

Evaluation of the reaction of sunflower inbred lines and their F₁ hybrids to drought conditions using various stress tolerance indices

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Abstract

In this study, 21 genotypes of sunflower (*Helianthus annuus* L.) derived from a half diallel cross between six inbred lines were evaluated in both water-stressed and well-watered environments. In each environment, the genotypes were evaluated using a randomized complete block design with three replications. From the grain yield data, drought tolerance indices comprising of stability tolerance index (STI), mean productivity (MP), geometric mean productivity (GMP), harmonic mean (HM), stress susceptibility index (SSI), tolerance index (TOL), yield index (YI) and yield stability index (YSI) were calculated for every genotype. The resulting data were analyzed as obtained from a randomized complete block design. Significant differences among genotypes were observed for all drought tolerance indices except for SSI and YSI. High yield value in non-stress and stress environments was exhibited by genotypes 'LR4 × LR25' (14.02 g) and 'LR25 × C100' (3.84 g) respectively. The maximum value of STI (0.93), MP (8.72), GMP (6.91) and HM (5.48) indices was by genotype 'LR4 × LR25'. Correlation coefficients revealed that TOL, MP, GMP, STI, HM, and YI indices could effectively be used for screening of drought tolerant genotypes. Using MP, GMP, HM, TOL, YI and STI indices, genotypes UPGMA classification was done and three clusters were established that paralleled the biplot analysis results. According to results in this study, 'LR4 × LR25' is the most drought tolerant genotype which was clustered as group A. We suggest that tolerance indices including MP, GMP and HM are suitable for sunflower drought tolerant genotypes selection.

Additional key words: biplot; diallel cross; *Helianthus annuus* L.; multivariate analysis; water-stressed condition, yield stability.

Resumen

Evaluación de la reacción de líneas puras de girasol y sus híbridos F₁ a las condiciones de sequía mediante diversos índices de tolerancia al estrés

En este estudio, 21 genotipos de girasol (*Helianthus annuus* L.) derivados de un cruce medio dialélico entre seis líneas puras se evaluaron con y sin estrés hídrico. Para cada ambiente, los genotipos se evaluaron usando un diseño de bloques completos al azar con tres repeticiones. De los datos de rendimiento de grano se calcularon los índices de tolerancia a la sequía para cada genotipo: índice de estabilidad de la tolerancia sexual (ITS), productividad media (MP), productividad media geométrica (GMP), media armónica (HM), índice de susceptibilidad al estrés (SSI), índice de tolerancia (TOL), índice de rendimiento (YI) e índice de estabilidad del rendimiento (YSI). Los datos resultantes se analizaron como obtenidos a partir de un diseño de bloques completos al azar. Se observaron diferencias significativas entre los genotipos en todos los índices de tolerancia a la sequía a excepción de SSI y YSI. Los genotipos 'LR4 × LR25' y 'LR25 × C100' exhibieron un alto rendimiento en ambos ambientes (14,02 y 3,84 g, respectivamente); 'LR4 × LR25' presentó el valor máximo de los índices STI (0,93), MP (8,72), GMP (6,91) y HM (5,48). Los coeficientes de correlación revelaron que los índices TOL, MP, GMP, STI, HM y YI podrían ser utilizados para la selección de genotipos tolerantes a la sequía. Utilizando los índices MP, GMP, HM, TOL, YI y STI, se hizo una

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clasificación UPGMA de los genotipos y se establecieron tres grupos análogos a los resultados del análisis biplot. De acuerdo a los resultados de este estudio, 'LR4 × LR25', del grupo A, es el genotipo más tolerante a la sequía. Se concluye que los índices de tolerancia MP, GMP y HM son adecuados para la selección de genotipos tolerantes a la sequía en girasol.

Palabras clave adicionales: análisis multivariado, biplot; cruce dialélico; estabilidad del rendimiento; estrés hídrico; *Helianthus annuus* L.

Introduction

Sunflower (*Helianthus annuus* L.) is one of the most important oil crops due to its high content of unsaturated fatty acids and a lack of cholesterol (Razi and Assad, 1998). Although sunflower is moderately tolerant to water stress, its production is greatly affected by drought conditions (Pasda and Diepenbrock, 1990). Evidence indicated that drought stress during vegetative phase, flowering and seed filling period causes considerable decrease in yield and oil content of sunflower (Razi and Assad, 1999; Ali *et al.*, 2009). Several research findings show that plant height, leaf area index and number of green leaves were reduced with no irrigation (Vivek and Chakor, 1992; Agele, 2003; Turhan and Baser, 2004; Poormohammad Kiani *et al.*, 2009). D'Andria *et al.* (1995) concluded that sunflower yield components such as seed weight is high in irrigation environment compared to non-irrigated conditions. Vasiliu (1988) reported a high seed yield ranging from 2.64 t ha⁻¹ in non irrigated condition to 3.34 t ha⁻¹ with irrigation at 50% field capacity. Similarly, Vijay (2004) mentioned that achene yield in irrigated conditions is higher than non-irrigated one. One of the sunflower breeding goals is establishing resistance to environmental stresses such as drought stress. For this reasons improved tolerance to drought has been a goal but unfortunately, success in breeding for drought tolerance has been limited because (I) it is controlled by several genes, and their simultaneous selection is difficult (Richards, 1996; Yeo, 1998; Flowers *et al.*, 2000); (II) tremendous effort is required to eliminate undesirable genes tightly linked to favorable ones, that are also incorporated during breeding (Richards, 1996); and (III) there is a lack of efficient selection procedures particularly under field conditions (Ribaut *et al.*, 1997; Kirigwi *et al.*, 2004). Generally, different strategies have been proposed for the selection of relative drought-

