



RESEARCH PAPER

OPEN ACCESS

Substitution analysis of adaptation using nonparametric stability estimators

Nasrin Hatamy¹, Ezatollah Farshadfar^{*2}

¹*Department of Agronomy and Plant Breeding, Kermanshah Branch, Islamic Azad University, Kermanshah, Iran*

²*Campus of Agriculture and Natural Resources, Razi University, Kermanshah, Iran*

Article published on July 09, 2014

Key words:

Abstract

One important step in the genetic analysis of adaptation is identification of the chromosomal location of the genes controlling phenotypic stability. The present investigation was therefore carried out to locate QTLs monitoring stability in wheat. The experiment was conducted in a randomized complete block design with three replications under three different irrigated and rainfed environments using wheat substitution lines. The results of combined analysis of variance showed highly significant differences for genotypes (G), environments (E) and G×E interaction indicating the presence of genotypic variability, different responses of genotypes to different environments and possible localization of QTLs controlling yield and yield stability. Non-parametric stability statistics, Si⁽¹⁾ introduced substitution lines, 4D, 5A, 4B and 2A; Si⁽²⁾: 4D, 5A, 2A, and 4B; Si⁽³⁾: 4D, 4B, 2A and 5A and Si⁽⁴⁾: 3A, 4B, 5A and 4D as phenotypically stable accessions, while non-parametric stability estimators NPi⁽¹⁾, NPi⁽²⁾, NPi⁽³⁾ and NPi⁽⁴⁾ discriminated 3A, 4B and 4D as stable entries. Ysi introduced 4D as the most stable substitution line. According to Biplot analysis QTLs monitoring simultaneously yield and yield stability were distributed on chromosomes 3A, 5A, 3B, 4B and 4D of wheat and they can be transferred to wheat through chromosome engineering for enhancement of yield and yield stability. Based on rank sum (RS) method the most desirable stable substitution lines were identified as 3A and 4B. It can be concluded that QTLs controlling adaptation are distributed on different chromosomes of wheat.

*Corresponding Author: Ezatollah Farshadfar ✉ e_farshadfar@yahoo.com

Introduction

Among crop plants, wheat 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). 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 and phenotypic stability is a major objective in plant breeding programs (Bayoumi *et al.*, 2008).

Phenotypes are a mixture of genotype (G), environment (E) and interactions (GEI) between them. The GE interaction is a major problem in the study of quantitative traits because it reduces the association between genotypic and phenotypic values and complicates the process of selecting genotypes with superior performance (Delacy *et al.*, 1996; Yan, 2002). Therefore, the first goal of plant breeders in a crop breeding program is the development of genotypes which are stable or adapted to a wide range of diversified environments (Farshadfar, 2011).

Stability analysis methods are categorized in two parametric and non-parametric groups (Huhn, 1996; Sabaghnia *et al.*, 2006). The nonparametric procedures have

the following advantages over the parametric stability methods: they reduce the bias caused by outliers, no assumptions are needed about the distribution of the observed values, they are easy to use and interpret, and additions or deletions of one or few genotypes do not cause much variation of results (Huhn, 1996; Truberg & Huhn, 2000; Kaya *et al.*, 2003; Adugna & Labuschagne, 2003).

Nassar and Huhn (1987) and Huhn (1996) reported four nonparametric measures of phenotypic stability as: (1) $S_i^{(1)}$ the mean of the absolute rank differences of a genotype over the n environments (2) $S_i^{(2)}$ the

variance among the ranks over the n environments (3) $S_i^{(3)}$ and $S_i^{(4)}$ the sum of the absolute deviations and sum of squares of rank for each genotype relative to the mean of ranks, respectively.

Thennarasu (1995) proposed the nonparametric statistics $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ based on ranks of adjusted means of the genotypes in each environment and defined stable genotypes as those whose position in relation to the others remained unaltered in the set of environments assessed.

Rank-sum (Kang, 1988) and simultaneous selection for yield and stability (Y_{si}) (Kang & Pham, 1991) are other nonparametric stability statistics where both yield and Shukla's (1972) stability variance are used as selection criteria. This statistics assigns a weight of one to both yield and stability and enables the identification of high-yielding and stable genotypes.

