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Evaluation of Safflower (*Carthamus* spp.) Genotypes in Multi-Environment Trials by Nonparametric Methods

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Abstract: The objectives of this study were to identify of the 16 safflower (*Carthamus* spp.) genotypes that have both high and stable yield performance across different environments through apply nonparametric measures and study on the relationship among nonparametric stability statistics. Yield data of the 16 safflower genotypes selected from Iran/ICARDA joint project grown in 18 rain fed environments during 2003-05 in Iran was collected. Results of nonparametric tests of $G \times E$ and a combined ANOVA across environments indicated the presence of both crossover and usual crossover interactions and genotypes varied significantly for the grain yield. In this study, low values of sum of yield ranks and Shukla's stability variance, Rank Sum (RS), were associated with high yield, but the other nonparametric stability methods were not significantly correlated with mean yield. According to RS, three genotypes viz, G2, G14 and G16 were the best. Measure for general adaptability (TOP) high value indicates widely adapted genotype, according to TOP measure the genotypes G7 followed by G4 and G16 were relatively adapted. Regarding to RS and TOP, G16 (PI-537598) was the best genotype, which has high TOP value and low RS value also has the highest yield. So, could be selected as an adapted and stable genotype among all genotypes, although according to other nonparametric measures G16 was not selected as stable genotype.

Key words: Multi environment trials, nonparametric measures, safflower, stability

INTRODUCTION

Parametric and nonparametric methods for estimating the Genotype \times Environment ($G \times E$) interactions and phenotypic stability are used in plant breeding programs (Kaya *et al.*, 2003). Several parametric methods such as variance component, multivariate analysis, regression methods and cluster analysis techniques have been proposed for the estimation and partitioning of $G \times E$ interactions (Huehn, 1990; Sabaghnia *et al.*, 2006). Nonparametric measures for stability based on ranks provide a viable alternative to the existing parametric measures based on the absolute data. Stability measures based on ranks require no statistical assumptions about the distribution of the phenotypic values. They are easy to use and interpret and as compared with parametric measures are less sensitive to errors of measurement. Furthermore, addition and deletion of one or a few observations is not as likely to cause great variation in the estimation as would be the case for parametric stability measures (Nassar and Huehn, 1987; Kaya *et al.*, 2003). Nassar and Huehn (1987) proposed four nonparametric measurements of the phenotypic stability (1) $S_1^{(1)}$ is the

mean of the absolute rank differences of a genotype over then environments, (2) $S_1^{(2)}$ is the variance among the ranks over the n environments, (3) $S_1^{(3)}$ and (4) $S_1^{(4)}$ are the sum of the absolute deviations and sum of squares of ranks for the each genotype relative to the mean of ranks, respectively (Sabaghnia *et al.*, 2006).

Kang (1988) assigned ranks for the mean yield, with the genotype having the highest yield receiving the rank of 1 and ranks for the stability variance of Shukla (1972), with the lowest estimated value receiving the rank of 1. The sum of these two ranks provides a final index, in which the genotype with the lowest rank-sum is regarded as the most desirable. Fox *et al.* (1990) suggested a non parametric superiority measure for the general adaptability. They used stratified ranking of the cultivars and ranking was done at each environment separately: the proportion of sites at which the cultivar occurred in the top, middle and bottom third of the ranks was computed to form the nonparametric measures TOP, MID and LOW, respectively. A genotype that occurred mostly in the top third (high value of TOP) was considered as widely adapted genotype. Thennarasu (1995) proposed the nonparametric statistics $Np_1^{(1)}$, $Np_1^{(2)}$, $Np_1^{(3)}$ and $Np_1^{(4)}$

based on ranks of adjusted mean of the genotypes as those whose position in relation to the others remained unaltered in the set of environments assessed as stability measures.

