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Appraising of drought tolerance relying on stability analysis indices in canola genotypes simultaneously, using selection index of ideal genotype (SIIG) technique: Introduction of new method

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ABSTRACT: The objective of this study was to develop a methodology to appraise best genotypes based on parametric and nonparametric stability methods using selection index of ideal genotype (SIIG) technique. This technique is one decision making method that is very simple to implement. According to this technique, the best genotype (stable genotype) would be the one that has the least of deviation from the positive ideal parameter and has the most of deviation from the negative ideal parameter. The positive ideal parameter is a parameter with maximizes the stability and minimizes the instability, whereas the negative ideal parameter is a parameter with maximizes the instability and minimizes the stability. In this study, we work out a practical example to demonstrate the SIIG technique for evaluate the yield stability of some genotypes of canola using parametric and nonparametric stability methods. Six canola genotypes were evaluated at five environments in two growing seasons (2011-2012). In this investigation, parametric and nonparametric stability procedures have revealed useful implications for plant breeding research towards selection of drought tolerance genotypes. Principal component analysis pointed out that the first two PCs described 87.93% of the variance of stability procedures and mean yield; also this Biplot revealed that stability procedures can be classified into six groups. Finally, results from this study, indicated that SIIG technique would serve as a better platform to identify stable and high yielding genotypes using a set of stability methods, simultaneously.

Key words: Canola, Genotype × environment interaction, Stability analysis, SIIG technique

Abbreviation: b_i: regression coefficient; CV_i: coefficient of variation; IG_i: ideal genotype; GEI: genotype × environment interaction; $NPi^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$: Thennarasu's non-parametric stability statistics; PC: principal component; PI: superiority index; $\bar{R}$: mean of rank; R_i^2: coefficient of determination; SDR: standard deviation of rank; S^2d_i: deviation from regression; S^2_{xi}: environmental variance; $S_i^{(1)}$: mean of absolute rank difference; $S_i^{(2)}$: sum of square deviations; $S_i^{(3)}$: variance among the ranks over environments; SIIG: selection index of ideal genotype; $S_i^{(6)}$: sum of absolute deviation; W_i^2: Wricke's ecovalence; σ_i^2: stability variance

INTRODUCTION

Identification of high yielding and stable genotypes across variable environments has been a continued challenge to plant breeders worldwide (Alwala *et al.,* 2010). Yield stability depends on plant characteristics, such as resistance or tolerance to environmental stress factors. By determining factors responsible for genotype × environment interaction or stability/instability, breeders can improve cultivar stability. Resistance or tolerance to biotic or abiotic stress is essential for stable performance (Duvick, 1996). Sources of increased crop productivity include enhanced yield potential, improved yield stability, heterosis, modified plant types, gene pyramiding and exotic and transgenic germplasm (Khush, 1993). It is important to identify the factors that are responsible for GEI.

Different parametric stability methods have been investigated and proposed to study genotype × environment interaction. Wricke (1962) moved a proposal using GEI for each genotype as a stability procedure. Francis and Kannenberg (1978) used the environmental variance (S_i^2) and the coefficient of variance (CV_i) to define stable genotypes. Shukla (1972) suggested an unbiased estimated using stability variance of genotypes. Eberhart and Russell (1966) developed linear regression and suggested the use of mean squares of deviation from linearity as stability method when describing the performance of one genotype across environments.

Also Lin and Binns (1988) proposed the cultivar performance measure and defined superiority index (PI) of genotype ith as the mean square of distance between genotype i^{th} and the genotype with the maximum response.

Different nonparametric stability procedures have been proffered to study and interpret the GEI. Nassar and Huehn (1987) and Huehn (1979) suggested nonparametric procedures of stability $S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$ and $Si^{(6)}$ based on the classification of the cultivars in different environments and also Thennarasu (1995) introduced nonparametric procedures $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ based on ranks of corrected means of the cultivars in each environment. Nonparametric procedures have been used based on the ranks of cultivars in different environments, and cultivars with similar rankings in environments are categorized as stable genotypes.

Selection index of ideal genotype (SIIG) technique, proposed in this paper, is one that is very simple and easy to implement. According to this technique, the best genotype would be the one that has the least deviation from the positive ideal parameter and the most deviation from the negative ideal parameter. The positive ideal parameter is a parameter with maximizes the stability and minimizes the instability, whereas the negative ideal parameter is a parameter with maximizes the instability and minimizes the stability. In other words, the positive ideal parameter is composed of all the best values attainable of stability, whereas the negative ideal instability consists of all the worst values attainable of stability. In fact, SIIG technique is derived from technique for order preference by similarity to ideal solution (TOPSIS) method (Hwang and Yoon, 1981).

