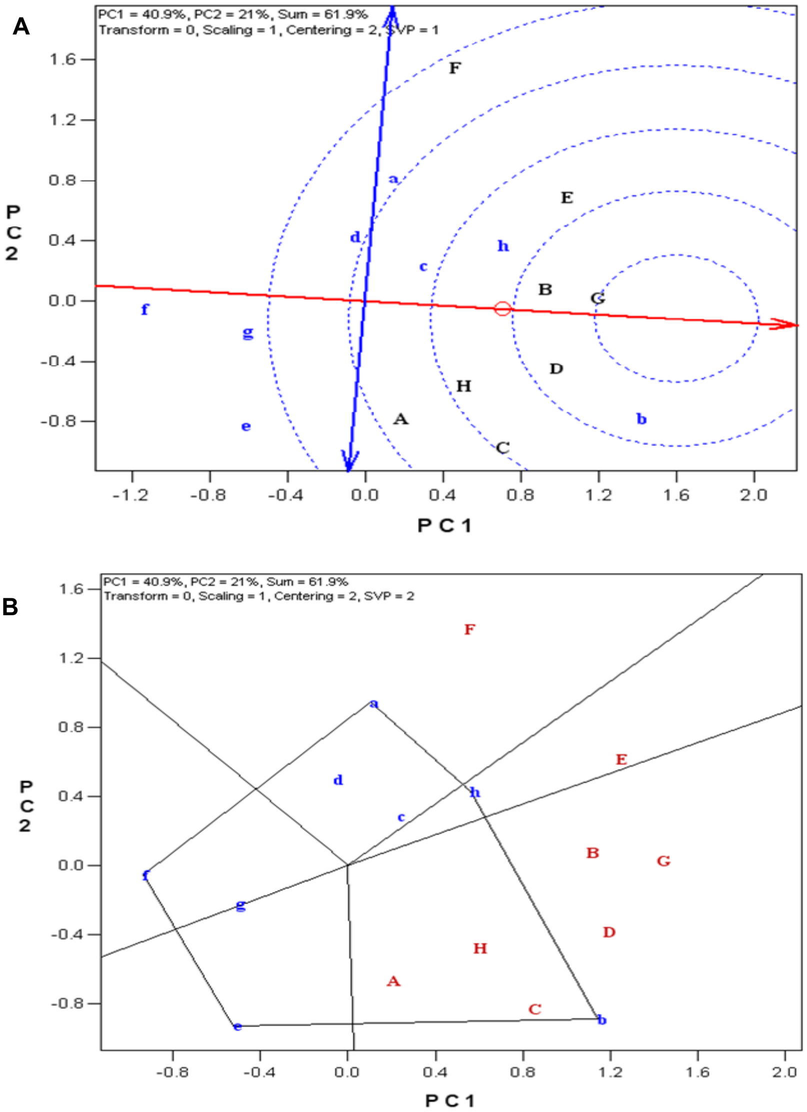

Fig. 3 Biplot showing (**A**) average tester coordinate (ATC) view and (**B**) polygon view of eight parents for Leaf water potential (LWP) in rainfed condition. Uppercase letters are testers and lowercase letters are entries of eight parents. Parents are: Plainsman (A), Regina (B), Capelle desprez (C), Chinese spring (D), Shakha (E), Saberbeg (F), Karchia (G) and Kobomugi (H).