Many statistical procedures have been proposed to study the G×E (Westcott, 1986; Crossa, 1990; Lin and Binns, 1994; Kang and Gauch, 1996). Most of these procedures, however, fail to distinguish between significant crossover and noncrossover (usual) interaction (Baker, 1990). Nonparametric statistical procedures for the test of crossover interactions have been developed in the field of medicine and can be applied to G×E interactions in MET (Truberg and Huehn, 2000). These procedures are the Bredenkamp method (Bortz *et al.*, 1990; Bredenkamp, 1974; Huehn and Leon, 1995), the Hildebrand method (Bortz *et al.*, 1990), the Kubinger method (Kubinger, 1986; Bortz *et al.*, 1990) and the van der Laan-de Kroon method (de Kroon and van der Laan, 1981). These methods for the test of G×E provide a useful alternative to parametric methods such as the analysis of variance (ANOVA) currently used, which is based on original data value. The objectives of this study were to (i) identify safflower genotypes that have both high yield and stable yield performance across different environments (ii) apply nonparametric tests to investigate the crossover and noncrossover interaction in multi environment trials (MET) and (iii) study the relationship among nonparametric stability statistics.

MATERIALS AND METHODS

This study was carried out with 16 safflower (*Carthamus* spp.) genotypes in 18 environments (year-location combinations during the 2003-2005) that were presented in Table 1. Experiments were conducted in

Randomized Completely Block Design (RCBD) with four replications in each environment. Sowing procedure was done by hand in 1.5×4 m plots, consisting of five rows with 30 cm row spacing. Seeding rate was 30 seeds m⁻² for the each location. Fertilizer application was 40 kg ha⁻¹ Nitrogen and 60 kg ha⁻¹ P₂O₅ at planting and 40 kg ha⁻¹ Nitrogen as top dressing in early spring. Yield (kg ha⁻¹) was obtained by converting the grain yields obtained from plot to hectare.

Statistical approaches for an analysis of (G×E) interactions and appropriate tests of significance have been divided into two distinct groups: parametric and non parametric. The parametric approach is ANOVA that is based on the original absolute yield data from the two way classification with genotypes (rows) and environments (columns). The nonparametric approaches use the ranks of genotypes in different environments. Two types of the nonparametric statistical procedures Bredenkamp method (Bredenkamp, 1974; Huehn and Leon, 1995; Sabaghnia *et al.*, 2006) and van der Laan-de Kroon method (de Kroon and van der Laan, 1981; Huehn and Leon, 1995) were used. The method of Bredenkamp (Bredenkamp, 1974; Huehn and Leon, 1995; Mohammadi *et al.*, 2007) is based on the usual model for interactions: Interactions are defined as deviations from the additivity of main effects and in the van der Laan-de Kroon (de Kroon and van der Laan, 1981; Huehn and Leon, 1995) method it was used for test of the crossover G×E [G×(E) is rank changes of the genotypes within environments and E×(G) is rank changes of environments within genotypes(de Kroon and van der Laan, 1981)]. These statistical methods are approximately chi-square distributed with (L-1) (M-1) degree of freedom, where L = No. of genotypes and M = No. of environments (Huehn and Leon, 1995) and the nonparametric stability

Table 1: Years, locations, names and origin of genotypes and annual precipitations for the each environment

| Environment | Years | Location | Precipitation (mm) | Genotypes | Symbols | Origin of genotypes |
|-------------|---------|-------------|--------------------|-----------|-------------|-------------------------|
| 1 | 2002-03 | Sararood | 424.4 | G1 | CH-5 | America |
| 2 | 2002-03 | Ardebil | 274.0 | G2 | PI-250537 | World Bank of Safflower |
| 3 | 2002-03 | Ghamloo | 354.0 | G3 | Syrian | Syria |
| 4 | 2002-03 | Gonbad | 444.7 | G4 | CW-74 | America |
| 5 | 2002-03 | Shirvan | 301.0 | G5 | Dincer | Turkey |
| 6 | 2002-03 | Khoram abad | 335.4 | G6 | Zarghan279 | Iran |
| 7 | 2003-04 | Sararood | 588.0 | G7 | LRV-55-245 | Iran |
| 8 | 2003-04 | Ardebil | 282.0 | G8 | PI-198290 | World Bank of Safflower |
| 9 | 2003-04 | Ghamloo | 425.0 | G9 | Hartman | America |
| 10 | 2003-04 | Gonbad | 492.8 | G10 | Gila | America |
| 11 | 2003-04 | Shirvan | 251.0 | G11 | Kino-76 | ICARDA |
| 12 | 2003-04 | Khoram abad | 466.7 | G12 | Yenice | Turkey |
| 13 | 2004-05 | Sararood | 431.5 | G13 | PI-537636 | World Bank of Safflower |
| 14 | 2004-05 | Ardebil | 286.2 | G14 | PI-537636-s | World Bank of Safflower |
| 15 | 2004-05 | Ghamloo | 333.7 | G15 | LRV-51-51 | Iran |
| 16 | 2004-05 | Gonbad | 700.6 | G16 | PI-537598 | World Bank of Safflower |
| 17 | 2004-05 | Shirvan | 242.2 | | | |
| 18 | 2004-05 | Khoram abad | 482.9 | | | |

