

Chromosomal Localization of QTLs Controlling Genotype × Environment Interaction in Wheat Substitution Lines Using Nonparametric Methods

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Abstract

To locate the genes controlling grain yield stability, substitution line of *Cheyenne* (as donor) into the genetic background of *Chinese Spring* (as recipient) and their parents were used in a randomized complete block design with three replications under two different conditions (rain-fed and irrigated) for two years. Interrelationship among nonparametric measures showed that non-parametric statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, δr and δgy were significantly ($P < 0.01$) correlated and exhibited negative and significant ($P < 0.01$) correlation with grain yield, while the statistics RS, TOP and Kr revealed positive and significant correlation with grain yield. The results of Spearman's rank correlation were confirmed by Ward's hierarchical cluster analysis. Principal components analysis indicated that the two first components explained 92.68% (77.71 and 14.97% by components 1 and 2, respectively) of the total variance. Screening nonparametric estimates using biplot technique based on two first components classified the stability measures in 2 groups. 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.

Keywords: wheat substitution lines, adaptation, non-parametric methods, chromosomal location

1. Introduction

The result of researches indicated that wheat grain yield was a quantitative trait and the effect of environment on it is very large, therefore the knowledge about the construction of genotype × environment (GE) interaction is necessary. GE interaction is the differential response of genotypes evaluated under different environmental conditions. It is a complex phenomenon as it involves environmental (agro-ecological, climatic and agronomic) conditions and all physical and genetic factors that determine the plant growth and development (Mohammadi et al., 2009). The GE interaction reduces association between phenotypic and genotypic values and leads to bias in the estimates of gene effects and combining ability for various characters sensitive to environmental variations. Such traits are less amenable to selection (Farshadfar et al., 2000).

Various statistical methods have been investigated and proposed to study GE interactions (Zali et al., 2011). The choice of the best methodology depends on some factors, such as the number of genotypes and environment available, environmental variation, mathematical model fit to the data set, stability concept adopted and the facility to apply and interpret the results (Farshadfar et al., 2012). 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.

Thenarasu (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.

A nonparametric superiority measure suggested by Fox et al. (1990) for general adaptability. They used stratified ranking of the cultivars in each environment to determine the proportion of sites in which each cultivar occurred in the top, middle, and bottom third of the ranks, forming the nonparametric measures TOP, MID and LOW, respectively.

Rank-sum (Kang, 1988) and simultaneous selection for yield and stability (Ys_i) (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. Ketata et al. (1989) suggested the plotting mean rank across environments (Kr) against standard deviation of ranks (σ_r) for all genotypes and plotting mean grain yield across environments (gy) against standard deviation (σ_{gy}) of grain yields for all genotypes as a nonparametric stability statistics.

Genetic materials such as alien additions, substitutions, translocations, deletions, monosomes, ditelosomes, and nullisomes are valuable genetic resources for both plant breeding and basic research (Szakacs & Molnar-Lang, 2010). Substitution lines are justified 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 locating QTLs controlling seed yield stability in wheat substitution lines of Cheyenne (as donor) into the genetic background of Chinese Spring (as recipient) and screening nonparametric stability indices.

2. Materials and Methods

To locate QTLs controlling yield and yield stability, 23 genotypes consists of 21 substitution line series of *Cheyenne* (as donor) into the genetic background of *Chinese Spring* (as recipient) and their parents 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 two different environments (irrigated and rain-fed) 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 semiarid with mean annual rainfall of 378 mm. Minimum and maximum temperature at the research station were -27°C and 44°C, respectively. Each replication consisted of 23 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 (E_{i1} : irrigation condition of the first year, E_{r1} : rainfed condition of the first year, E_{i2} : irrigation condition of the second year and E_{r2} : rainfed condition of the second year), while genotypes as fixed factors. At the harvesting time grain yield was measured for each plot.

2.1 Statistical Analysis

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

2.1.1 Nassar and Huhn (1987) Method

Four nonparametric measures of phenotypic stability of Nassar and Huhn (1987) 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.

