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Stability some sunflower genotypes across divergent environments

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Abstract: Simultaneously identify superior performing in terms of seed yield and seed oil content and broad adaptation across a wide range of different environments is an important target for sunflower breeder. So, 10 sunflower genotypes were evaluated across the eight various environments created by sowing at four locations i. e. Kafr El Hamam/ Sharkia, Shandaweel /Sohag, Tag El Ezz/ Dakahlia and Al Arish/ North Sinai Agricultural Research Stations, Agricultural Research Center (ARC), Egypt during the two successive summer seasons 2018 and 2019 using randomized complete block designs with four replications in each environment. Results showed that mean squares due to environments, genotypes and their interaction were highly significant for seed yield and seed oil content. Most stability approaches revealed that high performing stable genotypes were L240 for seed yield and Sakha 53, L110 and L235 for seed oil content under divergent environments. Hence, these four stable sunflower genotypes could be behaved as good breeding materials stock for sunflower improvement.

Keywords: AMMI; genotype × environment interaction; GGE; stability statistics; sunflower (*Helianthus annuus* L).

Introduction

Sunflower (*Helianthus annuus* L.) is an important oil seed crop not only in Egypt but also in the world. Sunflower breeder seeks to develop genotypes with superior performing and broad adaptation across a wide range of environments. Although

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sunflower is a temperate zone crop, yield potential of sunflower is greatly influenced by fluctuating of environmental conditions. In other words can be noted that, environmental changes either climatic or edaphic conditions are considered limiting factors for seed yield and seed oil content as earlier reported by Abd El-Satar et al. (2015), Khomari and Mohammadi (2017) and Sofalian et al. (2019). Hence, a considerable attention should be given to identify the interaction of genotype with a wide range of different environments, especially climatic and edaphic conditions in the sunflower breeding program. Accordingly, identify high performing genotypes in terms of seed yield and seed oil content with wider adaptability is an integral objective of sunflower breeding programs.

For this purpose, several models have been proposed to measure the stability of sunflower genotypes across a wide range of environments represented in regression slope value (Finlay and Wilkinson 1963), deviation from regression (Eberhart and Russell 1966), Alpha and Lambda of Tai's model (1971) and AMMI stability value (ASV) proposed by Purchase (1997) based on the AMMI model's IPCA1 and IPCA2 scores for each genotype along with grand mean. Moreover, the additive main effects and multiplicative interaction (AMMI) model as suggested by Gauch (1988, 1992) and the genotype main effect plus G × E interaction (GGE) models as suggested by Yan (2002) are the most frequently utilized models for graphing in biplots. AMMI and GGE Biplots analyses of the first two principal components were used to illustrate these relationships (Gabriel, 1971 and Kempton, 1984).

From above mentioned facts, the present study was carried out to simultaneous select for high seed yield and seed oil content, and stable sunflower genotypes under different environmental conditions.

Materials and methods

Genetic materials

Ten sunflower genotypes Sakha53, L990, L245, L240, L110, L125, L230, L880, L235 and L19 were received from sunflower breeding program, Oil Crops Research Department, Field Crops Research Institute, Agricultural Research Center, Giza, Egypt.

Site description

A field experiment was conducted at the experimental Farm of four Agricultural Research *Stations* i. e. Kafr El Hamam/ Sharkia, Shandaweel /Sohag, Tag El Ezz/ Dakahlia and Al Arish/North Sinai during the two successive summer seasons 2018 and 2019. Soil samples (0–30 cm) collected from the experimental site and analyzed for the physical and chemical analysis of soil as suggested by Jackson (1973) and results are summarized in Table 1.

Table 1: Soil texture, pH, organic matter, EC, salt concentration in soil, latitude and longitude of field stations.

Code	Growing season (summer)	Governorate/Research station	Soil texture	pH	Organic matter (g/kg)	EC (dsm^{-1})	Latitude	Longitude
E_1	1st June 2018	Sharkia/Kafr El Hamam	Clay loam	7.5	1.95	2.56	30° 58’	31° 50’
E_2	1st June 2018	Shandaweel/Sohag	Clay loam	7.8	1.51	0.42	26° 33’	31° 41’
E_3	1st June 2018	Dakahlia/Tag El Ezz	Clay	8.05	1.26	10.12	31° 36’	30° 57’
E_4	1st June 2018	North Sinai/Al Arish	Sandy	7.12	0.22	6.82	31° 05’	33° 50’
E_5	15th June 2019	Sharkia/Kafr El Hamam	Clay loam	7.4	2.85	2.12	30° 58’	31° 50’
E_6	15th June 2019	Shandaweel/Sohag	Clay loam	7.6	1.66	0.54	26° 33’	31° 41’
E_7	15th June 2019	Dakahlia/Tag El Ezz	Clay	7.19	1.52	9.6	31° 36’	30° 57’
E_8	15th June 2019	North Sinai/Al Arish	Sandy	7.15	0.42	6.35	31° 05’	33° 50’

Experimental design

Seeds of mentioned genotypes were evaluated in eight various environments created by sowing at four locations i. e. Kafr El Hamam/ Sharkia, Shandaweel/Sohag, Tag El Ezz/Dakahlia, and Al Arish/ North Sinai Agricultural Research *Stations*, ARC, Egypt during the two successive summer seasons 2018 and 2019. Experimental layout was performed in a randomized complete block design with four replications in each environment. Each plot consisted of five ridges, 60 cm apart, 3 m long, and 30 cm between hills.