tolerant and resistant genotypes, as Fisher and Maurer (1978) reported that achene yield in drought environment could be considered as drought-resistance index. While Blum (1988) mentioned that selection of genotypes for drought resistance must be associated with selection for high yield in non-stress environments. Hence, by calculation of genotypes yield in drought and well-watered environments, one could select resistant genotypes to drought. There are several selection indices for screening drought resistance genotypes such as geometric mean productivity (GMP) (Fernández, 1992), mean productivity (MP) (Rosielle and Hamblin, 1981), harmonic mean (HM) (Jafari *et al.*, 2009), stress susceptibility index (SSI) (Fischer and Maurer, 1978), yield stability index (YSI) (Bousslama and Schapaugh, 1984), yield index (YI) (Gavuzzi *et al.*, 1997), stress tolerance index (STI) (Fernández, 1992) and tolerance index (TOL) (Rosielle and Hamblin, 1981) that identify susceptible and resistance genotypes based on their yields in stress and non-stress environments. The best selection index must be able to distinguish genotypes that have uniform superiority in both stress and non-stress environment. Fernández (1992) reported that mungbean (*Vigna radiata* L.) genotypes selection based on STI and GMP indices resulted in genotypes that have high tolerance and high yield. Clarke *et al.* (1992) used SSI index to distinguish between wheat (*Triticum aestivum* L.) genotypes. According to Sio-Se Mardeh *et al.* (2006), MP, GMP and STI were best indices under moderate stress in wheat. The objectives of present study were evaluation of several drought tolerance indices as well as to identify drought-tolerant genotypes in sunflower.

Material and methods

Five sunflower recombinant inbred lines (RILs) together with their paternal line were selected on the

Abbreviations used: CV (coefficient of variation); GMP (geometric mean productivity), HM (harmonic mean), MP (mean productivity), PCA (principal component analysis), RIL (recombinant inbred line), SSI (stress susceptibility index), STI (stability tolerance index), TOL (tolerance index), YI (yield index), YSI (yield stability index), (Y_p) (yield in non-stress condition), Y_s (yield in stress condition), UPGMA (unweighted pair group method with arithmetic mean).

basis of their contrasting responses to water stress and different agronomical characteristics revealed in our previous experiments (Poormohammad Kiani *et al.*, 2007a,b, 2008, 2009). The RILs used in this experiment were F₉ pure lines which were developed through single seed descent from F₂ plants derived from a cross between 'PAC2' and 'RHA266'. RHA266 was obtained from a cross between wild *H. annuus* and *peredovik* by USDA and PAC2 is an INRA-France inbred line from a cross between *H. petiolaris* and 'HA61' (Gentzmittel *et al.*, 1995). This public RILs population is widely used for genetic analysis of complex traits in sunflower (Poormohammad Kiani *et al.*, 2007a,b, 2008, 2009; Darvishzadeh *et al.*, 2007; Abou Al Fadil *et al.*, 2007). The six genotypes were grown and crossed in a diallel mating system without reciprocals to produce 15 F₁ hybrid combinations. The parental genotypes and their F₁ hybrids were grown in the greenhouse under controlled conditions. Plants were individually grown in plastic pots containing a mixture of 40% soil, 40% compost and 20% sand as described (Poormohammad Kiani *et al.*, 2007a,b). Temperature was maintained at 25/18 ± 2°C (day/night) and relative humidity at about 65/85 ± 5%. Supplementary light was provided to obtain 16-h light period. Twenty-one genotypes including 15 F₁ hybrids plus 6 parental lines were evaluated in well-watered and water-stressed conditions. In each condition, the genotypes were evaluated using a randomized complete block design with three replications. In order to simulate natural water deficit conditions similar to field, a progressive water stress from mild stress to severe stress was imposed on 45-day-old plants at stage near flower bud formation (R₁) (Schneiter and Miller, 1981) for a period of 12 days (Poormohammad Kiani *et al.*, 2007a,b). Both well-watered and water-stressed plants were weighed and water lost replaced carefully. Well-watered (control) plants received sufficient water to maintain soil water content close to field capacity. Water-stressed plants were subjected to a progressive water stress and irrigated with a water volume of 60%, 50% and 40% of field capacity (each 4 days) during 12 days and continued up to harvest. Plants were harvested at maturity, and then the grain yield was recorded for every plot. The drought tolerance indices were calculated for every genotype using the corresponding well-watered and water-stressed plots. The resulting data were analyzed as obtained from a randomized complete block design. Drought tolerance indices were calculated using the equations cited in Table 1.