2.1.2 Thenarasu (1995) Method

Consisted of four nonparametric stability 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 using Nassar and Huehn (1987)'s definition.

2.1.3 Kang Method

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 RS value is considered the most desirable (Akcura & Kaya, 2008).

2.1.4 Fox et al. (1990) Method

The methodology described by Fox et al. (1990) was the fourth set in this study. In this technique the genotypes in each environment was ranked in the TOP, MID and LOW third of trial entries. A genotype that occurred mostly in the top third (high TOP value) was considered as a widely adapted cultivar.

2.1.5 Ketata et al. (1989)

The nonparametric stability statistic reported by Ketata et al. (1989) was the last set of nonparametric stability statistic used in this study. In this method a genotype is considered stable if its Kr or gy value is relatively consistent in all the environments. *i.e.*, showing low Kr or high gy and having a low σ_r (Flores et al., 1998; Akcura & Kaya, 2008).

Genotype ranks were calculated for grain yield and thirteen different nonparametric stability statistics and spearman's rank correlation between each pair of nonparametric statistic ranks were measured to determine relationships between statistics.

Ward's hierarchical clustering procedure was determined for grouping of nonparametric stability statistics and genotypes based on statistic ranks of genotypes (Abdulahi, et al., 2007). Principal component analysis was performed for two way table of genotypes and statistics (Mohammadi et al., 2007).

3. Results

3.1 Interrelationship Among Nonparametric Measures

The nonparametric stability measures of $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, Δr and Δgy were significantly ($P < 0.01$) correlated and had a negative and significant ($P < 0.01$) correlation with grain yield (gy) (except $S_i^{(1)}$, $S_i^{(2)}$ and Δr). Stability statistics RS, TOP and Kr also exhibited a positive and significant correlation with gy (Table 1). The results of spearman's rank correlation were confirmed by Ward's hierarchical cluster analysis. Dendrogram of statistics clustering (Figure 1) based on ranking of substitution lines and different stability statistics showed that 13 nonparametric statistics and grain yield could be divided into two major groups. The first group contains statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, Δr and Δgy and the second group contains RS, TOP, Kr and gy.

Table 1. Spearman's rank correlation coefficients between the nonparametric stability statistics

| Statistics | gy | $S_i^{(1)}$ | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | $NP_i^{(1)}$ | $NP_i^{(2)}$ | $NP_i^{(3)}$ | $NP_i^{(4)}$ | Δr | Δgy | RS | TOP |
|--------------|---------|-------------|-------------|-------------|-------------|--------------|--------------|--------------|--------------|------------|-------------|--------|--------|
| $S_i^{(1)}$ | -.243 | | | | | | | | | | | | |
| $S_i^{(2)}$ | -.375 | .935** | | | | | | | | | | | |
| $S_i^{(3)}$ | -.664** | .792** | .908** | | | | | | | | | | |
| $S_i^{(6)}$ | -.771** | .746** | .852** | .975** | | | | | | | | | |
| $NP_i^{(1)}$ | -.573** | .880** | .941** | .946** | .936** | | | | | | | | |
| $NP_i^{(2)}$ | -.760** | .720** | .846** | .980** | .988** | .927** | | | | | | | |
| $NP_i^{(3)}$ | -.799** | .687** | .814** | .961** | .985** | .921** | .992** | | | | | | |
| $NP_i^{(4)}$ | -.744** | .783** | .850** | .960** | .985** | .954** | .968** | .973** | | | | | |
| Δr | -.375 | .935** | 1.000** | .908** | .852** | .941** | .846** | .814** | .850** | | | | |
| Δgy | -.534** | .899** | .962** | .963** | .929** | .980** | .928** | .902** | .931** | .962** | | | |
| RS | .614** | -.374 | -.407 | -.563** | -.658** | -.566** | -.622** | -.657** | -.662** | -.407 | -.501* | | |
| TOP | .876** | -.187 | -.328 | -.574** | -.649** | -.490* | -.653** | -.687** | -.620** | -.328 | -.464* | .394 | |
| Kr | .983** | -.280 | -.397 | -.677** | -.779** | -.588** | -.766** | -.802** | -.760** | -.397 | -.556** | .538** | .875** |

*,**: Significant at the 0.05 and 0.01 probability levels, respectively.