biparental mating (Rastogi *et al.* 2010). The biplot (**Fig. 2B**) was divided into five sectors, with entries a, d, e, f and g as the vertex entries. The biplot indicated that entry g was the best mating partners for G, C, and H; entry f produced best hybrids with tester F, B and D; entry d and a were the best mating with E and A respectively. The biplot indicated No tester fell in the e sector, suggesting that entry e produced the poorest hybrids with some or all of the testers (Butorac *et al*. 2004). A single tester, A, fell into sector a, indicating that Pure line A was the best mating for A. Since G was in the sector g, all crosses between genotype g with C, G and H were not heterotic (Malla *et al*. 2010). Thus, the combination G × G (Pure line G) is the best among all crosses involving G, This condition also was similar in the f sector. In **Fig. 2B**, since D was not in the sector d, crosses between genotype D and E was heterotic. According to **Fig. 2A**, H was at the center of the concentric ring, suggesting that it was the ideal parent. Entry A and E were the farthest on the positive side of the ATC abscissa. Since RWC is suitable indicator for evaluate drought tolerance in wheat (Geravandi *et al*. 2011), thus the best combination for drought tolerance Based on the results of GCA and SCA were: nine hybrids involving G × G, G × H, G × C, F × F, F × B, F × B, F × D, A × A and D × E. These results suggested that the hybrids between G with G, H and C have the three tolerance genes (A1, A2, D2) and the hybrids between F with F, D and B have set of the three droughts tolerance genes (A1, A2, and D1). Also the crosses A × A and D × E have the two tolerance genes (A1 and D2) and (A1 and D1), respectively. Ahmad *et al.* (2009) reported additive, dominance as well as additive × additive genetics effects for RWC in cotton.

Leaf water potential

Crop plants avoid drought stress by enhanced capture of soil moisture, by limited crop water loss, and by retaining cellular hydration despite the reduction in LWP (Blum, 1985). LWP is considered to be a reliable parameter for quantifying plant water stress response (Golestani and Assad 1998). The biplot for LWP explained 61.9% (40.9 and 20% by PC1 and PC2, respectively) of the total variation (**Fig. 3**). Based on ATC abscissa, entries b and h have high GCA and f, g and e have low GCA. While entries a, d and c have intermediate GCA. Entry b had highest GCA followed by b > h > c > a ≈ d > e ≈ g > f. To explain the differences in GCA can be hypothesized that entries a, d and c (Group 2) had an additive gene (A1) for drought tolerance relative to entries f, g and e (Group 1), also entries b and h (Group 3) had an additional gene (A2) relative to Group 2 (**Fig. 3A**). Entries a, e and b had highest SCA effects due to their largest projections onto the ATC. Based to PC2 axis, the two heterotic groups (F and E) × (A, H, C and D) were observed with different dominant tolerance genes (D1 and D2). The biplot (**Fig. 3B**) was divided into five sectors, with entries b, h, a, f and e as the vertex entries.