statistics $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$ (Nassar and Huehn, 1987; Sabaghnia *et al.*, 2006; Mohammadi *et al.*, 2007); $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (Thennarasu, 1995; Mohammadi *et al.*, 2007); RS (Kang, 1988) and TOP, MID and LOW (Fox *et al.*, 1990) were used.

RESULTS AND DISCUSSION

Genotype×environment: The results (Table 2) indicated that both noncrossover and crossover interactions [G×(E) and E×(G)] were significant according to Brdenkamp (1974) (for non crossover) and the van der Laan-de Kroon (1981) (for crossover) procedures. These results were in agreement with the ANOVA method, but provided more specific information about the nature of (G×E). For each genotype, Z_1 and Z_2 values (Nassar and Huehn, 1987; Kaya *et al.*, 2003; Mohammadi *et al.*, 2007) were calculated based on the ranks of adjusted data and summed over the genotypes to obtain Z values (Table 3). It is seen that Z_1 sum = 29.180 and Z_2 sum = 29.877. Since both of these statistics were more than the critical value $\chi^2 = 29.0$ ($p = 0.05$, $df = 15$), significant differences in rank stability were found among the 16 genotypes grown in 18 environments. On inspecting the individual Z values, it was found that the genotypes were significantly unstable relative to others, because they showed large Z values, in comparison with the critical value $\chi^2 = 3.84$, ($p = 0.05$, $df = 1$). The $S_i^{(1)}$ and $S_i^{(2)}$ statistics are based on ranks of genotypes across environments and they give equal weight to each environment. Genotypes with fewer changes in rank are considered to be more stable (Becker and Leon, 1988). Nevertheless, these two statistics ranked genotypes similarity for stability. For example, according to both $S_i^{(1)}$ and $S_i^{(2)}$, G2 had the smallest changes in ranks and is thus, regarded as the most stable genotype unlike G1 and G9. The next most stable genotype was G8. Two other nonparametric statistics $S_i^{(3)}$ and $S_i^{(6)}$ combine yield and stability based on yield ranks of genotypes in each environment and these parameters measure stability in units of the mean rank of each genotype (Nassar and Huehn, 1987; Sabaghnia *et al.*, 2006). The lowest value for the each of these statistics indicates maximum stability for a certain genotype. G2 followed by G8 and G14 were the most stable according to the $S_i^{(3)}$ and $S_i^{(6)}$ parameters, respectively. Mean yield of G6 followed by G5 were the lowest among the genotypes tested. The observed highest mean yield has been taken from G16 and followed it by G1 and G9 (Table 3).