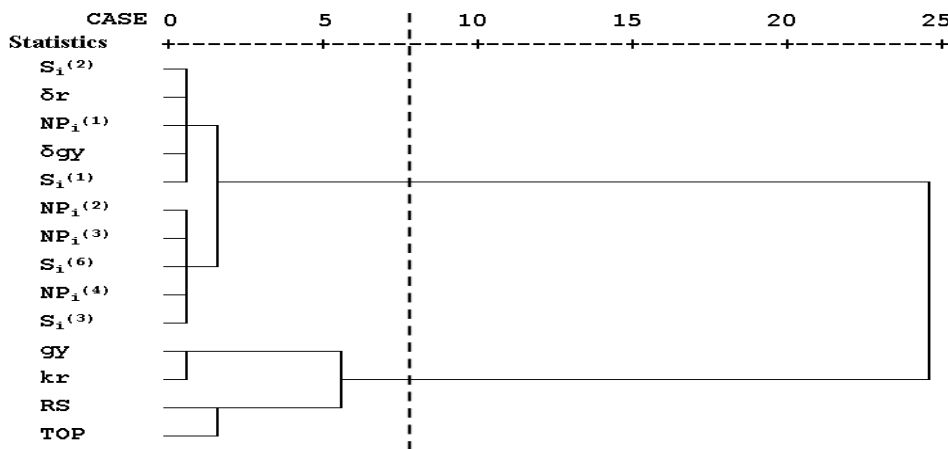


Figure 1. Dendrogram of Ward's hierarchical clustering based on ranks of nonparametric measures and mean grain yield

3.2 Assessment of Stable Genotypes

The results of 13 nonparametric stability measures and grain yield for 21 substitution lines and their parents and the ranks of genotypes based on nonparametric stability statistic are presented in Table 2 and 3, respectively.

Table 2. Non-parametric stability statistics for grain yield of 21 substitution lines and their parents