Agricultural practices

Sunflower genotypes seeds under study were hand-planted on ridges, 60 cm apart, 3 m long, and 30 cm between hills. Plants of sunflower genotypes under study were thinned at 15 days after sowing to secure one plants hill^{-1}. All other cultural practices were applied as recommended.

Data collected

Plants of three ridges from each plot were harvested for determining seed yield per m^2 and converted to recorded seed yield in kg fed^{-1}. Seed oil content was determined according to (AOAC 1990).

Statistical analysis

Mean values for seed yield and seed oil content subjected to analysis of variance for each environment using randomized complete block design with four replications according to Gomez and Gomez (1984). Bartlett's test (Table 2) indicated that the presence of homogeneity of variance, which allowed the combined analysis of variance over locations and years to be perform.

To judge on the magnitude of sunflower genotypes interaction with environments, data of seed yield and seed oil content were analyzed using three statistically models such as combined analysis of variance, joint linear regression model as suggested by Eberhart and Russell (1966) and AMMI model (Gauch 1992) as well as the E and G × E interaction biplot analysis (Yan 2002). Accordingly, regression slope value (Finlay and Wilkinson 1963), deviation from regression (Eberhart and Russell 1966), Tai's (1971) environmental effects (α_i) and deviation from the linear response (λ_i) and AMMI's stability values (Purchase 1997) along with grand mean. AMMI analysis (Gauch 1992) was performed. All statistical analyses were carried out using GEA-R (Pacheo et al. 2015) and MS-EXCEL (2007) with spreadsheet formula commands.

Table 2: Bartlett's test of error variances for all studied traits.

Item	Seed yield	Seed oil content
Bartlett's' test value	3.72	12.48
$X^2_{0.05}$	38.89	38.89
Significance	NS	NS

Results and discussion

Analysis of variance

A combined analysis of variance (Table 3) is an effective method used to identify the presence of genotype by environment interaction from replicated multi-environment trials. This analysis depicted highly significant differences among sunflower genotypes, locations, years and their interactions with respect to seed yield, and seed oil content. Significant interaction of genotypes with environments and its components for seed yield and seed oil content, suggest that genotypes varied across environments either years or locations, on genetic variability among the genotypes and possibility of selection for stable genotypes. These finding are in agreement with the results reported by Abd El-Satar et al. (2015), Khomari and Mohammadi (2017) and Sofalian et al. (2019). The partitioning of sum of squares for the seed yield and seed oil content indicated that environments contribute to (90.78% & 17.33) i. e. year (3.21 & 4.01), location (87.40% & 12.37), and Year × Location (0.17 & 0.93); genotypes (1.73% & 6.77) and GEI (5.09% & 41.60) i. e. Year × Genotype (1.25% & 6.77), Location × Genotype (2.84% & 19.94), and Year × Location × Genotype (0.99% & 14.89) as in Table 3. This indicates the highest influence of environment on seed yield and seed oil content performance of sunflower genotypes.

The joint linear regression analysis (Table 3) as suggested by Eberhart and Russell (1966) was performed through the means over replication for each genotype in each environment. This analysis showed also highly significant differences among sunflower genotypes, environments and their interaction for seed yield and seed oil content. This indicated that tested sunflower genotypes considerably differed in their response to environmental differences. Furthermore, highly significant mean squares of environment plus interaction (genotype by environment) and its components i. e. environment (linear), genotype by environment (linear) interaction and pooled deviation (non-linear) from regression model, indicating that predictable (linear) and unpredictable (non-linear) components were contributed in the genotype by environment interaction. Also, highly significant genotype by environment (linear) interaction, revealed that the presence of genetic differences among genotypes in their regression on environmental index, while highly significant pooled deviation of most genotypes indicated that the direction of most genotypes from linearity was highly significant. These finding are in agreement with the results reported by Abd El-Satar et al. (2015), Khomari and Mohammadi (2017) and Sofalian et al. (2019).

AMMI model has been achieved great successes in recently years in assessing the interaction of genotypes with environments. In this regard, the AMMI

Table 3: Regular combined analysis of variance and partitioning the proper source of variation according to each of Eberhart and Russell model and AMMI model for seed yield and seed oil content.