Results of the Thennarasu's (1995) nonparametric stability statistics, which are calculated from ranks of adjusted yield means, are shown in Table 3 and the ranks

of the genotypes according to these parameters are given in Table 4. According to the first method ($NP_i^{(1)}$), G2 was followed by G8 and G14 were stable in comparison with the other genotypes. These genotypes had the lowest value of $NP_i^{(2)}$ and were stable due to of the high values for $NP_i^{(2)}$. The stabilities of G7 followed by G16, G3 and G4 were low (Table 2). $NP_i^{(3)}$, identified G2 as the most stable genotype. The next most stable genotypes were G14 and G8 which had low mean yield performance. The unstable genotypes based on $NP_i^{(3)}$ were G7 followed by G15 and G16, which G15 and G7 had low mean yield but G16 had the highest mean yield. So there is not any relationship between $NP_i^{(3)}$ and mean yield (Table 5). Stability parameter $NP_i^{(4)}$ identified G2 as a stable genotype, followed by G14 and G8; but like $NP_i^{(3)}$, identified G7, G15 followed by G16 as unstable. The genotypes with the lowest rank-sum (RS) are the most favorable. According to the RS statistic, G2 followed by G14 and G16 had the minimum value for RS and therefore were stable genotypes with high yield (Table 3). According to the RS statistic, the undesirable genotypes were found as G7 and G15. Similarly, According to Foxs *et al.* (1990) measurements, a genotype usually found in the top third of entries across environments (TOP) can be considered relatively well adapted and stable. According to TOP parameter the genotypes G7 followed by G4, G16 and G11 relatively adapted. Regarding to RS and TOP, G16 is the best genotype which has high TOP value and low RS value also has the highest mean yield, so could be selected as an adapted and stable genotype among all genotypes, although relative to other genotypes G16 is an unstable genotype, the reason is, other nonparametric measures indicate stability and high yield has not any effect on their value.

Interrelationship among nonparametric measures:

The Spearman's rank correlations between each pair of nonparametric stability measures were calculated (Table 5) and demonstrate a high positive significant rank correlation between $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$. The measurements of $S_i^{(3)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ had significantly negatively correlated with the percentage of environments in which it ranked in the top third of genotypes (TOP). The parameters, $S_i^{(3)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ were positively correlated with RS ($p < 0.05$). Mean yield rank had positive correlation with RS ($p < 0.05$). Clustering of the 10 nonparametric rank measures and mean yield rank grouped these measures in four groups: 1. $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ measures that show only stability, 2. $S_i^{(6)}$ parameter, 3. RS and Y (mean yield rank) and 4. TOP measure.

Table 2: The tests statistics for the (G×E) interaction using parametric (ANOVA) and nonparametric (Bredenkamp and Laan-Kroon) methods on 16 genotypes grown in 18 environments

| SOV | df | Non parametric method | | | |
|-----------------|-----|---|--|---|-------|
| | | Parametric method ANOVA (F) [†] | Bredenkamp (Non-crossover interaction) χ ² -statistic | Laan-Kroon (Crossover interaction) G×(E) χ ² -statistic E×(G) χ ² -statistic | |
| Environment (E) | 17 | 102.44** | 814** | 853** | 853** |
| Genotype (G) | 15 | 6.04** | 820** | 852** | 853** |
| G×E | 289 | 2.76** | 1616** | 1122** | 886** |

** significant at 0.01 probability level. [†]Environments (year and location) and genotypes were considered as random and fixed factors, respectively

Table 3: Mean values (Y) and nonparametric stability parameters for the grain yield and tests of nonparametric stability measures (Z₁ and Z₂) for the 16 safflower genotypes