In selection index of ideal genotype (SIIG) technique there were several properties: 1. Help to select stable genotypes using parametric and nonparametric methods. If for selection of stable genotypes, researchers can be used several stability methods simultaneously, presumably will increase the efficiency of selection. SIIG method is able to combine different stability methods to choices genotype ideal. 2. Simultaneous selection for yield and stability. 3. Each stability method (trait) can be examined according to its importance. 4. SIIG method is used for assessing the final ranking of the stable genotypes.

SIIG technique that was proposed in this paper (as new method in plant breeding) is a method that can select stable genotypes using parametric and nonparametric stability procedures. Therefore, in us research with practical research to explain the principles of this method. So far, there has been no discussion about application of SIIG technique in plant breeding, especially in stable genotypes selection. The purposes of this investigation were to (1) Assessment of stability six canola genotypes grown in two year for seed yield using different stability methods, (2) testing and application of SIIG method that can select stable genotype using a set of stability methods, simultaneously and (3) The main purpose of this study is to develop an understanding of application SIIG technique in plant breeding.

MATERIALS AND METHODS

This study was produced at the experimental farm of agricultural research institute and natural resources, Yazd, Iran. The experiment was conducted as split plot based on randomized complete block design with three replications. Irrigation regimes were considered as main plots and cultivars as subplots. Six winter rapeseed cultivars including SLM046, Tassilo, Karun, Adriana, Cooper and Lilian were evaluated based on their reputed differences in yield performance under irrigated and no irrigated. The irrigation regimes in first year included: E1 = well-watered (irrigation during full season); E2 = water deficit at flowering stage until podding stage and the irrigation regimes in second year included: E3 = well-watered (irrigation during full season); E4 = water deficit from stem elongation stage until flowering and; E5 = water deficit from flowering stage until podding stage.

Rapeseed seeds were hand sown as furrow method at 25 June in two years (2011-2012). Each plot consisted of 2 rows, 2 m length, 80 cm distance between rows, and 6 cm distance between plants. All plants were well-watered and received irrigation uniformly until the imposition of the treatments. Weeds were hand controlled continuously during rapeseed vegetative growth. Data on seed yield were taken from the two rows of each plot. After harvesting, seed yield was determined for each genotype at each drought stress and control treatments.

Methods of stability:

Analysis of variance was executed across environments (non-stress and stress conditions) in two years using SPSS software. The stability indexes were performed in correspond with Eberthart and Russell's (1996), the regression coefficient (b_i) and deviation from regression (S^2d_i), Pinthus's (1973) coefficients of determination (R_i^2), Lin and Binn's (1988) superiority index (PI), Wricke's (1962) ecovalance (W_i^2), Shukla's (1972) stability variance (σ_i^2), Francis and Kannenberg's (1978) coefficient of variability (CV_i) and environmental stability variance (S_i^2) were calculated for all genotypes using Excel software.

The four nonparametric stability methods ($S_i^{(1)}$, $Si^{(2)}$, $S_i^{(3)}$ and $S_i(6)$) were achieved in according to Huehn (1979) and Nassar and Huehn (1987), nonparametric stability measures ($NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$) were performed in correspond with Thennarasu (1995).

The relationships among the parametric, nonparametric methods and genotypes were carried out using principal component (PC) analysis.

SIIG method development for parametric and nonparametric stability procedures:

Selection index of ideal genotype (SIIG) technique was improved as following method to the selection of favorable genotypes using parametric and nonparametric stability procedures simultaneously. The basic concept of this technique was based on selecting the best genotypes (stable genotype) that should had the shortest deviation from the ideal parameter and the farthest deviation from the negative ideal parameter in a geometrical sense. In this method there were two hypotheses: 1. Ideal parameter: the one which had maximizes the stability and minimizes the instability for all genotypes considered. 2. Negative ideal parameter: the one which had maximizes the instability and minimizes the stability for all genotypes. SIIG method selects the genotype that was the closet to the ideal parameter and farthest from negative ideal parameter. In SIIG technique, supposes that we had m stability procedures (or trait) and n genotypes and we had the score of each stability method with respect to each genotype.

Assume in an examination having n genotypes, G1, G2, . . ., Gn and m stability methods or trait, T1, T2, . . ., Tm. Each genotype appraised regarding the m stability methods. All the values appointed to genotypes with respect to decision matrix marked by $X(xij)_{n\times m}$.