Source of variation	df	Seed yield		Seed oil content	
		MS	Percent	MS	Percent
Combined analysis					
Environment (E)	7	743,276.58**	90.78	43.66**	17.33
Year (Y)	1	183,768.89**	3.21	70.61**	4.01
Location (L)	3	1,669,847.45**	87.40	72.69**	12.37
Y × L	3	3,208.26**	0.17	5.64	0.93
Reps/E	24	518.95	0.03	2.55	0.43
G	9	11,024.64**	1.73	13.27**	6.77
G × E	63	4,630.18**	5.09	11.64**	41.60
G × L	27	6,031.40**	2.84	13.02**	19.94
G × Y	9	7,987.21**	1.25	13.27**	6.77
G × Y × L	27	2,109.96**	0.99	9.72**	14.89
Pooled error	237	574.28		2.52	
Eberhart and Russell model					
Genotype (G)	9	2,756.16**	1.77	3.32**	10.31
Environment + G × E	70	19,623.71**	98.23	3.71**	89.69
(a) Env. (linear)	1	1,300,734.01**	94.69	76.41**	29.41
(b) G × E (linear)	9	2,307.22**	1.51	6.46**	22.39
(c) Pooled deviations	60	869.34**	3.80	2.09**	48.20
Environment (E)	7	185,819.14**	93.01	10.92**	26.38
G × E	63	1,157.55**	5.21	2.91**	63.31
Pooled error	240	143.40		0.63	
AMMI model					
Environment (E)	7	743,276.58**	93.01	43.66**	26.38
G × E	63	4,630.18**	5.21	11.64**	63.31
PC1	15	8,290.31**	42.63	22.01**	45.02
PC2	13	6,857.78**	30.56	16.94**	30.03
PC3	11	4,836.62**	18.24	6.90**	10.35
PC4	9	1,462.07**	4.51	6.40**	7.86
PC5	7	1,051.48	2.52	5.17*	4.94
PC6	5	577.31	0.99	2.09	1.43
PC7	3	529.11	0.54	0.95	0.39
Pooled error	240	573.59		2.52	

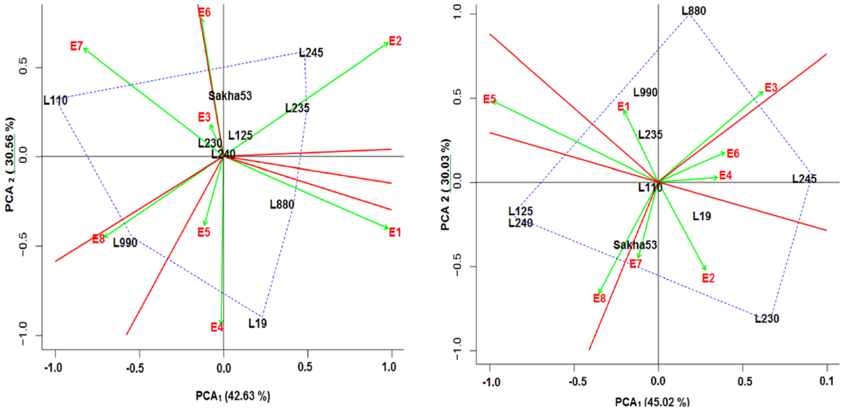
*, ** Significant at 0.05 and 0.01 probability level, respectively; PC: principal component.

analysis (Table 3) revealed a major contributor was environment (93.01 & 26.38) followed by interaction of genotype with environment (5.21 & 63.31%) in total phenotypic variation for seed yield and seed oil content, respectively. It further partitioned the interaction sum of squares of genotypes with environments into seven principal component analysis, four of these were highly significant. The first and second principal components were highly significant ($P < 0.01$), and explained 42.63 & 30.56% for seed yield and 45.02 & 30.03% for seed oil content of variation due to interaction of genotype with environments, respectively. They cumulatively accounted for 73.19% for seed yield and 75.05% for seed oil content of variation due to genotype by environment. These finding are in agreement with the results reported by Khomari and Mohammadi (2017) and Sofalian et al. (2019).

Highly significant interaction of genotype with environment was confirmed by combined analysis, joint linear regression analysis and AMMI analysis, hence this result encourages sunflower breeders to identify high values of seed yield and seed oil content of sunflower genotypes with their stability under various environmental conditions as well as given chance prepared to determine the stability degree for each genotype by several stability statistics.

AMMI biplot analysis

AMMI biplot graph for seed yield (Figure 1A) and seed oil content (Figure 1B) showed that, the eight environmental vectors were scattered into all four quadrants, meaning that indicates the lack of association among these environments. The environment (E-3 and E-4) has the shortest vector followed by (E5 and E6) for seed yield and seed oil content, respectively which indicates their low discriminating power. It can inferred that less force was exerted on genotypes to deviate from mean yield in these environments. On the other hand, long vectors of environment (E-4 and E-5), (E-2 and E3), (E-7 and E-8), (E-6 and E2), (E-1 and E7) and (E-8 and E1) for seed yield and seed oil content, respectively suggest that these environments enforced enough pressure on genotypes to exhibit their differences. Furthermore, the vertex genotypes L245, L235, L880, L19, L990 and L110 for seed yield and L880, L245, L230 and L240 for seed oil content were located far away from the origin, which exhibited the superior performance in particular environment and could be regarded as specifically adapted genotypes. The vertex genotype L245 and L235 interacted well with E-2 and E-6, L880 and L19 in E-4, E-1 and E-5, L990 in E-8 and L110 in E-7 for seed yield. On the other hand, the vertex genotype L880 interacted well with E-3 and E-1, L245 in E4 and E6, L230 in E-2 and E-7, L240 and L125 in E-8 for seed oil content. Majority of the genotypes i. e. L240, L230, L125 and Sakha 53 for seed yield and L110, L19, Sakha 53, L235 and L990 for seed oil content clustered around the origin which were most desirable and stable genotypes, as they less responsive to change environmental than the vertex genotypes.