Regardless of the definition of stability parameter one important question is whether stability is heritable or not? If stability is not heritable, then using this parameters in breeding programs is fruitless (Lin and Binn, 1991, 1994; Jalata *et al.*, 2011).

If stability is heritable, the next step in the genetic analysis is identification of the chromosomal location of the genes controlling the character (Farshadfar *et al.*, 2011b). Various techniques (biometrical, cytogenetic and molecular) have been used to locate the genes monitoring quantitative traits among which cytogenetic methods (monosomic, disomic and substitution analysis) have been widely used (Farshadfar *et al.*, 2012a).

Substitution lines in which a single pair of chromosomes from donor parent is substituted with the similar chromosome of the recipient parent, can be used for many purposes: 1) to study the location of the individual chromosomes or genes and determine their effect in genotypes with different genetic backgrounds, 2) to improve the agronomic value of cultivated wheat varieties by incorporating a

character and 3) to study the hybrid vigor (Khush, 1973).

The objectives of this study were (i) locating QTLs controlling seed yield stability in wheat substitution lines of Cappelle Desprez (as donor) into the genetic background of Chinese Spring (as recipient) and (ii) screening nonparametric stability indices.

Materials and methods

To locate QTLs controlling yield and yield stability, genotypes consisted of 21 substitution line series of *Capelle Desprez* (as donor) into the genetic background of *Chinese Spring* (as recipient) and were kindly provided from the gene bank of the Agricultural Research Institute of the Hungarian Academy of Sciences. The experiment was conducted in a randomized complete block design with three replications under three different environments (irrigated, pre-anthesis stress and post-anthesis stress) at the experimental farm of College of Agriculture, Razi University, Kermanshah, Iran (47°20' N latitude, 34° 20' E longitude and 1351.6 m altitude). Climate in the region is classified as semi-arid with mean annual rainfall of 378 mm. Minimum and maximum temperatures at the research station were -27°C and 44°C, respectively. Each replication consisted of 21 genotypes with 1.5 m length and 0.5 m wide and the distance between two plots was 30 cm. Single seeds were planted in two rows with 25 cm distance; in other word, harvest area was 0.75 m² per plot. The environments were considered as random factors while genotypes as fixed factors. At the harvesting time grain yield was measured for each plot.

Statistical analysis

The following non-parametric stability estimates were used for statistical analysis of phenotypic stability:

Nassar and Huhn (1987) introduced nonparametric measures of phenotypic stability: (1) $S_i^{(1)}$ the mean of the absolute rank differences of a genotype over the n environments (2) $S_i^{(2)}$ the variance among the ranks over the n environments (3) $S_i^{(3)}$ and $S_i^{(4)}$ the sum of the absolute deviations and sum of squares of rank for

each genotype relative to the mean of ranks, respectively.

Thennarasu (1995) reported four non-parametric stability statistics ($NPi^{(1)}$, $NPi^{(2)}$, $NPi^{(3)}$ and $NPi^{(4)}$) based on ranks of adjusted means of the genotypes in each environment and defined stable genotypes using Nassar and Huehn (1987)'s definition.

The third set was Kang's (1988) rank-sum (RS). In this method, both the highest yielding genotype and the genotype with the lowest stability variance are ranked 1 and after ranking all the genotypes the ranks by yield and by stability variance are added for each genotype and the genotype with the lowest rank sum (RS) value is considered the most desirable (Akcura & Kaya, 2008).

To understand better relationships, similarity and dissimilarity among stability estimators, principal component analysis (PCA), was performed. The softwares MSTAT-C, SPSS and STATISTICA were used for statistical analysis.

Results and discussion

Combined analysis of variance and mean comparisons

The results of combined analysis of variance showed highly significant differences ($P < 0.01$) for genotypes (G) and environments (E) (Table 1), indicating the presence of genotypic variability, different responses of genotypes to different environments and possible localization of QTLs controlling yield and yield stability in wheat (Farshadfar *et al.*, 2012b). The genotype (G) and environment (E) effects accounted for 7.97% and 78.60% of total sum of squares (TSS), respectively (Table 1). Genotype \times environment interaction (GEI) also revealed highly significant differences ($P < 0.01$) for grain yield. As GEI was significant, it was possible to proceed and calculate phenotypic stability (Lin *et al.*, 1986; Farshadfar and Sutka, 2003). The GEI accounted for 13.43% of TSS and was about 2 times more than the G effect. The large E and GEI in this study suggested the possible existence of different mega-environments

with different top-yielding genotypes (Yan and Kang, 2003). The results also revealed a differential yield performance among substitution lines across testing environments due to the presence of GEI. The presence of GEI complicates the selection process as GEI reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values (Crossa, 1990; Farshadfar *et al.*, 2012a).