The SIIG technique is composed of the following steps:

Step 1: Construct normalized selection matrix:

The normalization of the decision matrix was done using the following transformation for each r_{ij}.

$$r_{ij} = \frac{x_{ij}}{\sqrt{\sum_{i=1}^{n} x_{ij}^2}} \qquad i = 1, \dots, n; \qquad j = 1, \dots, m.$$

Where r_{ij} is the normalized stability methods or different trait value.

$$D = \begin{bmatrix} x_{11} & x_{12} & \cdots & x_{1m} \\ x_{21} & x_{22} & & x_{2m} \\ \vdots & & \ddots & \vdots \\ x_{n1} & x_{n2} & \cdots & x_{nm} \end{bmatrix} \rightarrow R$$
$$= \begin{bmatrix} r_{11} & r_{12} & \cdots & r_{1m} \\ r_{21} & r_{22} & & r_{2m} \\ \vdots & & \ddots & \vdots \\ r_{n1} & r_{n2} & \cdots & r_{nm} \end{bmatrix}$$

Step 2: Determine the positive ideal parameter (maximum stability) and negative ideal parameter (minimum stability) genotypes:

The positive ideal and negative ideal parameters are determined, respectively, as follows:

$$A^+ = \{r_1^+, r_2^+, \dots, r_m^+\}$$
$$A^+ = \{(\max\ r_{ij} \mid j \in \Omega_b), (\min r_{ij} \mid j \in j\,\Omega_c)\}$$

Where Ω_b is the set of maximum stability and Ω_c is the set of minimum instability.

$$A^- = \{r_1^-, r_2^-, \dots, r_m^-\}$$
$$A^- = \{(\min r_{ij} \mid j \in \Omega_b), (\max r_{ij} \mid j \in j\,\Omega_c)\}$$

Where Ω_b is the set of minimum stability and Ω_c is the set of maximum instability.

Step 3: Calculate the segregation measures for each genotype:

The two Euclidean distances for each genotype were calculated. The separation of each stability value from the positive ideal parameter is given as:

$$d_i^+ = \sqrt{\sum_{j=1}^{m} (r_{ij} - r_j^+)^2} \qquad i = 1, \dots, n$$

Similarly, the separation from the negative ideal parameter is given as:

$$d_i^- = \sqrt{\sum_{j=1}^{m} (r_{ij} - r_j^-)^2} \qquad i = 1, \dots, n$$

Step 4: Calculate the relative closeness to the ideal parameter:

The relative closeness (for selection stable genotypes) to the ideal parameters can be defined as:

$$SIIG = \frac{d_i^-}{d_i^+ + d_i^-} \qquad i = 1, 2 \dots, m, \qquad 0 \le SIIG \le 1$$

Step 5: Rank the preference order:

The best stable genotypes could now be decided according to preference rank order of SIIG. Therefore, the best genotype was the one that had the shortest distance to the positive ideal parameter. The relationship of genotypes reveals that any genotype which had the shortest distance to the positive ideal parameter guaranteed to had the longest distance to the negative ideal parameter. Eventually, we should select the genotypes with SIIG closet to 1.

In this study, we work with a practical example to demonstrate the SIIG method for evaluated the stability of some canola genotypes using parametric and nonparametric procedures. A case study of comparing 6 canola genotypes at five stress conditions (environment) using the stability methods.

RESULTS

The mean performance of grain yield over stress and non-stress conditions (environments) indicated the relative efficiency of the genotypes perused across stress conditions (Table 2). The genotypes mean yield ranged from 1372.1 (Cooper genotype) to 1851.7 kg h^{-1} (SLM046 genotype) displaying differences among the genotypes across stress and non-stress conditions.

A. Analysis of variance

The split plot variance analysis of mean yield (kg h^{-1}) of 6 rapeseed genotypes tested in 5 environments is indicated in Table 1.

The analysis of variance showed that rapeseed grain yield was significantly ($p<0.01$) affected by environment, genotypes and genotype × environment interaction. Environments significantly explained about 78.89% of the total sum of squares. A large yield variation explained by stress conditions demonstrated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield. Alone the small portion that is, 6.10% of the total sum of squares was attributed to genotypic effects. Genotype × environment interaction significantly indicated 13.64% of the total sum of squares variation in grain yield. The importance of the GEI sum of squares was 2.24 times larger than genotypes, showing there were sizeable differences in genotypic response across stress different conditions (Table 1). GEI makes difficult to select the best performing and most stable (tolerance to drought) genotypes is a momentous evaluation in plant breeding programs because it reduces the progress from selection in any one stress condition.

Table 1: Partitioning of the sum of squares (SS) and mean of squares (MS) from the split plot variance analysis of 6 canola genotypes yield.