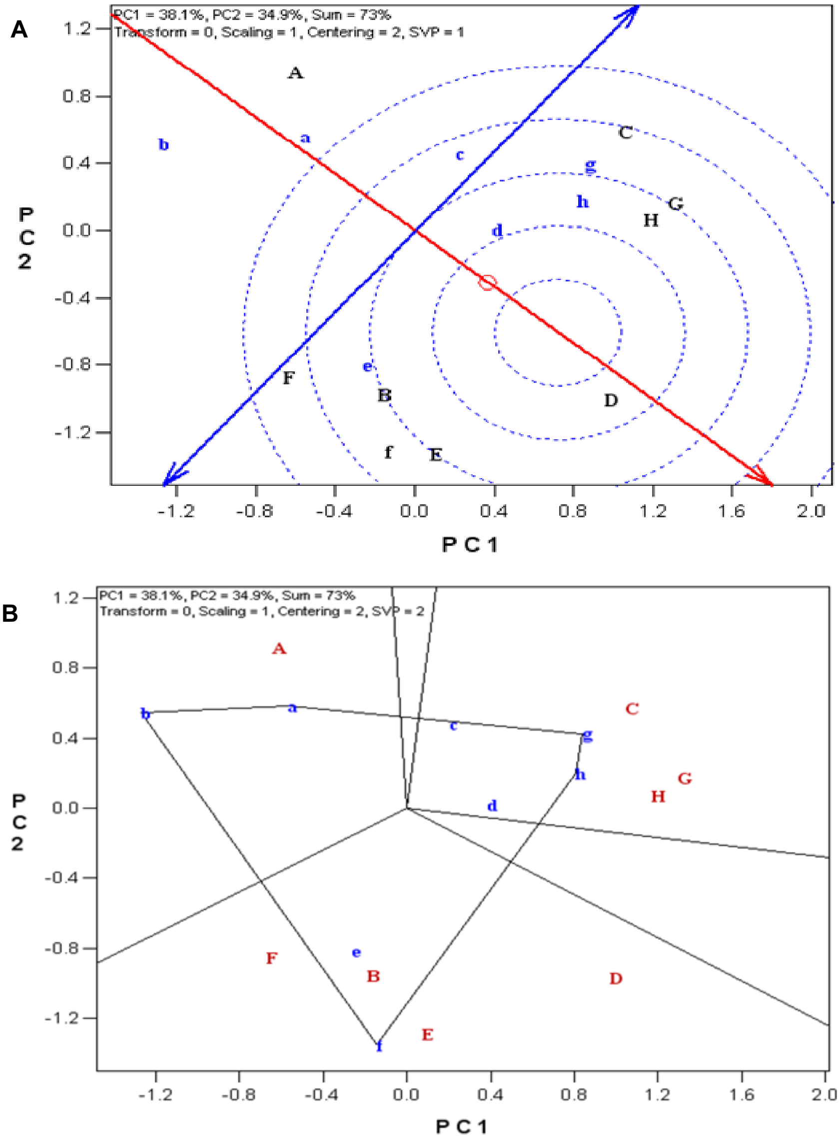

Fig. 4 Biplot showing (**A**) average tester coordinate (ATC) view and (**B**) polygon view of eight parents for relative water loss (RWL) in rainfed condition. Uppercase letters are testers and lowercase letters are entries of eight parents. Parents are: Plainsman (A), Regina (B), Capelle desprez (C), Chinese spring (D), Shakha (E), Saberbeg (F), Karchia (G) and Kobomugi (H).

The biplot indicated that entry b was the best mating partners for A, B, C, D, G and H. Since B was in the sector b, all crosses between genotype B with B, C, D, G and H were not heterotic (Bertoia *et al.* 2006). Thus, the combination B × B (Pure line B) is the best among all crosses involving B. The biplot indicated No tester fell in the e and f sectors, suggesting that entry e and f produced the poorest hybrids with some or all of the testers. Entry a and h were the best mating with F and E respectively. Since F and E was not in the sectors a and h, the crosses A × F and E × H were heterotic. According to the results, the best hybrids for drought tolerance were: eight hybrids involving B × A, B × B, B × C, B × D, B × G, B × H, A × F and H × E. The crosses B × A and B × D were the best hybrids relative to drought tolerance because they each integrated the four tolerance genes (A1, A2, D1, and D2). Due to the **Fig. 3A**, tester G was the best tester in all, as it was very close to the ideal tester. Whereas, F and A were the poorest tester as it is the least Representative of all testers. Jensen (1970) reported that the crosses involving high × low general combiners besides expressing favorable additive effects of high parent showed complementary gene action due to interaction between favorable genes contributed by the relevant parents.