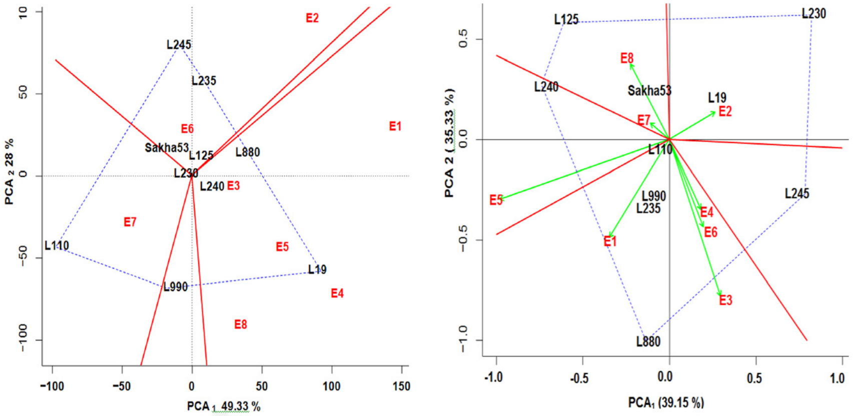


(A) (B)

Figure 1: AMMI biplots of 10 sunflower genotypes for seed yield (A) and seed oil content (B) across eight environments.

GGE biplot analysis

The associations of genotypes were distributed for seed yield (Figure 2A) and seed oil content (Figure 2B) in (4 and 5) sectors in which (3 and 4) sectors received environments, respectively. Hence, sectors of genotypes which have environments included with them, imply the association of genotypes with that specific environment. The five perpendicular lines divided the polygon view into four well defined sectors with genotypes L245, L19, L990 and L110 for seed yield and five sectors with genotypes L230, L245, L880, L240 and L125 for seed oil content as the corner or vertex genotypes. The environments E-6 and E-2 fell in the sector in which L245 was the vertex genotype for seed yield and the environment E-2 fell in the sector in which L230 was the vertex genotype for seed oil content. This means that L245 was the best genotype for E-6 and E-2 for seed yield and L230 adapted well with E2 for seed oil content. The environments E-1, E-3, E-4, E-5 and E-8 fell in the sector in which L19 was the vertex genotype for seed yield, meaning that L19 was the best genotype for these environments, whereas the environments E1, E3, E4 and E6 located in the sector in which L880 was the corner genotype for seed oil content, indicated that L880 interacted well with these environments. Environment seven fell in the sector in which L110 was the corner genotype for seed yield, so L110 was the best genotype in this environment, whereas the genotype L240 adapted well with E-5 as this environment located in the sector in which L240 was the vertex genotype for seed oil content. The genotype L125 interacted well with the environments E-7 and E-8 as they environments located in the sector in which L125

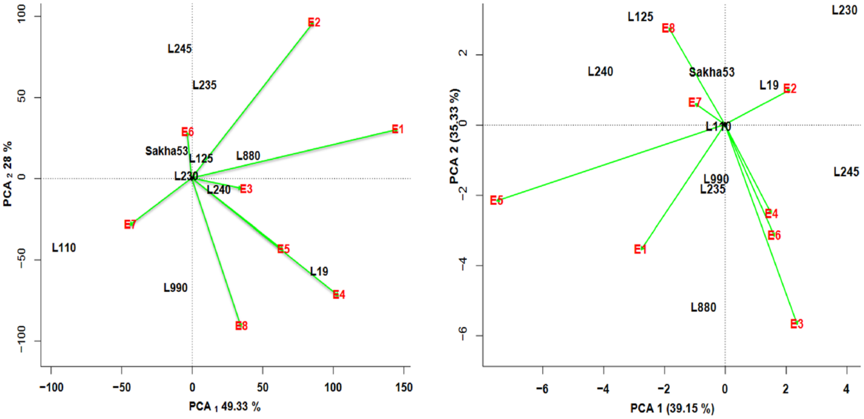


(A) (B)

Figure 2: "Which-won-where" pattern of GGE biplot of 10 sunflower genotypes for seed yield (A) and seed oil content (B) across eight environments.

was the vertex genotype for seed oil content. No environments fell in the sector in which L990 for seed yield and L245 for seed oil content were the vertex genotypes, indicating that this genotype was not the best in any of the environments.