Statistical analysis

The data were analyzed using the general linear model (GLM) procedure in the SAS software (SAS Institute Inc., Cary, NC, USA). Correlations between grain yield per plant in each of the water regimes and drought tolerance indices were determined using SAS PROC CORR. The Student-Newman-Keuls test was used for comparing mean performance of parents and F₁s. Multivariate statistical analysis as principle component analysis, biplot display, three dimensional plots, and cluster analysis were performed using the SPSS version 15.0 and STAT GRAPH softwares.

Results

There were significant differences among genotypes for yield under stress and non-stress conditions (Table 2). Significant differences among genotypes were observed for all drought tolerance indices except for SSI and YSI (Table 2). These results indicate that there is high genetic variation among genotypes, which could be an useful resource for selection of drought-tolerant germplasm. The experimental coefficient of variation (CV) varied from 18.45 to 30.92. However, for the majority of traits the values were less than 25% (Table 2). High yield value in non-stress and stress environments was exhibited by genotypes 'LR4 × LR25' (14.02 g) and 'LR25 × C100' (3.84 g) respectively (Table 3). The maximum value of STI (0.93), MP (8.72), GMP (6.91) and HM (5.48) indices was by genotype 'LR4 × LR25'. The highest value for YI (1.27) was from genotypes 'LR25 × C100' and 'LR4 × LR25' (Table 3). Genotype 'LR4 × LR25' had desirable yield in both environments and hence it is recommendable in arid and semiarid regions. A suitable index must have a significant correlation with yield in any of the two environments. To identify the best index of selection for drought-resistant genotypes, correlation coefficient between these indices and yield in non-stress condition (Y_p) as well as yield in stress condition (Y_s) was determined (Table 4). Correlation coefficients matrix (Table 4) revealed that TOL, MP, GMP, STI, HM, and YI indices could effectively be used for screening of drought resistant genotypes.

Principal component analysis (PCA) revealed that the first PCA explained 72.1% of the total data variation and had positive correlation with the performance under both stress and non-stress environments (Table 5).

Table 1. Drought tolerance indices used for evaluation of the reaction of sunflower inbred lines and their F₁ hybrids to drought conditions

Drought tolerance indices	Equation ¹	Reference
Stress susceptibility index	$SSI = \frac{1 - \left(\frac{Y_s}{Y_p}\right)}{1 - \left(\frac{\bar{Y}_s}{\bar{Y}_p}\right)}$	Fischer and Maurer, 1978
Geometric mean productivity	$GMP = \sqrt{(Y_s)(Y_p)}$	Fernández (1992) and Kristin <i>et al.</i> (1997)
Mean productivity	$MP = \frac{Y_s + Y_p}{2}$	Rosielle and Hambling (1981)
Harmonic mean	$HM = \frac{2(Y_p \cdot Y_s)}{Y_p + Y_s}$	Jafari <i>et al.</i> (2009)
Tolerance index	$TOL = Y_p - Y_s$	Rosielle and Hambling (1981)
Stress tolerance index	$STI = \frac{(Y_s)(Y_p)}{(\bar{Y}_p)^2}$	Fernández (1992)
Yield index	$YI = \frac{Y_s}{\bar{Y}_s}$	Gavuzzi <i>et al.</i> (1997)
Yield stability index	$YSI = \frac{Y_s}{Y_p}$	Bousslama and Schapaugh (1984)

¹ Y_s and Y_p are stress and optimal (potential) yield of a given genotype, respectively. \bar{Y}_s and \bar{Y}_p are average yield of all genotypes under stress and optimal conditions, respectively.

Thus the first dimension represents the yield potential and drought tolerance. In other words, this component was able to separate the genotypes with higher yield under both stress and non-stress conditions. The second PCA explained 26.35% of total data variation that have positive and high correlation with SSI but negative one by yield under stress conditions (Table5). Therefore it was the stress susceptibility dimension and

was able to separate the susceptible genotypes. Hence, selection of genotypes that have high PCA1 and low PCA2 are suitable for both stress and non-stress condition.