Relative water loss

RWL, LWP and RWC are among the main physiological index indicating plant water status in relation with drought tolerance. Water status considered as a good indicator for differential cultivar behavior facing water stress (Blum 1985; Golestani and Assad 1998). The first two principal components described 73% (PC1 = 38.1% and PC2 = 34.9%) of the total variation for RWL (**Fig. 4A**). Base on the biplot, entry f has high GCA, a, b and c have low GCA and d, e, h and g have intermediate GCA. The ranking of entries to The GCA effects were f > e ≈ h > g ≈ d > c > a > b. To illustrate differences in GCA can be hypothesized that entries d, e, h and g (Group 2) had an additive gene (A1) for drought resistance relative to entries a, b and c (Group 1), also entry f (Group 3) had an additional gene (A2) relative to Group 2 (**Fig. 4A**). Farshadfar *et al.* (2000) showed that the high GCA ratio and narrow sense heritability emphasizes the importance of additive gene action to drought tolerance. Entries f, e and g have the greatest distance from the ATC ordinate, so they had large SCA effects compared to other entries (**Fig. 4A**). The large SCA effects indicating the role of dominant gene action in their genetics; hence it may be necessary to resort to heterosis breeding (Butorace *et al.* 2004). The biplot (**Fig. 4A**) clearly indicates heterosis in crosses (F, B and E) × (C, G and H) with different dominant resistance genes (D1 and D2) to produced resistance hybrids. The polygon view of RWL content showed five sectors, namely a, b, f, g and h (**Fig. 4B**). The biplot indicated no tester fell in the a and h sectors, suggesting that,

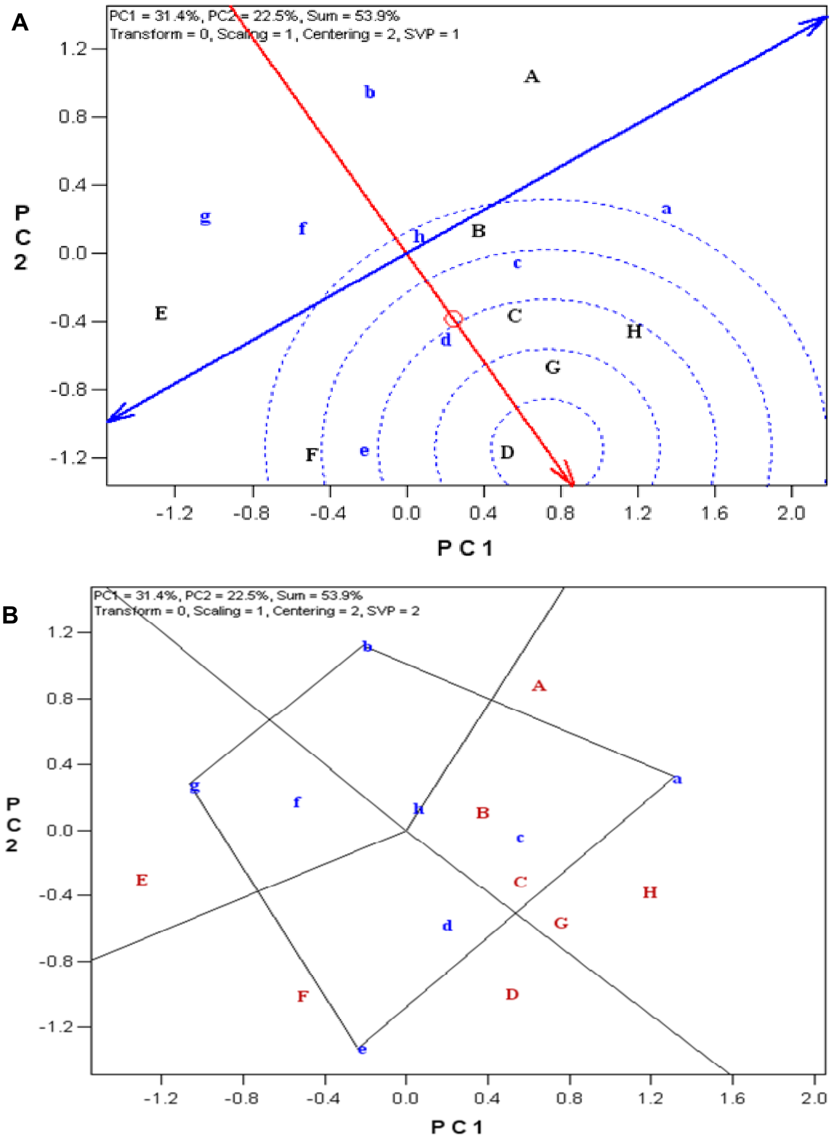

Fig. 5 Biplot showing (**A**) average tester coordinate (ATC) view and (**B**) polygon view of eight parents for chlorophyll fluorescence (CHF) in rainfed condition. Uppercase letters are testers and lowercase letters are entries of eight parents. Parents are: Plainsman (A), Regina (B), Capelle desprez (C), Chinese spring (D), Shakha (E), Saberbeg (F), Karchia (G) and Kobomugi (H).