S.O.V	Df	Sum of square	SS%	Mean of square
Total	89	42590928.7		
Replication	2	27187.7	0.06	13593.8^{ns}
environment	4	33996361	78.89	8499090^{**}
Ea	8	50841.5	0.12	6355.2
Genotypes	5	2629620	6.10	525924^{**}
Genotypes × environment	20	5881830	13.64	294092^{**}
Eb	50	507888.5	1.18	10157.8

^{ns} and **: non-significant and significant at 1% probability level, respectively.

Table 2: Yield, parametric stability procedures and its ranks on 6 canola genotypes grown in 5 environments.

Genotypes name	S_i^2	CV_i	W_i^2	σ_i^2	S^2d_i	b_i	R_i^2	PI	Yield
SLM046	497385 (3)	38.1 (2)	135528 (2)	26320 (2)	45123 (3)	0.991 (4)	93.2 (3)	16989 (1)	1851.7 (1)
Tassilo	239362 (1)	29.8 (1)	888826 (6)	30880 6 (6)	15010 7 (6)	0.518 (6)	52.97 (6)	149726 (4)	1643.6 (3)
Karun	780742 (6)	63.1 (6)	249362 (4)	69007 (4)	40329 (2)	1.261 (1)	96.13 (2)	208566 (5)	1401.2 (5)
Adriana	751490 (5)	53.4 (4)	363139 (5)	11167 4 (5)	95960 (5)	1.12 (3)	90.42 (4)	124312 (3)	1621.3 (4)
Cooper	615477 (4)	57.2 (5)	118125 (1)	19794 (1)	30241 (1)	1.121 (2)	96.31 (1)	230352 (6)	1372.1 (6)
Lilian	438773 (2)	38.2 (3)	205282 (3)	52477 (3)	63358 (4)	0.91 (5)	89.17 (5)	60656 (2)	1735.5 (2)
Mean	**553871**	**46.63**	**326710**	**98013**	**70853**	**0.987**	**86.37**	**131767**	**1604.2**

S_i^2: environmental variance; CV_i: coefficient of variation; W_i^2: Wricke´s ecovalence; σ_i^2: stability variance of Shukla; S^2d_i: deviation from regression; b_i: regression coefficient; R_i^2: coefficient of determination; PI: superiority index

B. Analysis of stability methods

The assessments of the 8 parametric stability methods and the ranks of genotypes pursuant to these procedures are given in Table 2. Correspond to CV_i and S_i^2 methods, Tassilo genotype had the lowest value, and thus was the most stable one and Karun genotype was the most unstable one. Considering both W_i^2 and σ_i^2 methods, Lilian and SLM046 genotypes were the most favorable ones, although Tassilo and Karun genotypes were the unstable ones.

Eberhart and Russell's (1966) method is one of the most widely used stability methods that investigates both linear and non-linear components of interaction in selecting the genotypes stability. In this method a variety with high mean, regression coefficient $b_i = 1$ and deviation from regression not significantly different from zero ($S^2d_i = 0$) is stable genotype. Thus simultaneous regarding of slope of linear regression and mean squares of deviations from regression, Cooper genotype was the most stable ones (Table 3).

The coefficient of determination (Ri^2) of the linear regression model ranged from 52.97 (Tassilo genotype) to 96.31 (Cooper genotype). Genotypes with high coefficient of determination (Ri^2) values can be appraised adequately via the joint linear regression model and the response of the genotypes to different environments can be foretold (Crossa, 1990).

According to R_i^2 values, Cooper and Karun genotypes were the most stable ones but hadn't high mean yield (Table 2). Regarding superiority index (PI) values, SLM046 and Lilian genotypes had the lowest value of PI, thus its were stable in collation with the other genotypes which had high mean yield.

Appraisals of the genotypes based on ten nonparametric different procedures and the ranks of genotypes in accord with these methods, which are calculated from ranks of adjusted yield means, are showed in Table 3.

The magnitude test for the null hypothesis that all the genotypes are equally stable was done using a χ^2 distribution. For each rape seed genotype, $Z_i^{(1)}$ and $Z_i^{(2)}$ values were calculated based on the rank of the data and summed over genotypes to obtain Z values (Table 3); $Z_i^{(1)}$ sum = 7.112 and $Z_i^{(2)}$ sum = 7.931. Because both of these statistics were less than the critical value χ^2 0.05, df: 6 = 12.6, thus no significant differences were detected in rank stability among the 6 genotypes grown in 5 environments (Table 3).