Table 1. Combined analysis of variance for grain yield across 3 environments.

| S.O.V | df | Sum of square | SS% | Mean of square |
|--------------------|-----|---------------|-------|----------------|
| Treatments | 62 | 1661.1 | | |
| Genotypes (G) | 20 | 132.4 | 7.97 | 6.62** |
| Environments (E) | 2 | 1305.7 | 78.60 | 652.85** |
| Interactions (GEI) | 40 | 223 | 13.43 | 5.58** |
| Pooled error | 122 | 371.3 | | 3.04 |

** : significant at 1% probability level

Maximum grain yield was attributed to substitution line 7A, followed by D7, 2B and 4B, while minimum grain yield belonged to genotype 4D (Table 2).

Table 2. Mean values and nonparametric stability statistics for grain yield of Substitution lines across 3 environments.

| Code | Yield | $S_i^{(1)}$ | $Z_i^{(1)}$ | $S_i^{(2)}$ | $Z_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | NP ₁ | NP ₂ | NP ₃ | NP ₄ | RSM | Y _{Si} | R | SDR |
|------|-------------|-------------|--------------|--------------|--------------|-------------|-------------|-----------------|-----------------|-----------------|-----------------|-----------|-----------------|--------------|-------------|
| 1A | 4.473 | 6.00 | 0.10 | 20.33 | 0.33 | 4.88 | 1.12 | 4.67 | 0.58 | 0.69 | 1.12 | 21 | 21 | 13.67 | 4.51 |
| 2A | 2.944 | 11.33 | 1.93 | 96.33 | 4.43 | 28.9 | 3.40 | 6.00 | 6.00 | 1.27 | 1.80 | 23 | 17 | 15.33 | 9.81 |
| 3A | 5.472 | 2.00 | 2.53 | 3.00 | 1.41 | 0.38 | 0.25 | 1.33 | 0.09 | 0.11 | 0.17 | 21 | 10 | 6.00 | 1.73 |
| 4A | 3.456 | 11.33 | 1.93 | 76.33 | 1.96 | 16.36 | 2.07 | 6.00 | 0.86 | 0.81 | 1.29 | 23 | 16 | 12.67 | 8.74 |
| 5A | 3.468 | 1.33 | 3.26 | 1.33 | 1.55 | 0.50 | 0.50 | 1.67 | 0.28 | 0.41 | 0.62 | 14 | 23 | 16.67 | 1.15 |
| 6A | 4.275 | 2.67 | 1.90 | 4.33 | 1.30 | 1.18 | 0.64 | 2.33 | 0.29 | 0.39 | 0.64 | 8 | 22 | 14.67 | 2.08 |
| 7A | 6.139 | 6.00 | 0.10 | 27.00 | 0.12 | 3.60 | 0.80 | 5.00 | 0.42 | 0.46 | 0.67 | 40 | 0 | 7.00 | 5.20 |
| 1B | 4.788 | 10.67 | 1.38 | 80.33 | 2.37 | 10.48 | 1.35 | 6.00 | 0.30 | 0.54 | 0.78 | 29 | 13 | 6.67 | 8.96 |
| 2B | 5.439 | 5.33 | 0.28 | 19.00 | 0.39 | 2.38 | 0.65 | 3.33 | 0.19 | 0.28 | 0.42 | 26 | 11 | 6.00 | 4.36 |
| 3B | 4.678 | 6.00 | 0.10 | 22.33 | 0.26 | 4.19 | 1.00 | 4.33 | 0.48 | 0.57 | 0.81 | 14 | 19 | 11.33 | 4.73 |
| 4B | 5.388 | 2.00 | 2.53 | 3.00 | 1.41 | 0.4 | 0.27 | 1.67 | 0.10 | 0.14 | 0.22 | 22 | 12 | 7.00 | 1.73 |
| 5B | 4.808 | 2.67 | 1.90 | 5.33 | 1.22 | 0.94 | 0.47 | 2.33 | 0.23 | 0.27 | 0.41 | 13 | 16 | 10.67 | 2.31 |
| 6B | 4.910 | 10.00 | 0.93 | 75.00 | 1.83 | 12.5 | 1.67 | 6.00 | 0.35 | 0.69 | 10.00 | 31 | 14 | 10.00 | 8.66 |
| 7B | 4.894 | 6.67 | 0.01 | 26.33 | 0.13 | 4.94 | 1.06 | 4.33 | 0.36 | 0.51 | 0.81 | 20 | 15 | 11.33 | 5.13 |
| 1D | 5.370 | 6.67 | 0.01 | 26.33 | 0.13 | 3.67 | 0.79 | 5.33 | 0.41 | 0.47 | 0.74 | 29 | 13 | 7.67 | 5.13 |
| 2D | 4.570 | 6.67 | 0.01 | 33.33 | 0.014 | 8.70 | 1.74 | 5.00 | 0.45 | 0.89 | 1.39 | 19 | 20 | 14.33 | 5.77 |
| 3D | 4.329 | 5.33 | 0.28 | 17.33 | 0.46 | 3.71 | 1.00 | 4.00 | 0.50 | 0.53 | 0.86 | 12 | 22 | 12.67 | 4.16 |
| 4D | 2.923 | 0.67 | 4.07 | 0.33 | 1.64 | 0.25 | 0.5 | 0.33 | 0.11 | 0.18 | 0.25 | 17 | 26 | 19.33 | 0.58 |
| 5D | 4.589 | 11.33 | 1.93 | 82.33 | 2.59 | 15.44 | 1.94 | 6.00 | 0.86 | 0.77 | 1.12 | 21 | 19 | 11.33 | 9.07 |
| 6D | 4.989 | 9.33 | 0.56 | 54.33 | 0.39 | 9.59 | 1.47 | 6.33 | 0.45 | 0.71 | 1.12 | 30 | 13 | 10.67 | 7.37 |
| 7D | 5.571 | 7.33 | 0.01 | 37 | 0.0001 | 4.63 | 0.88 | 4.67 | 0.25 | 0.41 | 0.58 | 29 | 9 | 6.00 | 6.08 |
| Mean | 4.64 | 6.25 | 25.76 | 33.86 | 23.93 | 6.55 | 1.12 | 4.13 | 0.65 | 0.53 | 0.80 | 22 | 15.76 | 11.00 | 5.11 |