Biplot presentation depicted genotypes 'RHA266 × C100', 'LR4 × LR25', 'RHA266 × LR55', 'LR55 × LR4', 'LR55 × LR25', 'RHA266 × C104', 'RHA266 × LR4', 'C104 × LR25', 'LR4 × C104', and 'LR55 × C104' lo-

Table 2. The mean squares of grain yield of sunflower genotypes under optimal and stress conditions, and calculated different drought tolerance indices

Source of variation	df ¹	Y _p ²	Y _s ³	SSI ⁴	TOL ⁵	MP ⁶	GMP ⁷	STI ⁸	HM ⁹	YI ¹⁰	YSI ¹¹
Replication	2	0.07 ^{ns}	0.21 ^{ns}	0.01 ^{ns}	0.005 ^{ns}	0.09 ^{ns}	0.17 ^{ns}	0.07 ^{ns}	0.25 ^{ns}	0.09 ^{ns}	0.02 ^{ns}
Genotype	20	0.99**	0.29**	0.02 ^{ns}	0.91*	0.60**	0.50**	0.103**	0.42**	0.12**	0.02 ^{ns}
Residual	25	0.30	0.09	0.03	0.40	0.16	0.13	0.03	0.12	0.04	0.02
CV ¹²		20.96	19.92	19.06	30.12	18.79	18.45	30.92	18.83	19.86	25.46

¹ df: degrees of freedom. ² Y_p: Yield of a given genotype in optimal (potential) conditions. ³ Y_s: Yield of a given genotype in stress conditions. ⁴ SSI: stress susceptibility index. ⁵ TOL: tolerance index. ⁶ MP: mean productivity. ⁷ GMP: geometric mean productivity. ⁸ STI: stress tolerance index. ⁹ HM: harmonic mean. ¹⁰ YI: yield index. ¹¹ YSI: yield stability index. ¹² CV: coefficient of variation. * and **: significant at 0.05 and 0.01 probability level, respectively. ns: not significant at 0.05 probability level.

Table 3. Average yield of sunflower inbred lines and their F₁ hybrids under optimal and stress conditions, and calculated different drought tolerance indices^a. Means followed by the same letter are not significantly different according to the Student-Newman-Keuls test

Code	Genotype	Y _P (g plant ⁻¹)	Y _S (g plant ⁻¹)	SSI	TOL	MP	GMP	STI	HM	YI	YSI
1	RHA266 × C100	8.17 ^{abc}	3.55 ^{ab}	0.91 ^a	4.62 ^{ab}	5.87 ^{abc}	5.38 ^{abc}	0.72 ^{abc}	4.94 ^{ab}	1.21 ^{ab}	0.43 ^a
2	LR25	5.10 ^{abc}	2.67 ^{ab}	0.78 ^a	2.42 ^{ab}	3.89 ^{abc}	3.61 ^{abc}	0.48 ^{abc}	3.37 ^{ab}	1.04 ^{abc}	0.54 ^a
3	LR25 × C100	6.98 ^{abc}	3.84 ^a	0.80 ^a	3.14 ^{ab}	5.42 ^{abc}	5.16 ^{abc}	0.70 ^{abc}	4.93 ^{ab}	1.27 ^a	0.56 ^a