The stability methods of Huehn (1979) including $Si^{(1)}$ and $S_i^{(2)}$ were suggested such that the ith genotype could be investigated stable in all environments under analysis if its groupings were similar in all stress conditions. Correspond both $Si^{(1)}$ and $Si^{(2)}$, Cooper genotype had the smallest variation in ranks and is therefore, regarded at the most stable of genotype unlike Tassilo genotype. The next most stable genotype was Lilian genotype. Ebadi-Segherloo *et al.* (2008) and Karimizadeh *et al.* (2013) pointed out that the $S_i^{(1)}$ and $S_i^{(2)}$ statistics are associated with the static or biological concept of stability. Therefore, these statistics define stability in the sense of homeostasis. Also genotype of Tassilo was the most unfavorable genotype based on $S_i^{(1)}$ and $S_i^{(2)}$ nonparametric methods (Table 3).

Two next nonparametric procedures of Huehn (1979), $Si^{(3)}$ and $Si^{(6)}$ combine yield and stability based on yield ranks of genotypes in each environment. These methods evaluate stability in units of the rank mean of each genotype (Huehn, 1979). The lowest value for each of these methods indicates most stability for a genotype. Lilian and Cooper genotypes were the most stable pursuant to the $S_i^{(3)}$ method, although them had the lowest minimum mean yield. Lilian and SLM046 genotypes indicated maximum stability correspond the $S_i^{(6)}$ method (Table 2).

Upshots of Thennarasu's (1995) nonparametric methods and the ranks of genotypes according to these methods, which are computed from ranks of adjusted yield means, are shown in Tables 2 and 3. According to these methods, SLM046 genotype had the lowest value of $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(6)}$, therefore it was stable in comparison with the other genotypes and had the high mean yield. Karun genotype had the highest value of $NP_i^{(1)}$ and $NPi^{(2)}$ and Tassilo genotype had the highest value of $NPi^{(3)}$ and $NPi^{(6)}$, thus they were unstable genotypes in comparison with the other genotypes. All of the Thennarasu's (1995) nonparametric methods have static concept of stability and define stability in the sense of homeostasis (Ebadi Segherloo *et al.*, 2008; Karimizadeh *et al.*, 2013).

Biplot analysis

In Fig. 1, a vector is drawn from the biplot origin to each marker of the stability procedures to simplify portrayal of the relationship among different stability methods. The correlation coefficient between any two stability procedures is approximated by the cosine of the angle between the vectors. Therefore, the most prominent relations correspond to Fig. 1 are: (1) strong positive association among $Si^{(1)}$, $Si^{(2)}$, S2di, SDR, σ_i^2, W_i^2 and $S_i^{(3)}$ as indicated by the small angles between their vectors, (2) high positive correlation among $NP_i^{(4)}$, $NP_i^{(3)}$, $S_i^{(3)}$ and $NP_i^{(1),\ (3)}$ strong positive association between regression $NP_i^{(2)}$ with PI, high correlation between S_i^2 with CV_i, between $\bar{R}$ with mean yield, as indicated by the small angles between their vectors, (4) strong negative correlation among mean yield and $\bar{R}$ statistic with PI and $NPi^{(2)}$, also negative correlation among mean yield and $\bar{R}$ statistic with Si^2 and CV_i (Fig. 1).

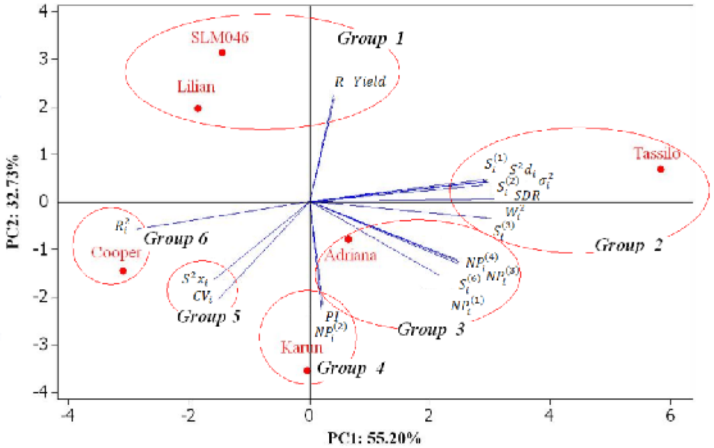

Fig. 1. Biplot based on first two principal components (PC1 and PC2) axes both parametric and nonparametric stability indices and 6 canola genotypes.