these entries were not the best mating partners with any of the genotypes (Yan and Kang 2003). Tester A fell in the b sector, indicating that entry b was the best crossing to produced resistance hybrid with A. Entry f was the best mating partners for F, B, E and D. also entry g was the best mating partners for G, C and H. Since G was in the sector g, all crosses between genotype g with H, C and H were not heterotic. Thus, the combination G × G (Pure line G) is the best among all crosses involving G in produced drought tolerance hybrids. This condition was also honest for sectors f. Thus, the combination F × F (Pure line F) is the best among all crosses involving F. According to **Fig. 4A**, tester D was the best tester in all, as it was very close to the ideal tester and A was the weakest tester, also it is the least Representative of all testers. The hybrid between F and B was the best hybrid relative to drought resistance because it has complex the four resistance genes (A1, A2, D1, and D2). The hybrids between G × D and A × B have set of the three drought resistance genes (A1, A2, and D1). As well as, the hybrids between F with F and E have set of the three drought resistance genes (A1, A2, and D2). Since drought resistance caused by the accumulation of these genes (Farshadfar *et al.* 2011c) thus the crossing F × F, F × E, F × B, G × D and A × B produced the best drought resistance hybrids.

Chlorophyll fluorescence

The biplot for CHF explained 53.9% (31.4 and 22.5% by PC1 and PC2, respectively) of the total variation (**Fig. 5**). Based on the biplot, entry e an d has high GCA, b, g, f and h have low GCA and entry a and c have intermediate GCA (**Fig. 5A**). The order of the entry based on GCA effects was: e > d > c ≈ a > h > f > g > b. According to the results can be hypothesized that entry a and c (Group 2) had an additive gene (A1) for drought tolerance relative to entries h, f, g and b (Group 1), also entries e and d (Group 3) had an additional gene (A2) relative to Group 2 (Yan and Hunt *et al.* 2002). It is clear the success of any hybridization programme chiefly depends on general combining ability of parents used in crossing programme (Rastogi *et al.* 2010). Entry e, g and a had highest SCA effects due to their largest projections onto the ATC (**Fig. 5A**). Based to PC2 axis, the testers seem fall into two groups: F and E in group 1 and A and H in group 2. Testers B, C, D and G falls between groups 1 and 2 and has a short vector. Groups 1 and 2 interacted positively to produce heterosis in terms of drought tolerance. They are two heterotic groups with different dominant tolerance genes (D1 and D2). These results clearly indicated heterosis in crosses (F and E) × (A and H). According to Malla *et al.* (2010), the predominance of SCA can easily detection of highly heterotic hybrids of economic importance. The biplot in **Fig. 5B** was divided into four sectors, with entries a, b, e and g as the vertex. The polygon view demonstrated that entry e produced good hybrid combinations with testers F and D due to CHF indicators. A single tester, E, fall in sector g, indicating that entry g was the best mating partner for E. The entry a was the best mating partners for A, B, C, G and H. Since A was in the sector a, all crosses between genotype a with A, B, C, G and H were not heterotic. Thus, the combination A × A (Pure line A) is the best among all crosses involving A in produced drought tolerance hybrids (Butorac *et al.* 2004). The biplot indicated no tester fell in the, b sector, suggesting that entry b produced the poorest hybrids with some or all of the testers. The best tester in this subset was parent D, as it is closest to the ideal tester represented by the center of the concentric circles (**Fig. 5A**). since CHF is a good indicators to demonstrated drought tolerance in plant (Farshadfar *et al.* 2011b), thus the best combination for drought tolerance Based on the results of GCA and SCA were: eight hybrids involving A × A, A × B, A × C, A × H, A × G, E × F, E × D and G × E. The crosses E × F was the best hybrid relative to drought resistance because it has complex the four resistance genes (A1, A2, D1, and D2). The hybrids between E and D have the three tolerance genes (A1, A2, and D2). So the crossing between A with G and B, have set of the three droughts tolerance genes (A1, D1 and D2). Farshadfar *et al.* (2011b) investigated the inheritance of Chlorophyll fluorescence in wheat reported dominance and additive effects as well as epistasis for this trait.