| Genotype | gy(g/plot) | Ketata et al. (1989) | | | Huhn (1979) | | | | Thennarasu (1995) | | | | Kang (1988) | Fox et al. (1990) |
|-----------|------------|----------------------|-------|---------|-------------|-------|--------|-------|-------------------|--------|--------|--------|-------------|-------------------|
| | | delta_gy | kr | delta_r | S1(1) | S1(2) | S1(3) | S1(6) | NP1(1) | NP1(2) | NP1(3) | NP1(4) | RS | TOP |
| 1A | 92.96 | 38.88 | 41.50 | 34.38 | 13.67 | 1182 | 85.42 | 2.80 | 31.75 | 0.86 | 0.79 | 0.72 | 31 | 25 |
| 2A | 96.97 | 20.50 | 38.50 | 15.95 | 6.33 | 254 | 19.82 | 1.40 | 9.75 | 0.24 | 0.29 | 0.21 | 29 | 50 |
| 3A | 84.35 | 19.03 | 49.00 | 17.45 | 6.08 | 305 | 18.65 | 1.14 | 8.00 | 0.17 | 0.20 | 0.13 | 38 | 25 |
| 4A | 76.26 | 23.99 | 58.75 | 23.84 | 8.92 | 568 | 29.02 | 1.34 | 14.00 | 0.25 | 0.29 | 0.18 | 36 | 0 |
| 5A | 71.91 | 30.43 | 61.25 | 27.56 | 11.83 | 760 | 37.20 | 1.52 | 22.00 | 0.37 | 0.41 | 0.37 | 27 | 0 |
| 6A | 82.15 | 32.54 | 53.75 | 30.35 | 12.92 | 921 | 51.40 | 1.92 | 26.50 | 0.50 | 0.52 | 0.49 | 22 | 0 |
| 7A | 91.67 | 38.69 | 43.75 | 35.98 | 12.50 | 1295 | 88.79 | 2.63 | 29.75 | 0.75 | 0.74 | 0.59 | 31 | 50 |
| 1B | 93.11 | 32.20 | 42.75 | 29.38 | 11.42 | 863 | 60.56 | 2.32 | 25.75 | 0.59 | 0.64 | 0.54 | 16 | 0 |
| 2B | 93.13 | 28.54 | 43.00 | 25.34 | 7.92 | 642 | 44.79 | 1.77 | 19.25 | 0.51 | 0.57 | 0.33 | 22 | 25 |
| 3B | 99.23 | 37.52 | 38.25 | 31.22 | 12.83 | 975 | 76.46 | 2.80 | 32.75 | 0.81 | 0.87 | 0.81 | 15 | 75 |
| 4B | 103.02 | 31.54 | 33.75 | 24.73 | 9.50 | 612 | 54.36 | 2.46 | 23.50 | 0.68 | 0.77 | 0.59 | 5 | 100 |
| 5B | 97.59 | 40.93 | 39.75 | 35.94 | 13.00 | 1292 | 97.48 | 2.94 | 32.25 | 0.91 | 0.87 | 0.71 | 21 | 75 |
| 6B | 98.01 | 43.34 | 37.25 | 37.23 | 16.17 | 1386 | 111.64 | 3.36 | 36.25 | 1.07 | 1.00 | 0.98 | 26 | 75 |
| 7B | 93.04 | 30.76 | 42.75 | 27.58 | 9.75 | 761 | 53.40 | 2.08 | 21.50 | 0.54 | 0.60 | 0.39 | 23 | 25 |
| 1D | 111.97 | 40.88 | 28.25 | 30.47 | 12.08 | 928 | 98.58 | 3.65 | 33.25 | 1.33 | 1.23 | 1.06 | 9 | 100 |
| 2D | 100.32 | 37.26 | 35.50 | 31.56 | 12.83 | 996 | 84.20 | 3.04 | 32.50 | 0.88 | 0.94 | 0.85 | 13 | 75 |
| 3D | 68.05 | 23.28 | 65.75 | 24.27 | 9.83 | 589 | 26.87 | 1.26 | 12.25 | 0.18 | 0.21 | 0.16 | 27 | 0 |
| 4D | 93.53 | 32.74 | 42.00 | 30.08 | 12.17 | 905 | 64.62 | 2.43 | 26.75 | 0.59 | 0.67 | 0.60 | 22 | 50 |
| 5D | 81.49 | 17.17 | 52.25 | 16.36 | 4.33 | 268 | 15.36 | 0.87 | 6.75 | 0.14 | 0.18 | 0.09 | 34 | 25 |
| 6D | 90.21 | 31.66 | 46.75 | 28.29 | 11.58 | 800 | 51.35 | 2.07 | 24.25 | 0.51 | 0.55 | 0.47 | 23 | 0 |
| 7D | 71.24 | 32.80 | 62.75 | 31.13 | 12.83 | 969 | 46.32 | 1.71 | 27.00 | 0.43 | 0.45 | 0.39 | 24 | 0 |
| Ch.Spring | 84.25 | 23.72 | 49.50 | 22.88 | 6.00 | 524 | 31.74 | 1.31 | 14.50 | 0.34 | 0.41 | 0.21 | 36 | 25 |
| Cheyenne | 71.59 | 27.97 | 62.75 | 26.73 | 10.67 | 714 | 34.15 | 1.45 | 18.75 | 0.30 | 0.33 | 0.25 | 22 | 0 |