Simultaneous selection for yield and stability based on all of parametric methods using SIIG technique

SIIG technique is method that was proposed in this paper (as new method in plant breeding) for select stable genotypes using all of parametric and nonparametric stability procedures, simultaneity. This technique is a decision making method to identify favorable genotypes using a set of stability methods, simultaneously. The basic principle is that the chosen genotypes should have the shortest distance from the positive ideal parameter and the farthest distance from the negative ideal parameter. We should select the genotypes in this method with SIIG closet to 1 ($0 \le SIIG \le 1$).

Stability should not be the only way for choice. Because, the most stable genotypes would not presently give the best yield. Hence, there is a need for procedure that peruses both yield and stability. Several methods of simultaneous selection for yield and stability and relationship among them were discussed by Kang and Pham (1991). Kang (1991, 1993) introduced three selection methods for simultaneous selection of yield and stability denominated: rank sum, modified rank sum and the yield - stability statistic (Y_{si}). The development Y_{si} demonstrated the significance and rationale of incorporating stability in selecting genotypes tested across a range of environments (Kang, 1993). The stability component in Y_{si} is based on Shukla's stability variance (1972). But stability components in SIIG model can be based on all method stability and there is no limitation. Therefore, in this method we simultaneously have used from all parametric methods and mean yield to select stable genotypes. Whole calculation process of SIIG method, for select of stable genotypes of 6 canola cultivars for simultaneous selection of yield and stability using the parametric methods and seed yield (Table 2) is presented in Tables 4 and 5. Results of SIIG method and the ranks of genotypes according to this statistic are given in Table 5. Results of SIIG technique indicated that SLM046 and Lilian genotypes in comparison with the other genotypes had the least of deviation from the positive ideal parameter (d^+ = 0.2798 and 0.3192 respectively) and has the most of deviation from the negative ideal parameter (d^+ = 1.1124 and 0.9660); therefore SLM046 and Lilian genotypes with maximum SIIG (0.799 and 0.753, respectively) were stable genotypes in comparison with the other genotypes and also had the high mean yield (Table 5). Whereas Tassilo genotype among genotypes had the most of deviation from the positive ideal parameter (d^+ = 1.0235) and has the least of deviation from the negative ideal parameter (d^- = 0.5613), thus it with minimum SIIG (0.354) was unstable genotype in comparison with the other genotypes, although this genotype had the high mean yield.

Simultaneous selection for yield and stability based on all of nonparametric procedures using SIIG technique

In SIIG method we simultaneously have used from all nonparametric methods and mean yield to select stable genotypes. All calculation process of SIIG technique, for select of stable genotypes of 6 canola cultivars using all of parametric methods and mean yield (Table 3), simultaneously is presented in Tables 6 and 7.

Table 3: Nonparametric stability procedures and its rank for seed yield and tests of nonparametric stability measures ($Z_i^{(1)}$ and $Z_i^{(2)}$) for 6 canola genotypes across environments.

Genotypes name	$S_i^{(1)}$	$Z_i^{(1)}$	$S_i^{(2)}$	$Z_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	$\bar{R}$	SDR
SLM046	2.0 (4)	0.0117	2.8 (5)	0.0065	2.43 (3)	1.39 (2)	0.8 (1)	0.16 (1)	0.283 (1)	0.389 (1)	2.4 (1)	1.673 (5)
Tassilo	2.8 (6)	2.3935	5.8 (6)	3.9672	6.44 (6)	2.89 (6)	2.0 (5)	0.4 (3)	0.624 (6)	0.833 (6)	3.4 (4)	2.408 (6)
Karun	1.8 (3)	0.0634	2.3 (3)	0.1817	3.83 (5)	2.67 (5)	2.2 (6)	1.1 (6)	0.538 (4)	0.750 (4)	4.6 (5)	1.517 (3)
Adriana	2.0 (4)	0.0117	2.7 (4)	0.0225	2.84 (4)	1.79 (4)	1.8 (4)	0.6 (5)	0.598 (5)	0.778 (5)	3.2 (3)	1.643 (4)
Cooper	1.0 (1)	2.8595	0.7 (1)	2.3460	1.27 (2)	1.45 (3)	1.0 (2)	0.5 (2)	0.377 (2)	0.500 (2)	4.8 (6)	0.837 (1)
Lilian	1.2 (2)	1.7722	1.2 (2)	1.4071	1.14 (1)	0.86 (1)	1.2 (3)	0.3 (3)	0.399 (3)	0.529 (3)	2.8 (2)	1.095 (1)
Mean	1.8		2.58		2.995	1.841	1.5	0.51	0.470	0.630	3.533	1.529

Test statistics

$\sum Z_i^{(1)} = 7.112$	$\sum Z_i^{(2)} = 7.931$
$E(S_i^{(1)}) = 1.944$	$E(S_i^{(2)}) = 2.917$
$V(S_i^{(1)}) = 0.309$	$V(S_i^{(2)}) = 2.095$