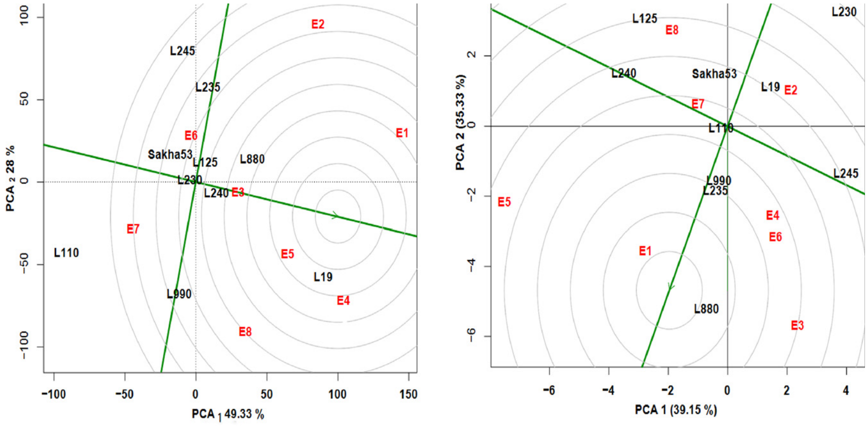
The scores of first two principal components (PC1 and PC2) cumulatively explained 77.33% for seed yield (Figure 3A) and 74.48% for seed oil content (Figure 3B) of the variation caused by GGE interaction. The scores of PC1 and PC2 were both in positive and negative direction signifying the differences in yield



(A) (B)

Figure 3: GGE biplot of 10 sunflower genotypes for seed yield (A) and seed oil content (B) across eight environments.

performance of genotypes across environments which lead to cross-over interaction (COI). Genotypes in the proximity of origin are considered as stable, while those far away from the origin are considered as responsive and sensitive to environments. Similarly, the length of environmental vectors suggests the strength of environment to incite variations in the yield performance of genotypes. Genotypes L245, L19, L990 and L110 for seed yield and L230, L245, L880, L240 and L125 for seed oil content were the most sensitive and responded well to the changing environments as indicated by their longer distances from the origin. Environments (E-2 and E-3) had the longest vector followed by (E-4 and E-5) and (E-1 and E1) for seed yield and seed oil content, respectively which implies that these environments had more strength than their other counterparts to force variation in the yield performance of genotypes. On the contrary, the short vectors of environments (E-3 and E-7) and (E-6 and E2) for seed yield, respectively indicate that they were steady and genotypes were consistent in their yield performance. Genotypes L230, L125, L240, Sakha 53 and L880 for seed yield and L110, L19, Sakha 53, L990 and L235 for seed oil content fell in the vicinity of origin and hence may be regarded as stable and widely adapted. It is visible in Figure 3 that environments (E-1 and E-2) and (E-3, E-5, E-4 and E-8) for seed yield and (E4, E6 and E3), (E1 and E5) and (E7 and E8) for seed oil content had close association which is evident by small angles among their vectors. Similarly, environments (E-3, E-5, E-4 and E-8) for seed yield and (E4, E6 and E3) for seed oil content were almost similar in response towards genotypes as they share the same quadrant while environments (E-7 and E-6) for seed yield and E2 for seed oil content were unique.

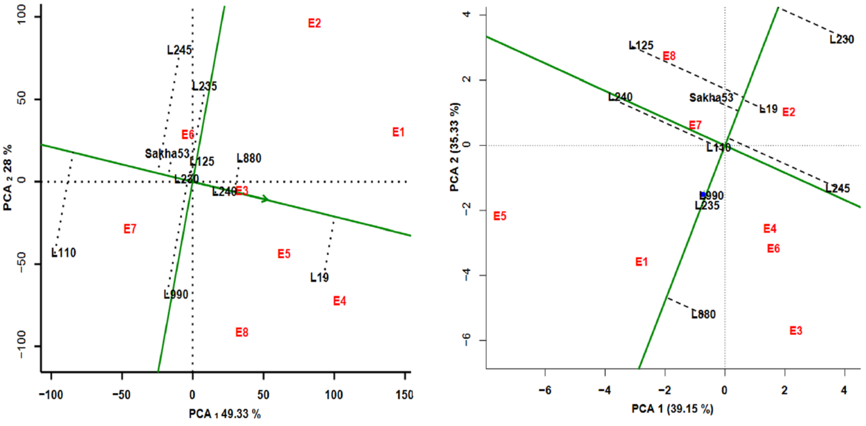


(A) (B)

Figure 4: Visualization of ideal environment and ideal genotype of GGE biplot based on seed yield (A) and seed oil content (B) for 10 sunflower genotypes across eight environments.