Table 3. Ranks of 13 nonparametric stability statistics and grain yield for 21 substitution lines and their parents

| Genotype | gy | $S_i^{(1)}$ | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | $NP_i^{(1)}$ | $NP_i^{(2)}$ | $NP_i^{(3)}$ | $NP_i^{(4)}$ | kr | δr | δgy | RS | TOP |
|-----------|----|-------------|-------------|-------------|-------------|--------------|--------------|--------------|--------------|----|------------|-------------|----|-----|
| 1A | 12 | 22 | 20 | 19 | 18 | 18 | 19 | 18 | 19 | 8 | 20 | 20 | 13 | 4 |
| 2A | 7 | 4 | 1 | 3 | 6 | 3 | 4 | 5 | 6 | 6 | 1 | 3 | 12 | 3 |
| 3A | 15 | 3 | 3 | 2 | 2 | 2 | 2 | 2 | 2 | 15 | 3 | 2 | 16 | 4 |
| 4A | 19 | 6 | 5 | 5 | 5 | 5 | 5 | 4 | 4 | 19 | 5 | 6 | 15 | 5 |
| 5A | 20 | 13 | 10 | 8 | 8 | 10 | 8 | 7 | 9 | 20 | 10 | 9 | 11 | 5 |
| 6A | 17 | 20 | 15 | 12 | 11 | 14 | 10 | 10 | 13 | 18 | 15 | 14 | 7 | 5 |
| 7A | 13 | 16 | 22 | 20 | 17 | 17 | 17 | 16 | 15 | 13 | 22 | 19 | 13 | 3 |
| 1B | 10 | 11 | 13 | 15 | 14 | 13 | 14 | 14 | 14 | 10 | 13 | 13 | 5 | 5 |
| 2B | 9 | 5 | 8 | 9 | 10 | 8 | 12 | 12 | 8 | 12 | 8 | 8 | 7 | 4 |
| 3B | 4 | 17 | 18 | 17 | 19 | 21 | 18 | 20 | 20 | 5 | 18 | 18 | 4 | 2 |
| 4B | 2 | 7 | 7 | 14 | 16 | 11 | 16 | 17 | 16 | 2 | 7 | 11 | 1 | 1 |
| 5B | 6 | 21 | 21 | 21 | 20 | 19 | 21 | 19 | 18 | 7 | 21 | 22 | 6 | 2 |
| 6B | 5 | 23 | 23 | 23 | 22 | 23 | 22 | 22 | 22 | 4 | 23 | 23 | 10 | 2 |
| 7B | 11 | 8 | 11 | 13 | 13 | 9 | 13 | 13 | 11 | 11 | 11 | 10 | 8 | 4 |
| 1D | 1 | 14 | 16 | 22 | 23 | 22 | 23 | 23 | 23 | 1 | 16 | 21 | 2 | 1 |
| 2D | 3 | 18 | 19 | 18 | 21 | 20 | 20 | 21 | 21 | 3 | 19 | 17 | 3 | 2 |
| 3D | 23 | 9 | 6 | 4 | 3 | 4 | 3 | 3 | 3 | 23 | 6 | 4 | 11 | 5 |
| 4D | 8 | 15 | 14 | 16 | 15 | 15 | 15 | 15 | 17 | 9 | 14 | 15 | 7 | 3 |
| 5D | 18 | 1 | 2 | 1 | 1 | 1 | 1 | 1 | 1 | 17 | 2 | 1 | 14 | 4 |
| 6D | 14 | 12 | 12 | 11 | 12 | 12 | 11 | 11 | 12 | 14 | 12 | 12 | 8 | 5 |
| 7D | 22 | 19 | 17 | 10 | 9 | 16 | 9 | 9 | 10 | 21 | 17 | 16 | 9 | 5 |
| Ch.Spring | 16 | 2 | 4 | 6 | 4 | 6 | 7 | 8 | 5 | 16 | 4 | 5 | 15 | 4 |
| Cheyenne | 21 | 10 | 9 | 7 | 7 | 7 | 6 | 6 | 7 | 22 | 9 | 7 | 7 | 5 |

The genotypes of 5D, 3A, 2A, 3D, 4A and recipient parent (Chinese Spring) revealed the highest stability based on the procedures of Nassar and Huehn (1987), Thennarasu (1995) and Ketata et al. (1989) (except Kr). According to the methods of Kang (1988), Fox et al. (1990) and Kr of Ketata et al. (1989) the genotypes 1D, 4B, 2D, 3B, 6B and 5B indicated the highest stability. These results were verified by Ward's hierarchical cluster analysis based on stability and mean yield (Figure 2).