$S_i^{(1)}$: mean of absolute rank difference of a genotype over environments; $S_i^{(2)}$: sum of square deviations of the rank; Z-statistics: measures of stability; $S_i^{(3)}$: variance among the ranks over environments; $S_i^{(6)}$: sum of absolute deviation; $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$: Thennarasu's nonparametric stability procedures; $\bar{R}$: mean of rank; SDR: standard deviation of rank

Results of SIIG technique displayed that Cooper and Lilian genotypes in collation with the other genotypes had the least of deviation from the positive ideal parameter (d^+ = 0.3147 and 0.3144, respectively) and have the most of deviation from the negative ideal parameter (d^- = 1.2859 and 1.2736, respectively); therefore Cooper and Lilian genotypes with maximum SIIG (0.803 and 0.802) were stable genotypes in comparison with the other genotypes based on yield and nonparametric stability methods (Table 7). Whereas Tassilo genotype among genotypes had the most of distance from the positive ideal parameter (d^+ = 1.2822) and has the least of distance from the negative ideal parameter (d^- = 0.5037), thus it with minimum SIIG value (0.282) was unstable genotype in comparison with the other genotypes.

Table 4: The normalized decision matrix of 6 canola genotypes for parametric methods and yield (matrix R).

Genotype name	S_i^2	CV_i	W_i^2	S^2d_i	R_i^2	PI	Yield
SLM046	0.3474	0.3231	0.1317	0.2247	0.4334	0.0457	0.4686
Tassilo	0.1672	0.2528	0.8640	0.7474	0.2466	0.4025	0.4160
Karun	0.5453	0.5351	0.2424	0.2008	0.4475	0.5606	0.3546
Adriana	0.5248	0.4529	0.3530	0.4778	0.4210	0.3342	0.4103
Cooper	0.4298	0.4851	0.1148	0.1506	0.4484	0.6192	0.3472
Lilian	0.3064	0.3240	0.1995	0.3155	0.4151	0.1630	0.4392

Table 5: The separation measures, the relative closeness coefficient (SIIG) and the ranking of 6 canola genotypes for parametric procedures.

Genotype name	d^+	d^-	SIIG	Rank
SLM046	0.2798	1.1124	0.799	1
Tassilo	1.0235	0.5613	0.354	6
Karun	0.7484	0.8298	0.524	4
Adriana	0.6699	0.6534	0.494	5
Cooper	0.7123	0.9660	0.576	3
Lilian	0.3192	0.9733	0.753	2

Table 6: The normalized decision matrix of 6 canola genotypes for nonparametric methods and yield (matrix R).

Genotypes names	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	$\bar{R}$	SDR	Yield
SLM046	0.4311	0.3741	0.2847	0.287	0.2055	0.1105	0.2379	0.2438	0.2690	0.4250	0.4686
Tassilo	0.6036	0.7751	0.7535	0.5966	0.5137	0.2763	0.5238	0.5225	0.3811	0.6117	0.4159
Karun	0.3880	0.3074	0.4482	0.5507	0.5650	0.7599	0.4516	0.4703	0.5156	0.3852	0.3546
Adriana	0.4311	0.3608	0.3323	0.3696	0.4623	0.4145	0.5026	0.4877	0.3587	0.4174	0.4103
Cooper	0.2156	0.0936	0.1488	0.3004	0.2568	0.3454	0.3165	0.3135	0.5380	0.2125	0.3472
Lilian	0.2587	0.1604	0.1336	0.1770	0.30820	0.2072	0.3351	0.3320	0.3138	0.2782	0.4392

Table 7: The separation measures, the relative closeness coefficient (SIIG) and the ranking of 6 canola genotypes for nonparametric procedures.

Genotypes name	d^+	d^-	SIIG	Rank
SLM046	0.5270	1.1251	0.681	3
Tassilo	1.2822	0.5037	0.282	6
Karun	1.0026	0.6933	0.409	5
Adriana	0.7482	0.7821	0.511	4
Cooper	0.3147	1.2859	0.803	1
Lilian	0.3144	1.2736	0.802	2

DISCUSSION

In this research several stability different methods are used for clarifying genotype × environment interaction. The most favorable genotype is the one that combines both high mean yield and stability performance together and so it is acceptable over a wide range of environmental stress conditions.

Breeders can use stability analysis methods to identify cultivars that have predictable performance and that respond positively to improvements in environmental conditions. Currently, plant breeders have a full hand of methods for the analyses of genotype yield adaptability and stability to help in the difficult task of identifying superior cultivars in different environmental conditions. Therefore, the choose 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).