4	LR4 × LR25	14.02 ^a	3.42 ^{ab}	1.06 ^a	10.61 ^a	8.72 ^a	6.91 ^a	0.93 ^a	5.48 ^a	1.20 ^{ab}	0.25 ^a
5	LR55 × C100	4.35 ^{bc}	1.43 ^{ab}	0.99 ^a	2.92 ^{ab}	2.89 ^{bc}	2.49 ^{abc}	0.34 ^{abc}	2.15 ^{ab}	0.77 ^{abc}	0.33 ^a
6	RHA266 × LR55	11.17 ^{ab}	2.92 ^{ab}	1.04 ^a	8.25 ^{ab}	7.05 ^{ab}	5.71 ^{ab}	0.77 ^{ab}	4.62 ^{ab}	1.11 ^{ab}	0.26 ^a
7	RHA266	2.57 ^{bc}	0.84 ^{ab}	0.99 ^a	1.73 ^b	1.70 ^{bc}	1.46 ^{bc}	0.20 ^{bc}	1.26 ^{ab}	0.50 ^{bc}	0.34 ^a
8	LR55 × LR4	7.09 ^{abc}	2.72 ^{ab}	0.94 ^a	4.38 ^{ab}	4.91 ^{abc}	4.34 ^{abc}	0.58 ^{abc}	3.86 ^{ab}	1.06 ^{abc}	0.40 ^a
9	C104 × C100	4.48 ^{bc}	0.78 ^{ab}	1.10 ^a	3.70 ^{ab}	2.63 ^{bc}	1.87 ^{bc}	0.25 ^{bc}	1.33 ^{ab}	0.57 ^{abc}	0.17 ^a
10	LR55 × LR25	7.97 ^{abc}	2.63 ^{ab}	0.99 ^a	5.34 ^{ab}	5.31 ^{abc}	4.53 ^{abc}	0.61 ^{abc}	3.90 ^{ab}	1.03 ^{abc}	0.33 ^a
11	RHA266 × C104	7.60 ^{abc}	2.64 ^{ab}	0.84 ^a	4.96 ^{ab}	5.12 ^{abc}	4.26 ^{abc}	0.58 ^{abc}	3.61 ^{ab}	1.05 ^{abc}	0.48 ^a
12	C104	4.51 ^{bc}	0.98 ^{ab}	1.07 ^a	3.53 ^{ab}	2.75 ^{bc}	2.10 ^{abc}	0.28 ^{abc}	1.61 ^{ab}	0.64 ^{abc}	0.22 ^a
13	RHA266 × LR4	11.00 ^{ab}	2.99 ^{ab}	1.04 ^a	8.01 ^{ab}	7.00 ^{ab}	5.69 ^{ab}	0.76 ^{ab}	4.65 ^{ab}	1.10 ^{ab}	0.26 ^a
14	LR4	5.74 ^{abc}	2.14 ^{ab}	0.96 ^a	3.60 ^{ab}	3.95 ^{abc}	3.51 ^{abc}	0.47 ^{abc}	3.12 ^{ab}	0.95 ^{abc}	0.38 ^a
15	RHA266 × LR25	6.55 ^{abc}	2.20 ^{ab}	0.83 ^a	4.35 ^{ab}	4.38 ^{abc}	3.72 ^{abc}	0.50 ^{abc}	3.18 ^{ab}	0.95 ^{abc}	0.48 ^a
16	LR55	4.05 ^{bc}	1.33 ^{ab}	0.98 ^a	2.73 ^{ab}	2.69 ^{bc}	2.28 ^{abc}	0.31 ^{abc}	1.95 ^{ab}	0.74 ^{abc}	0.35 ^a
17	C100	1.35 ^c	0.34 ^b	0.94 ^a	1.01 ^b	0.85 ^c	0.62 ^c	0.08 ^c	0.47 ^b	0.36 ^c	0.35 ^a
18	LR4 × C100	10.31 ^{abc}	1.97 ^{ab}	1.09 ^a	8.34 ^{ab}	6.14 ^{abc}	4.50 ^{abc}	0.61 ^{abc}	3.30 ^{ab}	0.90 ^{abc}	0.19 ^a
19	C104 × LR25	11.56 ^{ab}	3.15 ^{ab}	1.04 ^a	8.41 ^{ab}	7.36 ^{ab}	5.95 ^{ab}	0.80 ^{ab}	4.85 ^{ab}	1.14 ^{ab}	0.27 ^a
20	LR4 × C104	7.04 ^{abc}	2.66 ^{ab}	0.91 ^a	4.38 ^{ab}	4.86 ^{abc}	4.32 ^{abc}	0.58 ^{abc}	3.85 ^{ab}	1.01 ^{abc}	0.44 ^a
21	LR55 × C104	8.96 ^{abc}	2.67 ^{ab}	1.02 ^a	6.29 ^{ab}	5.82 ^{abc}	4.88 ^{abc}	0.66 ^{abc}	4.10 ^{ab}	1.06 ^{abc}	0.30 ^a