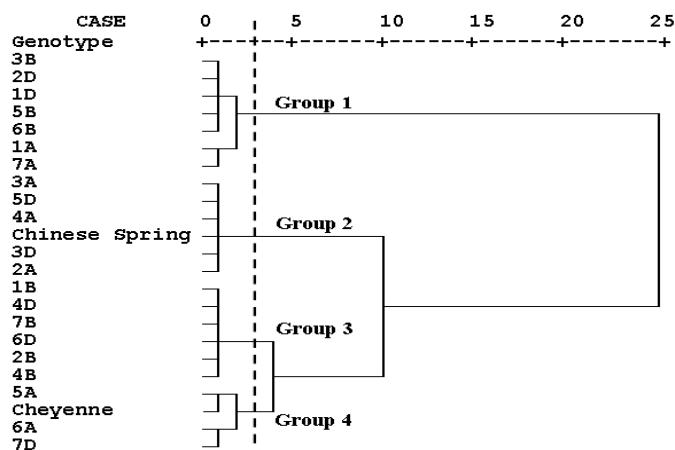


Figure 2. Dendrogram of Ward's hierarchical clustering of genotypes based on ranks of nonparametric statistics and mean grain yield

Cluster analysis of substitution lines grouped them into four distinct classes. The first group contained genotypes 3B, 2D, 1D, 5B, 6B, 1A and 7A which were stable based on mean yield and Kang (1988), Fox et al. (1990) and Kr of Ketata et al. (1989) methods. The second group consisted of genotypes 3A, 5D, 4A, 3D, 2A and recipient parent (Chinese Spring) which were stable based on Nssar and Huhn (1987) and Thennarasu (1995) procedures. The third and fourth groups included other genotypes and donor parent (Cheyenne) that had relatively low or moderate stability based on all nonparametric stability measures.

3.3 Principal Component Analysis

The first and second components accounted for 92.68% (77.71 and 14.97% by components 1 and 2, respectively) of total variations among the indices (Table 4).

Table 4. Eigen value, percentage of variance, cumulative variance, the first and second principal components

| Statistics | Component 1 | Component 2 |
|---------------------|-------------|-------------|
| gy | -0.743 | 0.645 |
| Kr | -0.753 | 0.610 |
| TOP | -0.688 | 0.607 |
| RS | -0.641 | 0.303 |
| $S_i^{(1)}$ | 0.791 | 0.546 |
| δr | 0.884 | 0.448 |
| $S_i^{(2)}$ | 0.884 | 0.448 |
| δgy | 0.954 | 0.272 |
| $NP_i^{(1)}$ | 0.963 | 0.214 |
| $S_i^{(3)}$ | 0.979 | 0.094 |
| $NP_i^{(3)}$ | 0.982 | -0.114 |
| $NP_i^{(2)}$ | 0.984 | -0.048 |
| $NP_i^{(4)}$ | 0.988 | -0.021 |
| $S_i^{(6)}$ | 0.993 | -0.052 |
| Eigenvalue | 10.88 | 2.10 |
| Percent of variance | 77.71 | 14.97 |
| Cumulative variance | 77.71 | 92.68 |

The statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, δr and δgy had the most positive portion in the first component and the statistics Kr, TOP, RS, $S_i^{(1)}$, δr , $S_i^{(2)}$ and grain yield exhibited the most positive portion in the second component. This result was confirmed by statistics cluster analysis.

The biplot of the first and second components (Figure 3) classified the stability estimates into 2 groups, the first group contains statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, δr and δgy with positive correlation (acute angle) and the second group contains RS, TOP, Kr and gy with positive correlation (acute angle) which is in complete agreement of cluster analysis.