Test statistics

$\sum Z_i^{(1)} = 25.76$

$\sum Z_i^{(2)} = 23.93$

$E(S_i^{(1)}) = 6.984$

$E(S_i^{(2)}) = 36.67$

$V(S_i^{(1)}) = 9.8$

$V(S_i^{(2)}) = 804.22$

$X^2 \text{ Sum} = 30.1$

$X^2 Z_1 Z_2 = 3.84$

S_i , Huehn's (1979) non-parametric stability statistics. NP_i , Thennarasu's (1995) non-parametric stability statistics. RSM and Y_{Si} , Kang's (1988 and 1993) stability statistics. R and SDR , Rank and standard deviation of rank.

Stability analysis procedures

Evaluations of the genotypes based on different non-parametric measurements with mean yield are presented in Table 2. For each genotype, $Z_i^{(1)}$ and $Z_i^{(2)}$ values were calculated based on the rank of the corrected data and summed over genotypes to obtain Z values (Table 2); $Z_i^{(1)sum} = 25.76$ and $Z_i^{(2)sum} = 23.93$. Since both of these statistics were less than the critical value $X^2 = 30.1$, therefore no significant differences were found in rank stability among the genotypes grown in 3 environments. The individual Z values, for genotypes, however were significantly

unstable relative to others, because they showed large Z values, in comparison with the critical value $X^2 = 3.84$.