Ideal environment is the one which has both the abilities of discriminating power for genotypes and representative of all the test environments, which is important in selection of widely adapted genotypes. Similarly, ideal genotype is the one which is high yielding yet stable in yield performance and consistently ranks highest in all test environments. It is visible from (Figure 4A) for seed yield and (Figure 4B) for seed oil content that environment (E-4 and E-1) were the best, followed by (E-1 and E-6) and (E-5 and E-4) for seed yield and seed oil content, respectively, as they were the most discriminating environment because of their large distance from the origin as well as representative environments for the evaluation of genotypes. It can be seen that genotypes L240, L230, L880, L125 and Sakha 53 for seed yield and L235, L990, L110, L19 and Sakha 53 for seed oil content have smaller projections on the Average tester coordinate y-axis, thus behaved them as ideal genotypes.

The ranking of genotypes based on mean values is illustrated in (Figure 5A) for seed yield and (Figure 5B) for seed oil content. It is visible that genotype L19 and L880 had higher mean seed yield and seed oil content, respectively with lesser stability which is indicated by its larger projection on ordinate. Similarly, L240, L880 and L125 for seed yield and L110, L235 and Sakha 53 for seed oil content are genotypes which performed above average and had better stability across environments and hence could be selected for diverse environments. The yield performance of genotypes L990, L235, L245 and L110 for seed yield and L230, L245 and L125 for seed oil content were highly influenced by environments as indicated by



(A) (B)

Figure 5: Genotype ranking pattern of GGE biplot based on seed yield and stability (A) and seed oil content and stability (B) for 10 sunflower genotypes evaluated across eight environments.

their long projection on ordinate in addition to their below average yield. Distribution of Tai (1971)'s parameters i. e. α and λ as genotypic stability can be estimated as shown in Table 4 and plotted on two orthogonal axes with a hyperbola that includes 80, 90 and 95% of the predicted values of parameter α as well as the two vertical lines denote the limits of the 95% confidence interval for parameter λ being

Table 4: Mean and some stability statistics for seed yield and seed oil content for 10 sunflower genotypes across eight environments.

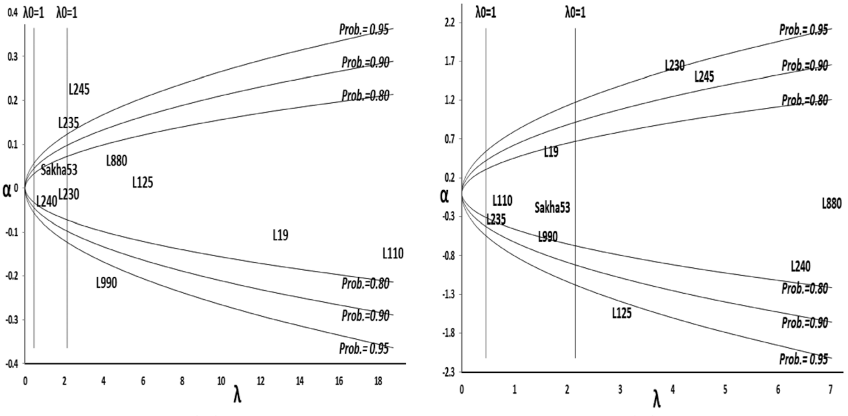
								Seed yield
Genotype	**Mean†, kg fed^{-1}**	b_i	**Tb = 0**	**Tb = 1**	S^2_{di}	α_i	λ_i	ASV_i
Sakha53	830.14	1.04	23.066**	0.991	121.143**	0.04	1.74	0.31
L990	825.74	0.79	11.226**	−3.037	493.550**	−0.21	4.17	0.88
L245	822.53	1.23	21.456**	3.983**	280.220**	0.23	2.78	0.89
L240	844.94	0.97	26.656**	−0.741	27.505**	−0.03	1.13	0.02
L110	799.34	0.85	5.745**	-0.984	2,727.082**	−0.15	18.77	1.43
L125	832.80	1.01	12.073**	0.176	773.238**	0.01	6.00	0.13
L230	827.91	0.99	19.250**	−0.243	196.537**	−0.01	2.24	0.11
L880	836.14	1.06	14.331**	0.870	572.098**	0.06	4.69	0.64
L235	827.72	1.15	22.396**	2.936*	197.699**	0.15	2.24	0.74
L19	873.00	0.90	7.236**	−0.844	1846.535**	−0.10	13.01	0.95
Mean	832.03							
LSD 5%	22.29	0.16						
LSD 1%	29.65	0.22						

								Seed oil content
Genotype	**Mean‡, %**	b_i	**Tb = 0**	**Tb = 1**	S^2_{di}	α_i	λ_i	ASV_i
Sakha 53	41.79	0.84	2.213	−0.430	0.490	−0.18	1.72	0.48
L990	41.61	0.50	1.341	−1.340	0.459	−0.54	1.63	0.51
L245	41.57	2.39	3.740**	2.177	2.527*	1.51	4.60	1.36
L240	41.95	0.15	0.197	−1.159	3.551**	−0.93	6.43	1.30
L110	41.84	0.92	3.643*	−0.315	−0.116	-0.09	0.77	0.05
L125	40.85	−0.41	−0.779	−2.667	1.539	−1.53	3.04	1.28
L230	40.62	2.52	4.155**	2.507*	2.210*	1.65	4.04	1.29
L880	42.75	0.89	1.166	−0.144	3.850**	−0.12	7.03	1.04
L235	42.32	0.70	2.986*	−1.256	−0.179	−0.32	0.65	0.29
L19	41.18	1.50	3.948**	1.316	0.499	0.54	1.70	0.37
Mean	41.65							
LSD 5%	1.09	1.05						
LSD 1%	1.45	1.39						