Substitution lines scattering based on biplot was also in consistent with the grouping of cluster analysis. The first component revealed the lowest value for genotypes 3A, 5D, 4A, 3D, 2A and Chinese Spring (Clustering group 2) and the most value for genotypes 1A, 7A, 6B, 5B, 3B, 2D and 1D (Clustering group 1). Group 3 and 4 showed relatively moderate values for the first component. Therefore, considering the first component the genotypes of group 1 had the most stability based on TOP, RS and kr statistics and mean of grain yield, beside the genotypes of group 2 had the most stability based on statistics of $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, δr and δgy . The second component was only able to separate the third group from the fourth group which both displayed relatively low or moderate stability based on all nonparametric statistics.

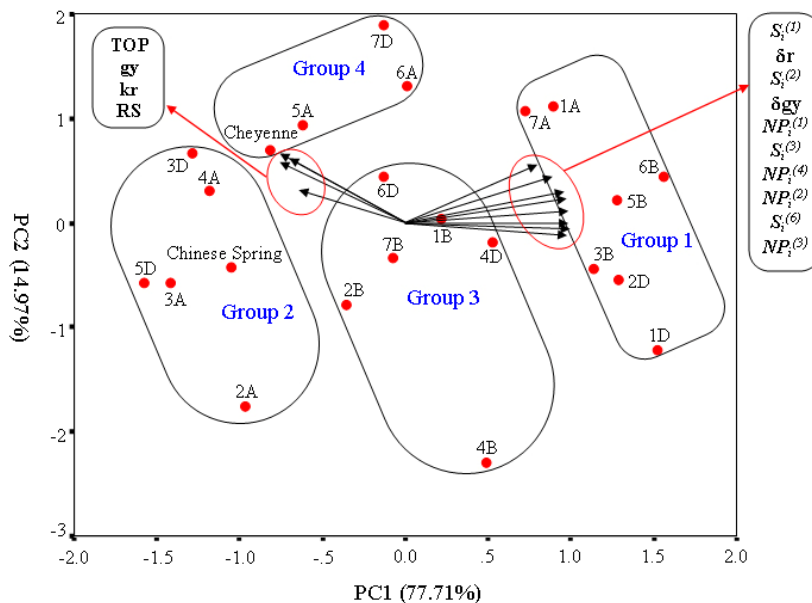


Figure 3. Biplot of nonparametric statistics and substitution lines based on two first components

4. Discussion

Stability analyses are very important in the development and evaluation of plant varieties because they reduce the genotypic stability values under diverse environments. Non-parametric methods were developed based on genotype ranking and the correlations among them were used for finding which one is repeatable in different crops and which ones are similar and can be used as an alternative to others (Mohammadi et al., 2009). Study of interrelationship among nonparametric measures based on Spearman's rank correlation, Ward's hierarchical cluster analysis and biplot of the first and second components showed two major groups of statistics. Analogous results were reported by Mohammadi et al. (2009) in bread wheat and Abdulahi et al. (2007) in Safflower. There are two concepts about stability; biological or static is the first concept which is based on this idea that stable genotype has a minimal variance for yield across environments (Becker & Leon, 1988; Akcura & Kaya, 2008). This concept of stability is not acceptable to most breeders and agronomists, who prefer genotypes with high mean yields and the potential to respond to agronomic inputs or better environmental conditions. This idea of stability may be called dynamic concept of stability (Becker, 1981; Akcura & Kaya, 2008). Our study indicated that the nonparametric statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$, $NP_i^{(4)}$, δr and δgy represent static concept of stability and are not correlated with mean yield, while statistics RS, TOP and Kr represent dynamic concepts of stability and are correlated with mean yield.

Regardless of the concept of stability and based on the most of the non-parametric stability estimates most of the QTLs controlling adaptation in wheat are distributed and located on chromosomes 2A, 3A and 4A in A genome and 3D and 5D in D genome. Using AMMI model Farshadfar and Sutka (2003) reported that chromosomes 4A carry the genes controlling general adaptation and QTLs responsible for specific adaptation to rainfed condition were located on chromosomes 3A and 3D in wheat which is in agreement of our results. 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.

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