According to Nassar and Huhn (1987) stability statistics, $S_i^{(1)}$ substitution lines, 4D 5A, 4B and 2A; $S_i^{(2)}$ 4D, 5A, 2A, and 4B; $S_i^{(3)}$ 4D, 4B, 2A and 5A and $S_i^{(4)}$ 3A, 4B, 5A and 4D were identified as phenotypically stable accessions.

Thennarasu (1995) non-parametric stability statistics $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ discriminated 3A, 4B and 4D as stable entries. Y_{Si} introduced 4D as the most stable substitution line. It can be concluded that QTLs controlling adaptation are distributed on different chromosomes of wheat.

Table 3. Ranks of yield, stability estimators, mean of ranks, standard deviation of ranks and rank sum of Substitution lines over three environments.

| Code | Yield | $S_i^{(1)}$ | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | NP_1 | NP_2 | NP_3 | NP_4 | Y_{Si} | SDR | Mean of ranks | RS |
|------|-------|-------------|-------------|-------------|-------------|--------|--------|--------|--------|----------|-----|---------------|------|
| 1A | 15 | 9 | 9 | 13 | 14 | 11 | 18 | 15 | 17 | 17 | 9 | 13.8 | 22.8 |
| 2A | 20 | 19 | 21 | 21 | 21 | 16 | 21 | 21 | 21 | 13 | 21 | 19.4 | 40.4 |
| 3A | 3 | 3 | 3 | 2 | 1 | 2 | 1 | 1 | 1 | 3 | 3 | 2 | 5 |
| 4A | 19 | 19 | 18 | 20 | 20 | 16 | 19 | 19 | 19 | 11 | 18 | 18 | 36 |
| 5A | 18 | 2 | 2 | 4 | 4 | 3 | 7 | 7 | 7 | 20 | 2 | 7.4 | 9.4 |
| 6A | 17 | 5 | 5 | 6 | 7 | 5 | 8 | 6 | 8 | 18 | 5 | 8.5 | 13.5 |
| 7A | 1 | 9 | 13 | 8 | 9 | 13 | 13 | 9 | 9 | 1 | 13 | 8.5 | 21.5 |
| 1B | 11 | 18 | 19 | 17 | 15 | 16 | 9 | 13 | 11 | 6 | 19 | 13.5 | 32.5 |
| 2B | 4 | 7 | 8 | 7 | 6 | 7 | 4 | 5 | 5 | 4 | 8 | 5.7 | 13.7 |
| 3B | 12 | 9 | 10 | 11 | 11 | 9 | 16 | 14 | 12 | 14 | 10 | 11.8 | 21.8 |
| 4B | 5 | 3 | 3 | 3 | 2 | 3 | 2 | 2 | 2 | 5 | 3 | 3 | 6 |
| 5B | 10 | 5 | 6 | 5 | 3 | 5 | 5 | 4 | 4 | 11 | 6 | 5.8 | 11.8 |
| 6B | 8 | 17 | 17 | 18 | 17 | 16 | 10 | 16 | 15 | 9 | 17 | 14.3 | 31.3 |
| 7B | 9 | 12 | 12 | 14 | 13 | 9 | 11 | 11 | 12 | 10 | 12 | 11.3 | 23.3 |
| 1D | 6 | 12 | 11 | 9 | 8 | 15 | 12 | 10 | 10 | 6 | 11 | 9.9 | 20.9 |
| 2D | 14 | 12 | 14 | 15 | 18 | 13 | 15 | 20 | 20 | 16 | 14 | 15.7 | 29.7 |
| 3D | 16 | 7 | 7 | 10 | 11 | 8 | 17 | 12 | 14 | 18 | 7 | 12 | 19 |
| 4D | 21 | 1 | 1 | 1 | 4 | 1 | 3 | 3 | 3 | 21 | 1 | 5.9 | 6.9 |
| 5D | 13 | 19 | 20 | 19 | 19 | 16 | 19 | 18 | 18 | 14 | 20 | 17.5 | 37.5 |
| 6D | 7 | 16 | 16 | 16 | 16 | 21 | 14 | 17 | 16 | 6 | 16 | 14.5 | 30.5 |
| 7D | 2 | 15 | 15 | 12 | 10 | 11 | 6 | 8 | 6 | 2 | 15 | 8.7 | 23.7 |

Principal component analysis

To better understand the relationships, similarities and dissimilarities among the non-parametric stability estimates, principal component analysis (PCA), based on the rank correlation matrix was used.