^a Indices: see Table 2.

cated adjacent to important drought resistance indices that confirm these genotypes being drought resistant (Fig. 1). Genotype 'LR4 × C100' was near to SSI and has high Y_P (seed yield in non-stress condition) value (Fig. 1). Therefore, this genotype had specific adaptability to non-stress environment. Some genotypes such as 'LR55 × C100', 'RHA266', 'C104 × C100', 'C104', 'LR4', 'RHA266 × LR25', 'LR55' and 'C100' belong to low yield and high drought sensitivity region in the

biplot space (Fig. 1). On the other hand, there was genetic variability among genotypes based on their drought resistance. Using important resistance indices comprising of MP, GMP, HM, TOL, YI and STI genotypes UPGMA classification was done and three clusters were established that paralleled the biplot analysis results (Fig. 2).

To identify the relationship among Y_P, Y_S and suitable resistance indices, three-dimensional graphs for

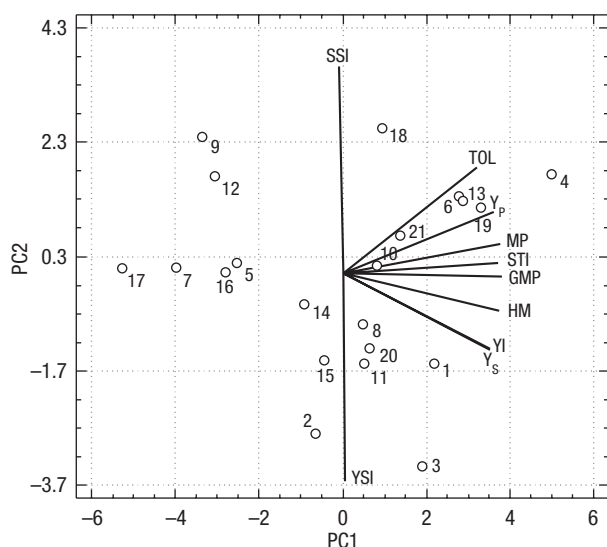
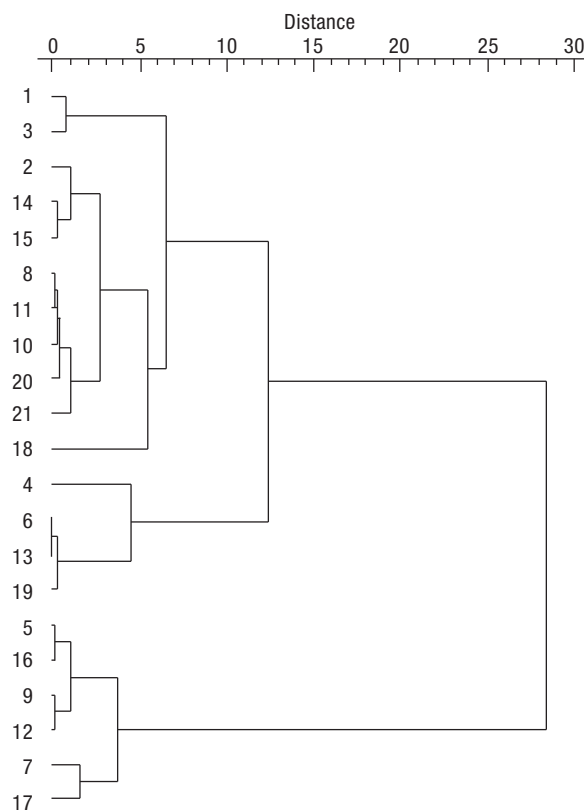
Table 4. Correlation between different drought tolerance indices and mean yield of sunflower inbred lines and their F₁ hybrids under optimal and stress conditions

Indices ¹	Y _P	Y _S	SSI	TOL	MP	GMP	STI	HM	YI
Y _S	0.673**								
SSI	0.421**	-0.253							
TOL	0.958**	0.433**	0.612**						
MP	0.982**	0.802**	0.275	0.886**					
GMP	0.921**	0.905**	0.120	0.772**	0.978**				
STI	0.886**	0.867**	0.124	0.744**	0.939**	0.963**			
HM	0.823**	0.969**	-0.039	0.628**	0.915**	0.979**	0.945**		
YI	0.674**	1.000**	-0.253	0.434**	0.802**	0.906**	0.867**	0.969**	
YSI	-0.423**	0.249	-1.000**	-0.612**	-0.278	-0.123	-0.127	0.036	0.249

¹ Indices: see Table 2. **: significant at 0.01 probability level.

Table 5. Eigen value and vectors of principal component analysis for potential yield (Y_P), stress yield (Y_S) and drought tolerance indices¹

Principal component	1	2	3
Eigen value	7.21	2.64	0.11
Percentage of variance	72.1	26.35	1.1
Cumulative percentage	72.1	98.45	99.51
Y_P	0.35	0.18	0.3
Y_S	0.34	-0.22	-0.37
SSI	-0.01	0.61	-0.33
TOL	0.31	0.31	-0.52
MP	0.37	0.09	0.15
GMP	0.37	-0.01	-0.06
STI	0.36	0.03	0.13
HM	0.36	-0.11	-0.27
YI	0.34	-0.22	-0.37
YSI	0.01	-0.61	0.36

¹ Indices: see Table 2.**Figure 1.** The genotype by trait biplots of sunflower breeding for resistance to drought stress trial. The traits are spelled out in lowercase letters, and each genotype is represented by numbers. Y_P : yield of a given genotype in optimal (potential) conditions. Y_S : yield of a given genotype in stress conditions. SSI: stress susceptibility index. TOL: tolerance index. MP: mean productivity. GMP: geometric mean productivity. STI: stress tolerance index. HM: harmonic mean. YI: yield index. YSI: yield stability index. 1: 'RHA266 × C100'. 2: 'LR25'. 3: 'LR25 × C100'. 4: 'LR4 × LR25'. 5: 'LR55 × C100'. 6: 'RHA266 × LR55'. 7: 'RHA266'. 8: 'LR55 × LR4'. 9: 'C104 × C100'. 10: 'LR55 × LR25'. 11: 'RHA266 × C104'. 12: 'C104'. 13: 'RHA266 × LR4'. 14: 'LR4'. 15: 'RHA266 × LR25'. 16: 'LR55'. 17: 'C100'. 18: 'LR4 × C100'. 19: 'C104 × LR25'. 20: 'LR4 × C104'. 21: 'LR55 × C104'.**Figure 2.** Dendrograph from cluster analysis of genotypes based on drought tolerance indices and grain yield of sunflower inbred lines and their F₁ hybrids, in both normal and stress environment. Genotype codes: see Figure 1.