KEY: Mean† = seed yield (kg/fed.); Mean‡ = seed oil content (%); b_i = Regression coefficient, S^2_{di} = deviation from regression; α_i and λ_i = Tai's stability parameters; ASV_i = AMMI stability value;* = significant at 5%; ** = significant at 1%.

equal to 1. Thus, the area within the hyperbola and the two vertical lines define the region as having “average stability, ($\alpha = 0$ & $\lambda = 1$)” whereas the area between the two vertical lines but outside the hyperbola defines the area as having “above average stability, ($\alpha < 0$ & $\lambda = 1$)” and the values ($\alpha > 0$ & $\lambda = 1$) will be referred to as below average stability as well as “perfect stability, ($\alpha = -1$ & $\lambda = 1$)” as perfect stable genotype rarely exist. Plotted Tai’s parameters α and λ regarding seed yield (Figure 6A) and seed oil content (Figure 6B) and Table 4 for the 10 genotypes across all eight environments, showed the genotypes L240, L230 and Sakha 53 for seed yield and L110, L19, Sakha 53, L990 and L235 for seed oil content were distributed in the average stability region at probability levels of 0.20, 0.10 and 0.05. Of these L240 (844.94 Kg) genotype had higher seed yield than grand mean (832.03 kg), whereas Sakha 53, L110 and L235 possessed higher seed oil content than grand mean (41.65%), thereby this genotype considered as breeding stocks in any further sunflower breeding program for satisfying stable high yielding genotype under divergent environments. From above mentioned results, plotted of Tai’s stability parameters α and λ detected that genotype L240 for seed yield and Sakha 53, L110 and L235 for seed oil content had average stability coupled with the highest mean values comparable to that of the grand mean.

Scatter plot of regression coefficient (bi) *versus* seed yield (Figure 7A) and seed oil content (Figure 7B) as seen in Table 4, the genotype L235 and L245 for seed yield and L245 for seed oil content showed better adaptability to favorable environmental conditions (bi > 1 and $\bar{x}i = \bar{x}$). The highest mean values were obtained from the genotype L240 for seed yield and L880 and L235 for seed oil content along with

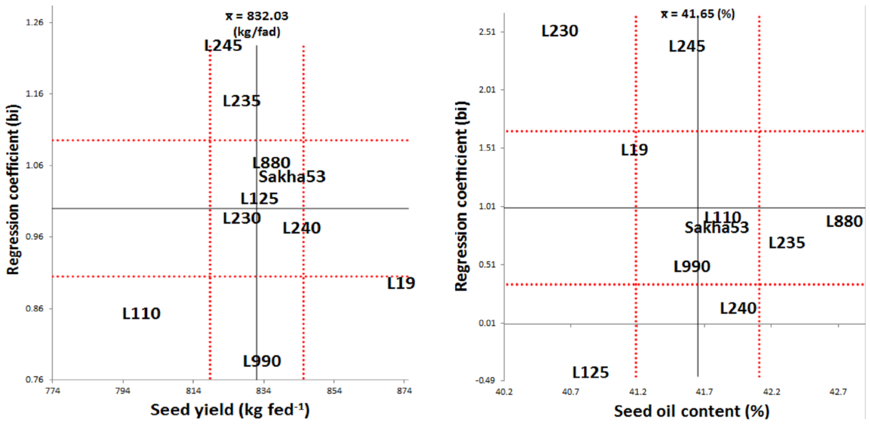


(A) (B)

Figure 6: Distribution of estimated stability statistics α and λ for (A) seed yield and (B) seed oil content based on Tai’s model for 10 genotypes grown in eight environments.