| Genotype | Y | S ₁ ^{(1)*} | Z ₁ [†] | S ₁ ^{(2)*} | Z ₂ [†] | S ₁ ⁽³⁾ | S ₁ ⁽⁶⁾ | NP ₁ ^{(1)†} | NP ₁ ^{(2)†} | NP ₁ ^{(3)†} | NP ₁ ^{(4)†} | TOP [‡] | MID [‡] | LOW [‡] | RS [¥] |
|----------|-----|--------------------------------|-----------------------------|--------------------------------|-----------------------------|-------------------------------|-------------------------------|---------------------------------|---------------------------------|---------------------------------|---------------------------------|------------------|------------------|------------------|-----------------|
| G1 | 869 | 6.549 | 3.925 | 32.928 | 5.986 | 56.607 | 10.472 | 5.278 | 0.556 | 0.564 | 0.662 | 28 | 17 | 56 | 18 |
| G2 | 791 | 3.752 | 6.255 | 10.889 | 4.712 | 22.514 | 13.743 | 2.444 | 0.306 | 0.390 | 0.456 | 22 | 50 | 28 | 5 |
| G3 | 744 | 5.438 | 0.040 | 21.294 | 0.000 | 45.250 | 12.548 | 4.056 | 0.624 | 0.561 | 0.680 | 33 | 44 | 22 | 16 |
| G4 | 711 | 5.157 | 0.062 | 19.441 | 0.144 | 46.116 | 9.770 | 3.722 | 0.620 | 0.598 | 0.720 | 44 | 39 | 17 | 17 |
| G5 | 624 | 4.758 | 0.789 | 16.706 | 0.906 | 35.500 | 14.310 | 3.167 | 0.422 | 0.497 | 0.595 | 22 | 56 | 22 | 20 |
| G6 | 547 | 4.647 | 1.137 | 16.448 | 1.012 | 33.779 | 18.727 | 3.222 | 0.379 | 0.476 | 0.561 | 28 | 61 | 11 | 20 |
| G7 | 689 | 6.033 | 1.332 | 27.899 | 1.940 | 64.188 | 13.696 | 4.444 | 0.988 | 0.695 | 0.816 | 56 | 22 | 22 | 24 |
| G8 | 682 | 3.961 | 4.691 | 12.118 | 3.660 | 26.870 | 7.357 | 2.667 | 0.381 | 0.441 | 0.517 | 28 | 56 | 17 | 15 |
| G9 | 814 | 6.235 | 2.186 | 28.941 | 2.596 | 50.897 | 11.793 | 4.500 | 0.429 | 0.541 | 0.645 | 28 | 22 | 50 | 18 |
| G10 | 737 | 6.157 | 1.830 | 28.353 | 2.214 | 51.643 | 10.391 | 4.556 | 0.456 | 0.554 | 0.660 | 28 | 22 | 50 | 22 |
| G11 | 723 | 5.085 | 0.133 | 19.477 | 0.138 | 35.904 | 8.024 | 4.000 | 0.500 | 0.465 | 0.551 | 39 | 22 | 39 | 17 |
| G12 | 689 | 4.863 | 0.519 | 17.242 | 0.705 | 35.649 | 7.784 | 3.722 | 0.496 | 0.491 | 0.591 | 33 | 44 | 22 | 17 |
| G13 | 753 | 6.196 | 2.004 | 28.340 | 2.206 | 52.878 | 11.397 | 4.667 | 0.519 | 0.568 | 0.680 | 28 | 28 | 44 | 19 |
| G14 | 778 | 4.477 | 1.792 | 16.016 | 1.202 | 29.000 | 7.537 | 3.056 | 0.306 | 0.414 | 0.477 | 11 | 50 | 39 | 8 |
| G15 | 634 | 5.961 | 1.079 | 26.105 | 1.034 | 54.712 | 10.647 | 4.111 | 0.587 | 0.612 | 0.735 | 33 | 39 | 28 | 24 |
| G16 | 994 | 6.052 | 1.405 | 26.941 | 1.422 | 54.960 | 12.029 | 4.500 | 0.692 | 0.605 | 0.726 | 39 | 28 | 33 | 12 |
| Sum | | | 29.180 | | | 29.877 | | | | | | | | | |

Test statistics

$$\begin{aligned}
 E(S_1^{(1)}) &= 5.31 & E(S_2^{(2)}) &= 21.25 \\
 \text{Var}(S_1^{(1)}) &= 0.389 & \text{Var}(S_2^{(2)}) &= 22.78 \\
 \chi^2 \text{ Sum}^* &= 25 & \chi^2 Z_1, Z_2^\dagger &= 3.84 \\
 \text{Grand mean} &= 736 \text{ kg ha}^{-1}
 \end{aligned}$$