CONCLUSION

The result of biplot analysis showed that the Parent A, F, B, F and E were The best general combiners with positive effects, for improvement of Y, RWC, LWP, RWL and CHF under drought conditions respectively, also parent C exhibited positive GCA for all traits. The high GCA ratio emphasizes the importance of additive gene action to drought tolerance. The crosses (A, C and H) × (B, F and G), (F and D) × (A, C and G), (F and E) × (A, H, C and D), (F, B and E) × (C, G and H) and (F and E) × (A and H) for Y, RWC, LWP, RWL and CHF were heterotic, respectively. The heterotic effect might be due to over dominance or epistatic effect of different dominant genes present in parents. It is considerable that all the heterotic crosses obtained through biplot analysis indicated similar heterotic effects for same crosses analyzed manually following standard formula, which confirmed the honest of the biplot in displaying the heterotic combinations. The polygon view of the biplot indicated combining A × G and F × E produced the best drought tolerance hybrids for all the traits by integrated the four tolerance genes (A1, A2, D1, and D2). The results showed additive gene effects mainly that control the physiological indicators of drought tolerance. Thus, genetic gain in developing tolerance in bread wheat can be achieved through selection.

REFERENCES

Ahmad RT, Malik TA, Khan IA, Jaskani MJ (2009) Genetic analysis of some morpho-physiological traits related to drought stress in cotton (*Gossypium hirsutum* L.). *International Journal of Agriculture and Biology* **11**, 235-240

Baker RJ (1978) Issues in diallel analysis. *Crop Science* **18**, 533-536

Bayoumi TY, Eid MH, Metwali EM (2008) Application of physiological and biochemical indices as a screening technique for drought tolerance in wheat genotypes. *African Journal of Biotechnology* **7 (14)**, 2341-2352

Bertoia L, Lopez C, Burak R (2006) Biplot analysis of forage combining ability in maize landraces. *Crop Science* **46**, 1346-1353

Blum A (1985) Breeding crop varieties for stress environments. *Plant Science* **2**, 199-238

Butorac J, Beljo J, Gunjaca J (2004) Study of inheritance of some agronomic and morphological traits in burley tobacco by graphic analysis of diallel cross. *Plant Soil and Environment* **50**, 162-167

Farshadfar E, Farshadfar M, Sutka J (2000) Combining ability analysis of drought tolerance in wheat over different water regimes. *Acta Agronomica Hungarica* **48 (4)**, 353-361

Farshadfar E, Ghanadha M, Zahravi M, Sutka J (2001) Generation mean analysis of drought tolerance in wheat (*Triticum aestivum* L.). *Acta Agronomica Hungarica* **49**, 59-66

Farshadfar E, Sutka J (2002) Screening drought tolerance criteria in maize. *Acta Agronomica Hungarica* **50 (4)**, 411-416

Farshadfar E, Mahjouri S, Aghaee A (2008a) Detection of epistasis and estimation of additive and dominance components of genetic variation for drought tolerance in durum wheat. *Journal of Biological Sciences* **8 (3)**, 548-603

Farshadfar E, Sabaghpour SH, Khaksar N (2008b) Inheritance of drought tolerance in chickpea (*Cicer arietinum* L.). *Journal of Applied Sciences* **8 (21)**, 3931-3937