The main advantage of using PCA over cluster analysis is that each statistics can be assigned to one group only (Khodadadi *et al.*, 2011).

The PCA1 and PCA2 axes which justify 87.65% of total variation, mainly distinguish the stability estimates in

different groups. One interesting interpretation of biplot is that the cosine of the angle between the vectors of two indices approximates the correlation coefficient between them. The cosine of the angles does not precisely translate into correlation coefficients, since the biplot does not explain all of the variation in a dataset. Nevertheless, the angles are informative enough to allow a whole picture about the interrelationships among the stability estimates (Yan and Kang, 2003). Biplot clustered the stability measures in 3 groups. Group 1 (G1) included Yield and RS. The PCs axes separated $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(4)}$ and SDR, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ as Group 2 (G2) and Ysi and R were classified as group 3 (G4). G1 introduced genotypes 3A and 3B as stable which showed high mean yield. All of the stability indices in G2 and G3 mainly discriminated genotypes 5A, 4B and 4D as stable (Fig. 1), hence according to Biplot analysis (Fig. 1) QTLs monitoring simultaneously yield and yield stability are distributed on chromosomes 3A, 5A, 3B, 4B and 4D of wheat and they can be transferred to wheat through chromosome engineering for enhancement of yield and yield stability.

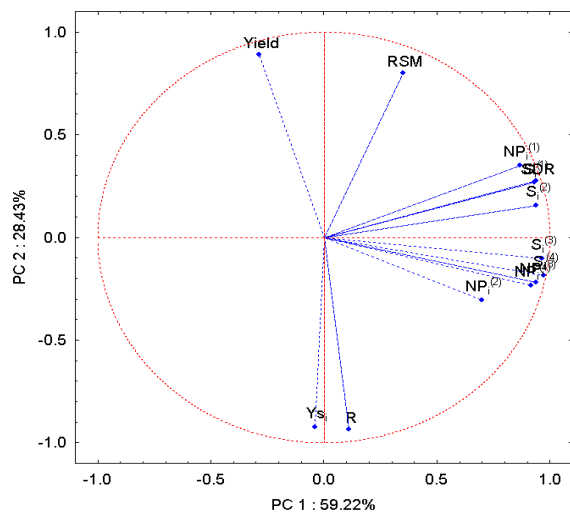


Fig. 1. Principal components and Biplot analysis for screening non-parametric stability estimators of wheat substitution lines over 3 environments.

Ranking procedure

The estimates of stability indicators (Table 2) exhibited that the identification of stable genotypes based on a single criterion was contradictory. For example, different estimators introduced different substitution lines. To determine the most desirable stable genotype according to the all indices mean rank and standard deviation of ranks of all stability criteria were calculated and summed (RS) based on RS the most desirable stable substitution lines lines were identified as 3A and 4B.

Non-parametric statistical procedures indicated that most of the QTLs involved in controlling phenotypic stability in barley are located on the chromosomes 3H and 4H (Farshadfar *et al.*, 2011a), and most of the genes controlling yield stability in *Agropyron* (Farshadfar, 2011) and Rye (Farshadfar *et al.*, 2011b) are located on chromosome 7E and 5R, respectively. Nonparametric statistical procedures and ranking method indicated that most of the quantitative trait loci (QTLs) involved in controlling phenotypic stability in wheat are located on the chromosomes 2A, 3A and 4A in A genome and 3D and 5D in D genome (Farshadfar *et al.*, 2012b).

References

Adugna W, Labuschagne MT. 2003. Association of linseed characters and its variability in different environments. *Journal of Agricultural Science* **140**, 285-296.

Akcura M, Kaya Y. 2008. Nonparametric stability methods for interpreting genotype by environment interaction of bread wheat genotypes (*Triticum aestivum* L.). *Genetic and Molecular Biology* **31**(4), 906-913.

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.