*S₁⁽¹⁾ statistics measures the mean absolute rank difference of a genotype over environments and S₂⁽²⁾ is the common variance of the ranks; the Z-statistics are measures of stability; ¥ χ² Z₁, Z₂: Chi-square for Z₁⁽¹⁾, Z₂⁽²⁾; χ² Sum: chi-square for sum of Z₁⁽¹⁾, Z₂⁽²⁾ † NP are the parameters of Thenarasu (1995); ‡TOP, MID and LOW are the parameters of Fox *et al.* (1990); ¥ RS is the rank-sum of Kang (1988)

Table 4: Ranks of the 16 safflower genotypes after yield data from 18 environments were analyzed for the (G×E) and stability using 10 different nonparametric methods

| Genotype | Y | S ₁ ⁽¹⁾ | S ₁ ⁽²⁾ | S ₁ ⁽³⁾ | S ₁ ⁽⁶⁾ | NP ₁ ⁽¹⁾ | NP ₁ ⁽²⁾ | NP ₁ ⁽³⁾ | NP ₁ ⁽⁴⁾ | TOP | RS |
|----------|----|-------------------------------|-------------------------------|-------------------------------|-------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|-----|----|
| G1 | 2 | 13 | 16 | 15 | 7 | 12 | 8 | 10 | 8 | 5 | 6 |
| G2 | 4 | 1 | 1 | 1 | 13 | 1 | 1 | 1 | 1 | 6 | 1 |
| G3 | 7 | 9 | 9 | 8 | 12 | 7 | 10 | 10 | 9 | 4 | 5 |
| G4 | 10 | 8 | 7 | 9 | 5 | 5 | 10 | 12 | 10 | 2 | 6 |
| G5 | 14 | 5 | 5 | 5 | 14 | 4 | 3 | 7 | 6 | 6 | 7 |
| G6 | 15 | 4 | 4 | 4 | 15 | 4 | 2 | 5 | 5 | 5 | 7 |
| G7 | 11 | 10 | 12 | 16 | 13 | 8 | 12 | 14 | 12 | 1 | 9 |
| G8 | 12 | 2 | 2 | 2 | 1 | 2 | 2 | 3 | 3 | 5 | 4 |
| G9 | 3 | 12 | 15 | 10 | 10 | 9 | 4 | 8 | 7 | 5 | 6 |
| G10 | 8 | 12 | 14 | 11 | 6 | 10 | 5 | 9 | 8 | 5 | 8 |
| G11 | 9 | 7 | 8 | 7 | 4 | 6 | 6 | 4 | 4 | 3 | 6 |
| G12 | 11 | 6 | 6 | 6 | 3 | 5 | 6 | 6 | 6 | 4 | 6 |
| G13 | 6 | 12 | 13 | 12 | 9 | 11 | 7 | 11 | 9 | 5 | 7 |
| G14 | 5 | 3 | 3 | 3 | 2 | 3 | 1 | 2 | 2 | 7 | 2 |
| G15 | 13 | 10 | 10 | 13 | 8 | 7 | 9 | 13 | 11 | 4 | 9 |
| G16 | 1 | 11 | 11 | 14 | 11 | 9 | 11 | 13 | 11 | 3 | 3 |

Nonparametric measurements for the stability based on ranks provide a useful alternative to parametric measures currently used which are based on absolute

data (Huehn, 1990). In this study, obtained results of the nonparametric tests for the (G×E) interactions were similar to combined ANOVA. Similar results were reported

Table 5: Spearman's rank correlation coefficients between the different nonparametric stability parameters for the grain yield in the 16 genotypes