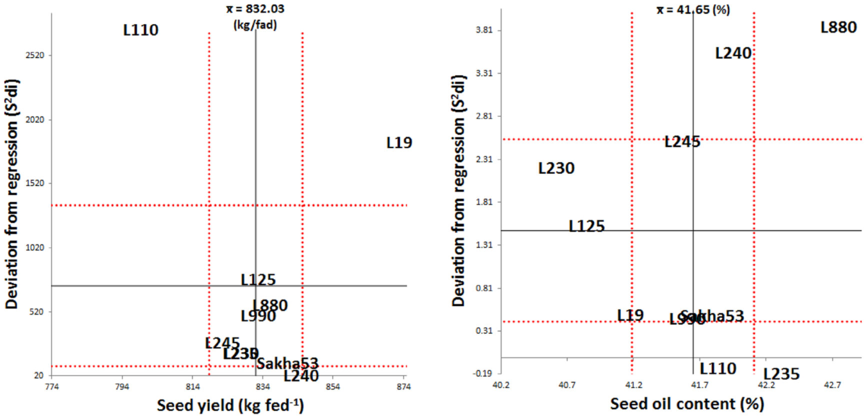
their b_i values nearly equal to unit, so they were accepted as having better adaptability to grow under more environmental changes ($bi = 1$ and $xi > x$). The lowest mean values were detected in L110 for seed yield and L125 for seed oil content with b_i values less than unity, hence they were accepted as having poor adaptability to unfavorable environmental conditions. The regression coefficient did not differ significantly from unity coupled with the lowest mean values were detected in the genotype L110 for seed yield and L125 for seed oil content, hence they were poor adaptability to all environmental conditions. Moreover, the genotypes L880, Sakha 53, L125, L230 and L240 for seed yield and L110, Sakha 53, L990, L880 and L235 showed average adaptability to all environmental conditions, as they the regression coefficients did not differ significantly from unity associated with mean values nearly equal to or higher than the grand mean. These genotypes can be considered as the most widely adaptable and stable genotypes in terms of seed yield and seed oil content.

Deviation from regression *versus* seed yield (Figure 8A) and seed oil content (Figure 8B) and in Table 4, the genotypes L110 for seed yield behaved as poor and L240 for seed oil content behaved as average adaptability to favorable environments conditions, as they had ($\bar{x}i < \bar{x}$ & high S^2_{di}) and ($\bar{x}i \approx \bar{x}$ & high S^2_{di}), respectively. Whereas, the different degrees of adaptability can be classified into average in the genotype L240 for seed yield and L110 for seed oil content and better in the genotype L235 for seed oil content to grow under unfavorable or poor agro-climatic conditions. Moreover, the widely adaptability degrees to all environmental conditions was classified into poor ($\bar{x}i < \bar{x}$ & medium S^2_{di}) in the genotype L230 and L125



(A) (B)

Figure 7: The relationship between the regression coefficients and seed yield (A) and seed oil content (B) for 10 sunflower genotypes across eight environments.

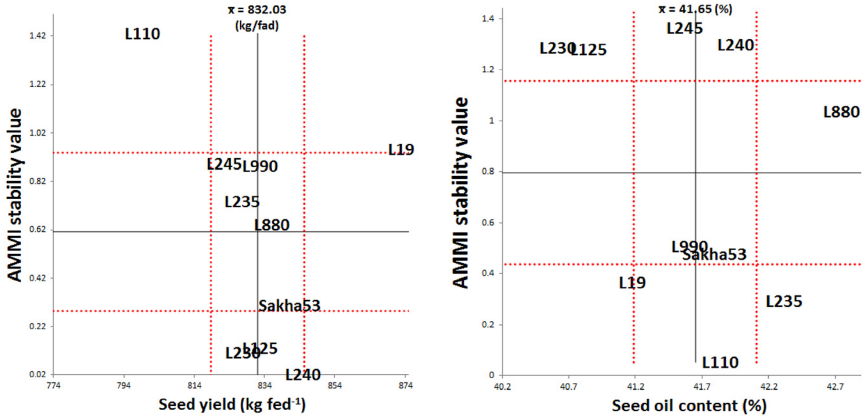


(A) (B)

Figure 8: The relationship between the deviation from regression and seed yield (A) and seed oil content (B) for 10 sunflower genotypes across eight environments.

for seed oil content and average ($\bar{x}i \approx \bar{x}$ & medium S^2_{di}) in the genotype L125, L880, L990, L245, L230, L235 and Sakha 53 for seed yield and L19, L990, Sakha53 and L245 for seed oil content.

ASV *versus* seed yield (Figure 9A) and seed oil content (Figure 9B) as well as in Table 4 at favorable environmental conditions, performance of the genotype L110 for seed yield and L230 and L125 for seed oil content ($\bar{x}i > \bar{x}$ & high ASV) were poor with compared to the best performance of the genotype L19 for seed yield ($\bar{x}i < \bar{x}$ &



(A) (B)

Figure 9: The relationship between the AMMI stability value and seed yield (A) and seed oil content (B) for 10 sunflower genotypes across eight environments.

high ASV). At unfavorable environmental conditions, adaptability was portioned into poor in the genotype L19 for seed oil content ($\bar{x}i < \bar{x}$ & low ASV), average in the genotypes L230, L125 and L240 for seed yield and L110 for seed oil content ($\bar{x}i \approx \bar{x}$ & low ASV) and better in the genotype L235 for seed oil content ($\bar{x}i > \bar{x}$ & low ASV). Moreover, performance of the genotypes L245, L990, L235, L880 and Sakha 53 for seed yield and L990 and Sakha 53 ($\bar{x}i \approx \bar{x}$ & medium ASV) was moderate to grow at all environmental conditions.

Conclusion

In conclusion, most stability approaches revealed that high performing stable genotypes were L240 for seed yield and Sakha 53, L110 and L235 for seed oil content under divergent environments. Hence, these four stable sunflower genotypes could be behaved as good breeding materials stock for sunflower improvement.

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