Farshadfar E, Mohammadi M, Haghparast R (2011a) Diallel analysis of agronomic, physiological and metabolite indicators of drought tolerance in bread wheat (*Triticum aestivum* L.). *International Journal of Plant Breeding* **5 (1)**, 42-47

Farshadfar E, Allahgholipour M, Zarei L, Kiani M (2011b) Genetic analysis of field and physiological indicators of drought tolerance in bread wheat (*Triticum aestivum* L.) using diallel mating design. *African Journal of Biotechnology* **10 (61)**, 13071-13081

Farshadfar E, Rasoli V, Teixeira da Silva JA, Farshadfar M (2011c) Inheritance of drought tolerance indicators in bread wheat (*Triticum aestivum* L.) using a diallel technique. *Australian Journal of Crop Science* **5 (7)**, 870-878

Genty B, Briantais YM, Baker NR (1989) The Relationship between quantum yield of photosynthetic electron transport and quenching of chlorophyll fluorescence. *Biochimica et Biophysica Acta* **990**, 87-92

Geravandi M, Farshadfar E, Kahrizi D (2011) Evaluation of some physiological traits as indicators of drought tolerance in bread wheat genotypes. *Russian Journal of Plant Physio*logy **58 (1)**, 69-75

Golestani S, Assad MT (1998) Evaluation of four screening techniques for drought resistance and their relationship to yield reduction ratio in wheat. *Euphytica* **103**, 293-299

Griffing B (1956) Concept of general and specific combining ability in relation to diallel crossing systems. *Australian Journal of Biological Sciences* **9**, 463-493

Jensen NF (1970) A diallel selective mating system for cereal breeding. *Crop Science* **10**, 629-635

Kaw RN, Khush GS (1986) Combining ability for low-temperature tolerance in rice. In: *Proceedings of an International Rice Genetics Symposium*, IRRI, Los Baños, Philippines, pp 593-612

Khalil IA, Saeed HN, Khan NU, Durrisha W, Nawaz I, Ali F, Sajjad M, Saeed M (2010) Combining ability in maize single cross hybrids for grain yield: A graphical analysis. *Sarhad Journal of Agriculture* **26 (3)**, 373-379

Kiani G, Nematzadeh GA, Kazemitabar SK, Alishah O (2007) Combining ability in cotton cultivars for agronomic traits. *International Journal of Agriculture and Biology* **9**, 521-522

Malla S, Ibrahim AMH, Glover KD, Berzonsky WA (2010) Combining ability for Fusarium head blight resistance in wheat (*Triticum aestivum* L.). *Communications in Biometry and Crop Science* **5 (2)**, 116-126

Ober ES, Bloa ML, Clark CJA, Royal A, Jaggard KW, Pidgeon JD (2005) Evaluation of physiological traits as indirect selection for drought tolerance in sugar beet. *Field Crops Research* **91**, 231-249

Rastogi A, Mishra BK, Srivastava M, Siddiqui A, Shukla S (2010) Biplot approach for identification of heterotic crosses in linseed (*Linum usitatissimum* L.). *Journal of Botany* **10**, 1-7

Sprague GF, Tatum LA (1942) General vs. specific combining ability in single cross of corn. *Journal of Agronomy* **34**, 923-932

Yan W (2001) GGE-biplot a windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Journal of Agronomy* **93**, 1111-1118

Yan W (2002) Singular value partitioning in biplot analysis of multi-environment trial data. *Journal of Agronomy* **94**, 990-996

Yan W, Hunt LA (2002) Biplot analysis of diallel data. *Crop Science* **42**, 21-30

Yan W, Kang MS (2003) GGE biplot analysis: A graphical tool for breeders. In: Kang MS (Ed) *Geneticists and Agronomist*, CRC Press, Boca Raton, FL, pp 121-158

Yang RC, Jana S, Clarke JM (1991) Phenotypic diversity and associations of potentially drought-responsive characters in durum wheat. *Crop Science* **31**, 1484-1491