Genotype × environment (stress and non-stress conditions) interactions are one of variation sources in any crop and the term stability is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. On the basis of this idea, genotypes with a minimum variance for yield across different environments are considered stable. Correspond to Huehn (1990), nonparametric procedures have the following advantages: they reduce the bias caused by outliers, no assumptions are needed about the distribution of observed values, they are easy to use and interpret and additions or deletions of one or a few genotypes do not cause much variation of results. As a result, many researchers applied different nonparametric methods to appraise stability (Zali *et al.,* 2011).

To better comprehend the associations among the parametric and nonparametric methods and to distinguish stable genotypes from others, principal component analysis based on the rank correlation matrix was used in two subjects of screening stability methods and genotypes. The first two PCs illustrated 87.93% of the variances in the original variables (Tables 2 and 3). The associations among different stability methods and genotypes are graphically revealed in a biplot of PC1 and PC2 (Fig. 1). The PC1 and PC2 axes mainly distinguish the parametric and nonparametric methods and genotypes in five different groups. Biplot analysis demonstrated that the first PC, 55.20% of the variation with $Si^{(1)}$, $Si^{(2)}$, $Si^{(3)}$, SDR, σi^2, S_2di, W_i^2, Si (6), $NPi^{(1)}$, $NPi^{(3)}$ and NPi $^{(4)}$. Thus, the first dimension can be named as the yield inconstancy. Considering the high and positive value of this PC on biplot, selected genotypes will be instability yield but high yield under drought stress and control conditions. The second PC revealed 32.73% of the total variability and had positive correlation with mean yield and mean rank ($\bar{R}$). Therefore the second component can be named as a stable and high yield dimension and it separates the stable genotypes with high yield from non stable ones. Mean yield groups with nonparametric procedure of $\bar{R}$ that we refer to group 1 stability procedure. The PCs axes separated nonparametric procedures ($Si^{(1)}$, $Si^{(2)}$, $Si^{(3)}$ and SDR) and parametric measures (σ_i^2, S^2d_i and Wi^2) (We refer to as group 2) from the statistics $S_i\,^{(6)}$, $NPi^{(1)}$, $NPi^{(3)}$ and $NPi^{(4)}$ (We refer to as group 3). Although PI groups with nonparametric measures of $NPi^{(2)}$ (group 4), S_i^2 with CVi (group 5) and R_i^2 was separated from the other classes (group 6).

The biplot analysis was also carried out for the ranks of genotypes obtained from different stability procedures (Fig. 1). In biplot, the PCs axes divided the genotypes into five groups. Group 1 included the genotypes of SLM046 and Lilian with good performance. The genotype of Tassilo in group 2 with high yields, but was not stable genotype to drought stress conditions. Group 3 consisted of the Adriana genotype with high mean yield and had relatively low stability to drought conditions. Group 4 included the genotype of Karun with low mean yield and low stability in stress drought and Cooper genotype was separated from the other group (group 6) with lowest yield but with high stability to more procedures.

The basic concept of SIIG method is that the chosen genotype should have the shortest deviation from the positive-ideal parameter and the farthest deviation from the negative-ideal parameter. We assumed that if each parameter or trait takes monastically increasing or decreasing variation, then it is easy to define an ideal parameter or trait. Such a solution is composed of all the best traits values achievable, while the none-ideal parameter is composed of all weak trait or parameter values achievable. The SIIG value is in range of 0-1. If it is close to 1, evaluating genotypes close to the ideal, else if it close to 0, evaluating genotypes close to the non-ideal.

CONCLUSIONS

The different parametric and nonparametric stability procedures can be proposed to select drought tolerant genotypes under different conditions (environments); therefore, in first stem to choice, these procedures could be useable for recognition of the best genotypes in different stress conditions. According to most nonparametric methods (SIIG method), Cooper and Lilian genotypes were stable in comparison with the other genotypes and also had the high mean yield; whiles Tassilo genotype was unstable genotype in contrast with the other genotypes. Correspond to most parametric procedures (SIIG method), SLM046 and Lilian genotypes were stable in comparison with the other genotypes whiles Tassilo genotype was unstable genotype in contrast with the other genotypes. The proposed measures (SIIG method) are comprehensive in the order in which amount of information increases. It is very effective in selection of ideal (best) genotypes using several different traits or indices simultaneously.

Therefore we propose that researches use of SIIG method to help choose an ideal genotypes using stability procedures, morphological and physiological traits, simultaneously and also simultaneous selection for yield and stability.

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