each one were also employed (Fig. 3). These graphs showed the ability of these indices to detect Fernández (1992) groups. By using these indices and Y_P and Y_S variables, three dimensional diagrams could partition the genotypes in four groups: (1) Genotypes producing high yield under both water stress and non-stress environments (group A), (2) genotypes with high yield under either non-stress (group B) or (3) stress (group C) environments, and (4) genotypes with poor performance under both stress and non-stress environments (group D). A suitable index must be able to distinguish group A genotypes from the other groups. Three dimensional plots corresponding to TOL, MP, GMP, STI, HM, and YI indices illustrated that genotypes 'RHA266 × C100', 'LR4 × LR25', 'RHA266 × LR55', 'LR55 × LR25', 'RHA266 × LR4', 'C104 × LR25' and 'LR55 × C104' are drought resistant; because they express uniform superiority in both stress and non-stress conditions (Group A). Among these indices, resistant genotype were revealed by STI, MP, GMP, HM indices (Genotype 'LR4 × LR25') opposite the resis-

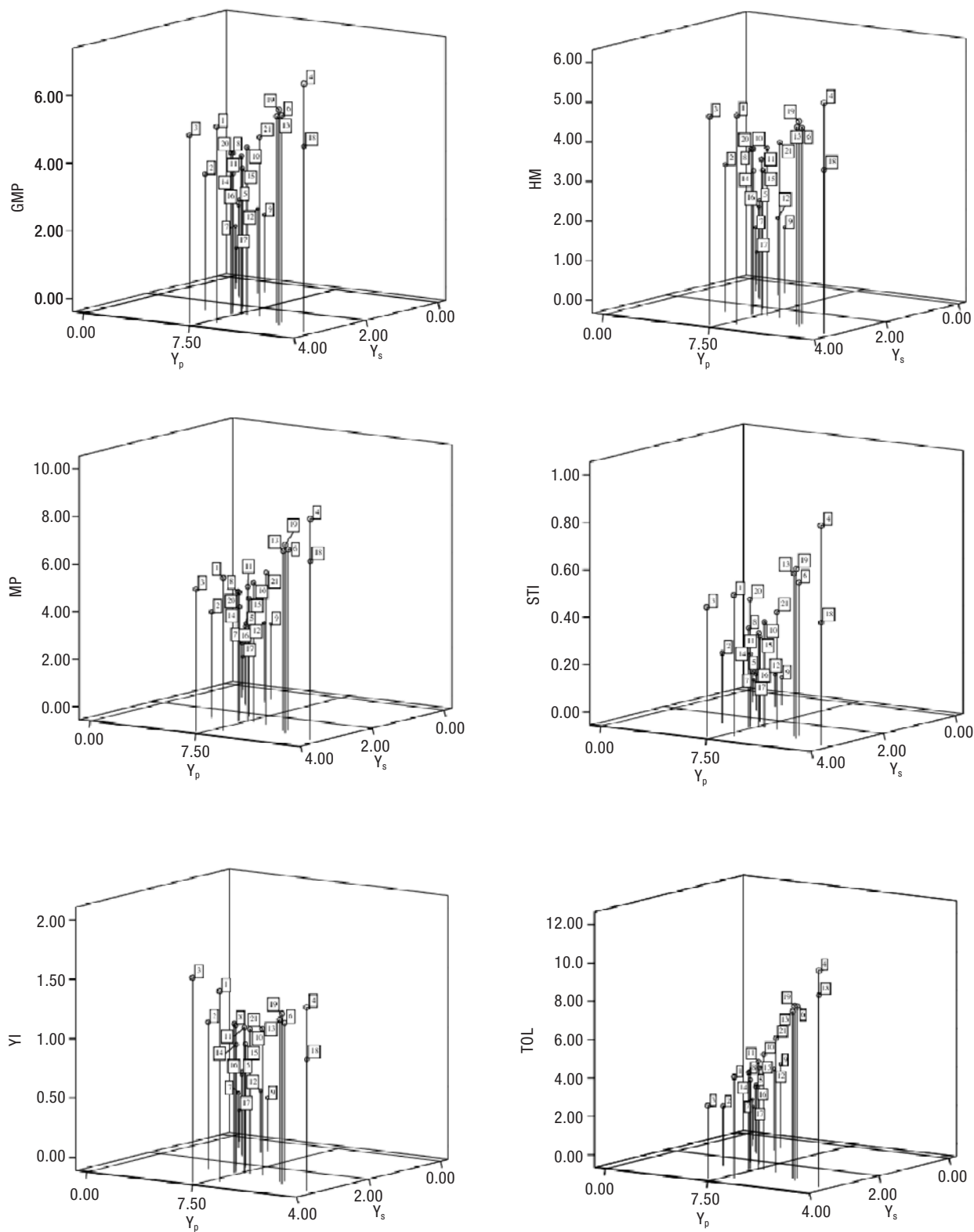


Figure 3. Tree dimension scheme of potential yield (Y_p), stress yield (Y_s) and geometric mean productivity (GMP), harmonic mean (HM), mean productivity (MP), stress tolerance index (STI) for sunflower inbred lines and their F1 hybrids. Genotype codes: see Figure 1.

tant genotypes revealed by TOL (genotypes 'LR25' and 'C100'); and by YI (genotype 'LR25 × C100').