- Crossa J.** 1990. Statistical analysis of multilocation trials. *Advances in Agronomy* **44**, 55–85.
- Delacy IH, Basford KE, Cooper M, Bull JK.** 1996. Analysis of multi-environment trials an historical perspective. *Plant Adaptation and Crop Improvement*. Eds. M. Cooper and G. L. Hammer. CAB international, UK
- Farshadfar E, Sutka J.** 2003. Locating QTLs controlling adaptation in wheat using AMMI model. *Cereal Research Communication* **31**, 249-254.
- Farshadfar E.** 2011. Chromosomal localization of the genes controlling adaptation in *Agropyron elongatum* using a new AMMI–based simultaneous selection index of yield and yield stability. *International Journal of Plant Breeding* **5**(2), 80–83.
- Farshadfar E, Zali H, Mohammadi R.** 2011a. Evaluation of phenotypic stability in chickpea genotypes using GGE-Biplot. *Annals of Biological Research* **2**(6), 282-292.
- Farshadfar E, Farshadfar M, Kiani M .** 2011b. Involvement of chromosome 5R carrying the genes controlling yield and yield stability in rye (*Secale Cereale* cv. Imperial). *European Journal of Scientific Research* **59**(3), 352-360
- Farshadfar E, Mohammadi M, Aghae M, Vaisi Z.** 2012a. GGE biplot analysis of genotype × environment interaction in wheat-barley disomic addition lines. *Australian Journal of Crop Science* **6**(6), 1074–1079.
- Farshadfar E, Safari H, Yaghotipoor A.** 2012b. Chromosomal Localization of QTLs Controlling Genotype × Environment Interaction in Wheat Substitution Lines Using Nonparametric Methods. *Journal of Agricultural Science* **4**(12), 18-26.
- 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.
- Huhn M.** 1996. Non-parametric analysis of genotype x environment interactions by ranks. In M. S. Kang, & H. G. Gauch, (Eds.). *Genotype by Environment Interaction*. pp. 213-228. Boca Raton: CRC Press.
- Jalata Z, Ayana A, Zeleke H.** 2011. Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian Barley (*Hordeum vulgare* L.) land races and crosses. *International J of Plant Breeding and Genetics* **5**, 44-52.
- Kang MS.** 1988. A rank-sum method for selecting high yielding stable corn genotypes. *Cereal Research. Communication* **16**, 113-115.
- Kang MS, Pham HN.** 1991. Simultaneous selection for yielding and stable crop genotypes. *Journal of Agronomy* **83**, 161-165.
- Kaya Y, Taner S, Ceri S.** 2003. Nonparametric stability analysis of yield performances in oat (*Avena sativa* L.) genotypes across environments. *Asian Journal of Plant Science* **2**, 286-289.
- Khodadadi M, Fotokian MH, Miransari M.** 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science* **5**(1), 17- 24.
- Khush GS.** 1973. *Cytogenetics of Aneuploids* (p. 301). New York: Academic Press.
- Lin CS, Binns MR, Lefkovitch LP.** 1986. Stability Analysis: Where Do We Stand? *Crop Science* **26**, 894-900.

Lin CS, Binns MR. 1991. Genetic properties of four stability parameters. *Theoretical Applied Genetetics* **82**, 505- 509.

Lin CS, Binns MR. 1994. Concepts and methods for analyzing regional trial data for cultivar and location selection. *Plant Breed Review* **12**, 271–297.

Nassar R, Huhn M. 1987. Studies on estimation of phenotypic stability: Tests of significance for nonparametric measures of phenotypic stability. *Biometric*, **43**, 45-53.

Sabaghnia N, Dehghani H, Sabaghpour SH. 2006. Nonparametric methods for interpreting genotype x environment interaction of lentil genotypes. *Crop Science* **46**, 1100-1106.

Shukla GK. 1972. Some statistical aspects of partitioning genotype-environmental components of variability. *Heredity* **29**, 237–245.

Thennarasu K. 1995. On certain non-parametric procedures for studying genotype-environment interactions and yield stability. *Indian Journal. of Genetics* **60**, 433-439.

Truberg B, Huhn M. 2000. Contribution to the analysis of genotype by environment interactions: Comparison of different parametric and non-parametric tests for interactions with emphasis on crossover interactions. *Journal of Agronomy and Crop Science* **185**, 267-274.

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

Yan W, Kang MS. 2003. *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists*. 1st Edn., CRC Press LLC., Boca Roton, Florida, 271.