| Parameters | $S_i^{(1)}$ | $S_i^{(2)}$ | $S_i^{(3)}$ | $S_i^{(6)}$ | $NP_i^{(1)}$ | $NP_i^{(2)}$ | $NP_i^{(3)}$ | $NP_i^{(4)}$ | TOP | RS |
|--------------|-------------|-------------|-------------|-------------|--------------|--------------|--------------|--------------|--------|--------|
| $S_i^{(2)}$ | 0.989** | | | | | | | | | |
| $S_i^{(3)}$ | 0.893** | 0.888** | | | | | | | | |
| $S_i^{(6)}$ | 0.054 | 0.069 | 0.131 | | | | | | | |
| $NP_i^{(1)}$ | 0.987** | 0.978** | 0.889** | 0.062 | | | | | | |
| $NP_i^{(2)}$ | 0.616* | 0.596* | 0.826** | 0.108 | 0.624** | | | | | |
| $NP_i^{(3)}$ | 0.718** | 0.683** | 0.898** | 0.240 | 0.695** | 0.909** | | | | |
| $NP_i^{(4)}$ | 0.699** | 0.667** | 0.879** | 0.233 | 0.678** | 0.919** | 0.996** | | | |
| TOP | -0.314 | -0.323 | -0.560* | 0.054 | -0.327 | -0.846** | -0.658** | -0.685** | | |
| RS | 0.438 | 0.462 | 0.517* | 0.263 | 0.426 | 0.328 | 0.527* | 0.516* | -0.264 | |
| Y | -0.435 | -0.418 | -0.277 | 0.091 | -0.442 | -0.116 | -0.044 | -0.044 | -0.106 | 0.550* |

*, **Significant at the 0.05 and 0.01 levels, respectively

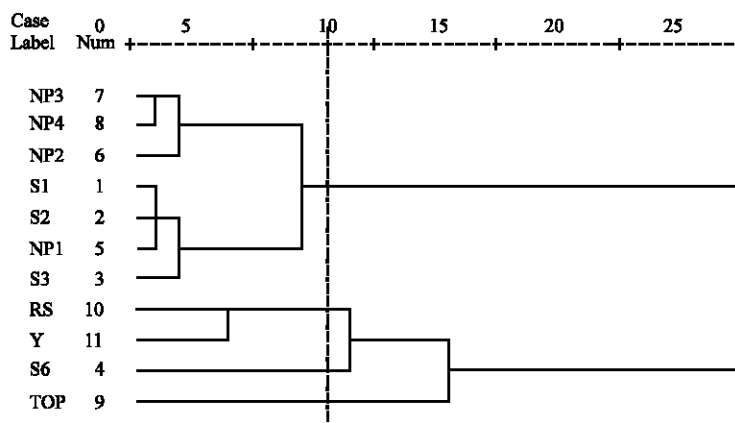


Fig. 1: Dendrogram presenting hierarchical clustering of 10 nonparametric rank measures and mean yield rank

by Huehn and Leon (1995) and Mohammadi *et al.* (2007), who recommended the Bredekamp test for non-crossover interaction and the van der Laan-de Kroon test for crossover interaction (Table 2).

We found that the three nonparametric statistics ($S_i^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$) (Nassar and Huehn, 1987; Mohammadi *et al.*, 2007) and the $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ parameters of Thenarasu (1995) clustered together as same-class statistics. These parameters classified genotypes as stable or unstable in a similar group. These parameters were positively and significantly correlated ($p < 0.01$), indicating that these measures were similar under different environmental conditions (Fig. 1 and Table 5). Consequently, only one of these parameters would be sufficient to select stable genotypes in a breeding program. Mohammadi *et al.* (2007) also found significantly positive correlations among these parameters in durum wheat. Scapim *et al.* (2000) found significantly positive correlations between $S_i^{(1)}$ and $S_i^{(2)}$ in maize. Flores *et al.* (1998) reported high rank correlations between $S_i^{(1)}$ and $S_i^{(2)}$ in faba bean and pea. These parameters are associated with the static concept of stability (Mohammadi *et al.*, 2007; Nassar and Huehn, 1987), as they define stability in the sense of homeostasis. The stability statistics of ($S_i^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$) and the $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ parameters represent static concepts of stability and are not correlated with

mean yield. Therefore, these stability statistics could be used as compromise methods to select genotypes with moderate yield and high stability. According to these measures, G2, G8 and G14 can be selected. In our study, positive significant correlation between RS and mean yield ($p < 0.05$) indicated that RS was the best parameter to identify high yielded genotypes. A low value of RS indicates the combination of high yield and high stability. According to RS, G2, G14 and G16 were the best genotypes. Consequently, we recommend use of RS as the best parameter to select superior genotypes.

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