Discussion

The CV values for yield in non-stress condition (Y_p) and yield in stress condition (Y_s) were 20.96 and 19.92, respectively. Concerning to calculated indices the values varied from 18.45 to 30.92 (Table 2). In general, CV value higher than 20% is considered to be high; however, may be possible to ignore from approximately high CV values when F test are significant and this item is found in several published research works (Takemoto *et al.*, 1988; Xu *et al.*, 2000; Aliyu and Awopetu, 2005; Zarei *et al.*, 2007; Okwuagwu *et al.*, 2008; Kandiç *et al.*, 2009; Sabu *et al.*, 2009). This however indicates that effect of genotypes was more pronounced on studied characters under two irrigation regimes (Aliyu and Awopetu, 2005). The inconsistent CV values reported in many studies as our one might be due to physio-genetic characteristics and degree of compatibility of the plant material, low number of individual per genotype in plot, low number of replication per genotype and/or variable environments in which the trial was carried out (Okwuagwu *et al.*, 2008).

As shown in Table 3, selection based on SSI index identified genotypes with relatively high Y_p but low Y_s and this is in agreement with Sio-Se Marde *et al.* (2006) findings in wheat. For the SSI index, the greater values correspond to greater susceptibility of genotype to stress. The main disadvantage of this index is that separated genotypes are not co-located in group A. Clarke *et al.* (1992) reported that SSI index does not differentiate between potentially drought resistant genotypes and similar limitation was also observed by White and Singh (1991) and Farshadfar and Sutka (2002). YI index that was proposed by Gavuzzi *et al.* (1997), was significantly correlated with stress and non-stress yield and therefore is a suitable criterion for drought resistance selection. However, Sio-Se Marde *et al.* (2006) reported that this index groups genotypes only based on their yield under stress condition and so does not discriminate genotypes belonging to group A. In this experiment, a reason for this significant correlation between yield in both conditions and this index may be due to less severe stress conditions. According to Tezara *et al.* (2002), 67% of field capacity is considered as mild stress and 33% is considered as severe

stress in sunflower. In this study, YSI index was not a desirable index because it had no significant relationship with both growing condition's yield. Stability is more important than high yield in non-stress conditions. This index shows the relative stability of yield with conditions changes and the higher the YSI, the more resistant the crop is. Selection based on TOL was efficient in improving yield under stress condition whereas the selected genotypes performed poorly under non-stress condition (Fernández, 1992). MP is mean yield for a genotype in two stress and non-stress conditions. MP can identify genotypes with high Y_p but with relatively low Y_s (group B) and thus it fails to distinguish group A from group B. By decreasing TOL and increasing MP, the relative tolerance increases (Rosielle and Hamblin, 1981; Fernández, 1992). GMP is more powerful than MP in separating group A genotypes and has a lower susceptibility to different amounts of Y_s and Y_p . Therefore MP, which is based on arithmetic mean, will be biased when the difference between Y_s and Y_p is high. The geometric mean is often used by breeders interested in relative performance since drought stress can vary in severity in field environments and over years (Fernández, 1992). A high STI demonstrates a high tolerance and the best advantage of STI is its ability to separate group A from others. STI index is calculated based on GMP index and therefore there is high positive correlation between these indices (0.963) and agree with Fernández (1992) and Mozaffari *et al.* (1996). The observed relationships between Y_p , Y_s and a few desirable criteria (GMP, MP and STI) are consistent with those reported by Fernández (1992) in mungbean (*Phaseolus aureus* Roxb.), Farshadfar and Sutka (2002) in maize (*Zea mays* L.) and Kristin *et al.* (1997) in common bean (*Phaseolus vulgaris* L.).

Results based on PCA and biplot analysis revealed that genotype 'LR4 × LR25' classified as group A is a drought resistant genotype that has reasonable yield in both stress and non-stress conditions. PCA and biplot application for screening resistant genotypes agreed with several studies by Fernández (1992), Farshadfar and Sutka (2003) and Golabadi *et al.* (2006). Result of UPGMA clustering method, based on desirable resistance indices, was in agreement with the output of biplot analysis and therefore by using genotypes that are located in separate groups and have maximum genetic distance, it is possible to analyze genetic parameters of these drought resistance indices.

Drought is considered as one of the most visible factors which affect grain yield and some of the consti-

tments of the seed oil of sunflower (Razi and Assad, 1999; Ali *et al.*, 2009). According to results in this study, the following suggestions are made: 1. In order to select a genotype with stable and high yield in non-irrigated and irrigated conditions, STI, MP, GMP, and HM are proposed as the more suitable indices. Selection by these indices can be useful to identify a cultivar with desirable yield in both stress and non-stress conditions (group A), although it is recommended that, the selection be done based on PCA results (namely by using several indices instead of only one index information). 2. In order to identify parents with high level of differences for confirmation of mapping population for QTL analysis, we suggest making a first selection according to MP, GMP, HM indices to have a maximum of segregating loci.

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